cases were interviewed concerning their educational, occupational, marital, parenthood, smoking, and social insurance status. Data were analyzed in relation with gender, age at diagnosis, stage of disease, and follow up duration.
Results: All 65 cases (M/F: 50/15) were >18 years of age (median 23, 18−40) at the time of study. Median age at diagnosis was 9 years (2−19). Median follow up time was 16 years (4−26). 12/65 cases (19%) had stage I; 29 (46%), II; 18 (29%), III; and 4 (6%), IV disease. 38/65 (59%) cases had a profession, 27/65 (41%) did not. 34/65 (52%) cases were working at a job. 58% of females didn't work compared to 31% of the male patients didn't ($p = 0.08$). 36/65 (56%) patients were non-smokers, 8 (12%) ex-smokers, and 21 (32%) smokers (3/15 females, 18/50 males; $p = 0.06$). 3 females and 11 males (14/65; 21.5%) were married; 6/14 (43%) (M/F = 3/3) had offsprings. 54/65 (83%) cases had any kind of social insurance; all females had social insurance compared to 74% of the males ($p = 0.02$). There was no significant difference in employment, smoking, marital status, and having social insurance between the cases according to age at diagnosis (<10 or >10 years), and follow up time (<15 or >15 years), and having university education; also between gender and marital status. There was no significant difference between early (I-II) or advanced stages (III-IV) and having higher education, employment, smoking, marital status or having social insurance ($p > 0.05$).
Conclusions: That educational status of our patients was not inferior than the normal population is satisfying. All patients should be advised not to smoke. In this series HD survivors did not have important disadvantages in social life. Patients should be encouraged to continue education, work, marry and so have a better quality of life.

Breast Cancer

Oral presentations (Mon, 24 Sep, 10.45−12.15)
Breast cancer – preclinical

2000 ORAL

Quantification of free circulating tumor DNA in plasma as a diagnostic marker for breast cancer

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Background: Breast cancer is the leading cause of cancer death in women worldwide. There is a need to develop new approaches that may facilitate earlier diagnosis and more effective treatments. Increased knowledge of molecular pathogenesis of breast cancer offers a basis for the use of molecular markers in biologic fluids for early detection, as well as identification of higher-risk individuals.
The purpose of our study was to determine whether the amounts of circulating DNA could discriminate between breast cancer patients and healthy individuals by using real-time PCR based DNA quantification methodology and determine the kinetics of circulating plasma DNA in surgically treated patients.
Material and Methods: Our standard protocol for quantification of cell free plasma DNA involved 175 consecutive patients with breast cancer and 80 healthy controls. The quantification was perfomed by real-time PCR amplification of the human telomerase reverse transcriptase gene (hTERT).
Results: We found increased levels of circulating DNA in breast cancer patients compared to control individuals (105.2 vs 77.06 ng/ml, $p < 0.001$). We also found statistically significant differences in circulating DNA amounts in patients before and after breast surgery (105.2 vs 59.0 ng/ml, $p = 0.001$). Increased plasma cell free DNA concentration was a strong risk factor for breast cancer, conferring an increased risk for the development of this disease (OR, 12.32; 95% CI, 2.09−52.28; $p < 0.001$). High levels of plasma DNA were also correlated with a decrease in patients' overall survival ($p = 0.043$). There were no association between clinicopathological parameters and concentrations of cell free circulating DNA.
Conclusions: Diagnostic assays based on blood sample analysis are becoming an area of study with growing interest, mainly because of the simplicity of sampling and the future potential of automation of the technical methods for clinical applicability. In conclusion, cell-free DNA is significantly increased in plasma of breast cancer patients, which is associated with an increased risk for the development of this disease and decrease of patient's survival. Therefore, quantification of circulating DNA by real-time PCR may be a good and simple tool for early detection of breast cancer with potential to clinical applicability together with other current methods used for monitoring the disease.

Plasma DNA concentration as a risk factor for breast cancer

		Patients (n = 175) N (%)	Controls (n = 80) N (%)	OR*	95% CI*	P*
High [fcDNA]	Yes	99 (56.6)	73 (91.2)	8.01	3.49−18.38	<0.001
	No	76 (43.4)	7 (8.8)			
Very high [fcDNA]	Yes	133 (76.0)	78 (97.5)	12.32	2.90−52.28	<0.001
	No	42 (24.0)	2 (2.5)			

*For High [fcDNA], $P < 0.001$, OR = 6.48 and 95% CI: 2.76−15.20; For Very high [fcDNA], $P = 0.003$, OR = 9.30 and 95% CI: 2.14−40.35, using logistic regression analysis adjusted by age.

2001 ORAL

Circulating tumor cells (CTCs) in peripheral blood of primary breast cancer patients – Results from the translational research program of the German SUCCESS-Trial

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Background: In metastatic breast cancer, the presence of CTCs has been shown to be associated with bad prognosis and their persistence predicted lack of treatment efficacy. Only limited data, however, has been published in the adjuvant setting. We evaluated the role of CTCs in peripheral blood at primary diagnosis and during adjuvant chemotherapy, endocrine and bisphosphonate treatment within the SUCCESS-trial (n = 3658 pts.)
Methods: We analyzed methods of 23 ml of peripheral blood from 1767 N+ and high risk N− primary breast cancer patients before systemic treatment. 852 of these patients have undergone follow-up blood sampling after completion of chemotherapy. The presence of CTCs was assessed with the CellSearch System (Veridex, Warren, USA). Briefly, after immunomagnetic enrichment with an anti-Epcam-antibody, cells were labeled with anticytokeratin (8, 18, 19) and anti-CD45 antibodies to distinguish epithelial cells and leukocytes.
Results: 10% of pts with a blood sampling before systemic treatment (n = 170) showed >1CTC before the start of systemic treatment (mean 13, range 2–827). While we found 2 CTCs in 5% of patients, 3% had 3−5 CTCs and 1% 6−10 and >10 CTCs each. The presence of CTCs did not correlate with tumor size ($p = 0.07$), grading ($p = 0.30$), hormonal status ($p = 0.54$) or Her2-Status of the primary tumor ($p = 0.26$). However, we observed a significant correlation with the presence of lymph node metastases ($p = 0.015$). None of 24 healthy individuals showed more than 1 CTC.
Among those 852 patients with follow-up blood sampling after the completion of cytostatic treatment, 11% were CTC positive before starting systemic treatment (mean 7, range 2–166), while 7% of patients presented with >1CTC after completion of chemotherapy (mean 6, range 2−84). Of those, initially CTC positive, 10% remained positive (n = 9) and 90% had a negative CTC test after chemotherapy (n = 82). Of those initially CTC negative, 93% remained negative (n = 711), whereas 7% returned with a positive CTC test (n = 50) ($p = 0.24$).
Conclusions: The SUCCESS-trial is the first trial to perform the detection of CTCs in a large number of primary breast cancer patients with this highly standardized and easily applicable approach. If the observed persistence of CTCs after completion of adjuvant chemotherapy is prognostically relevant, will have be further evaluated with longer follow-up.

2002 ORAL

Low SIAH2 expression in breast cancer is associated with resistance to endocrine therapy

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Background: Low expression levels of Seven-in-Absentia Homolog 2 (SIAH2) were observed in our microarray and quantitative real-time PCR