10.3 ($\pm$15.4) vs. 3.5 ($\pm$6.1), p = 0.018, respectively. These mean values were neither correlated with Gleason score, nor PSA, nor risk groups. Mean number of pathological voxels for patients with a tumor $\geqslant$T2b−c was: 6.31 ($\pm$7.43) and 4.09 ($\pm$7.64) if $\leqslant$T2a (p = 0.03). The mean number of pathological voxels was significantly correlated with increased PSA: (OR: 1.80 [95% CI 1.016–1.149], p = 0.013). No correlation was found with the Gleason score. Patients with intermediary risk have a significantly higher number of pathological voxels than in the low risk group (OR: 1.075 [95% CI 1.009–1.145], p = 0.025). A similar result was found for high risk pts with respect to the intermediary group.

Conclusion: At 3 T, biomarkers expressing the relative Choline content and number of pathological voxels were powerful parameters for the localisation of PCa and could be helpful for determining the prognosis more accurately.

PP38

Proteomic analysis of plasma from BRCA1/BRCA2 mutation carriers as modifier risk factor of breast cancer

A.B. Custodio, P. Pérez-Segura, J.J. Zamorano, A.J. López-Farré, E. Olivera, J. Puente, E. Díaz-Rubio. *Hospital Universitario Clínico San Carlos, Spain*

Background: BRCA1 and BRCA2 mutations were estimated to cause cumulative lifetime risks of breast cancer of 70% by 70 years. However, there is a marked variation of phenotypic expression among BRCA mutation carriers. Identification of markers that can be used to refine estimates of a woman's individual cancer risk appears to be warranted in order to individualizing prevention strategies. The aim of this study was to analyze using proteomics modifications in the plasma protein map from BRCA1/2 mutation carriers with respect to a control group, as well as potential differences between cancer patients (CP) and cancer-free carriers (CFC). Preliminary results were presented at ICACT 2009 (abstract 237).

Materials and Methods: We use two-dimensional gel electrophoresis and mass spectrometry to analyze plasma levels of the following proteins in 40 female BRCA mutation carriers (22 BRCA1 − 10 CP and 12 CFC − and 18 BRCA2 − 12 CP and 6 CFCs): fibrinogen (fgg), haptoglobine (hap), serotransferin (ser), convertase (con), alpha1-antitrypsin (AAT), apolipoprotein A-I (APO AI) and A-IV (APO AIV) and C-reactive protein (PCR). The control group included 10 age-matched non-carriers without personal or family history of cancer. We also use the PD-QUEST software to determine the total protein count for each group.

Results: AAT 4 (p = 0.038), 5 (p = 0.023) and 6 (p = 0.037), hap 4 (p = 0.023) and APO AI 2 (p = 0.038) and 5 (p = 0.013) were increased in plasma from BRCA2 mutation carriers with respect to BRCA1 ones. BRCA1 CFC showed increased levels of AAT 6 (p = 0.058) and APO AIV (p = 0.004) when compared to BRCA1 CP. No significant differences were found in the protein map between BRCA2 CP and CFC. BRCA2 CP when compared with BRCA1 showed increased levels of AAT 6 (p = 0.023), APO AI 2 (p = 0.038) and 5 (p = 0.019) and APO AIV (p = 0.010) and decreased levels of con 3 (p = 0.023). Fgg 2 (p = 0.001) and 3 (p = 0.001), ser 4 (p = 0.001) and con 1 (p = 0.041), 2 (p = 0.006), 3 (p = 0.001), 4 (p = 0.001) and 5 (p = 0.001) were found significantly increased in plasma from CFC with respect to the control group. No significant differences were found in the total protein count among groups using PD-QUEST.

Conclusion: BRCA2 mutation carriers showed a favorable plasma protein map when compared with BRCA1 ones, as well as observed in control group with respect to BRCA1/2 carriers. Moreover, BRCA1 CFC had better prognosis proteomic profile than BRCA1 CP. The confirmation of these results in a larger cohort is required before proteomic analysis could be used to guide prevention strategies among BRCA mutation carriers.

PP17

The predictive value of HLA Class I tumor cell expression and tumor infiltration by regulatory T cells for chemotherapy in patients with early breast cancer

E. de Kruijf, J. van Nes, A. Sajet, H. Putter, S. Osanto, F. Speetjens, V. Smit, G.J. Liefers, C. van de Velde, P. Kuppen. *Leiden University Medical Center, the Netherlands*

Background: Additional prognostic and predictive factors may direct tailored treatment in early breast cancer and thus decrease morbidity and mortality rates. We hypothesized that T cell immune interactions affect tumor development and therefore clinical outcome. Therefore, we examined the clinical impact of human leukocyte antigen (HLA) class I tumor cell expression and regulatory T cell (Treg) infiltration in breast cancer.

Materials and Methods: Our study population (n = 677) consisted of all early breast cancer patients primarily treated with surgery in our center between 1985 and 1994. Formalin-fixed paraffin-embedded tumor tissue was used for immunohistochemical staining with HCA2 and HC10 (recognizing HLA Class I) and Foxp3 (recognizing Treg) antibodies. HLA

class I expression was evaluated by combining results from HCA2 and HC10 antibodies and was classified into three groups: loss, downregulation and expression. Treg infiltration was defined as complete absence or presence of Treg.

Results: Remarkably, only in patients treated with chemotherapy after surgery, both presence of Treg (p = 0.01; Hazard Ratio (HR): 2.04) and expression of HLA class I (p = 0.002; downregulation HR: 2.11; loss HR: 3.34) resulted in less relapses over time, independently of other clinicopathological parameters. Treg and HLA class I were not of influence on outcome in patients who did not receive chemotherapy. An interaction between chemotherapy and HLA class I (p < 0.001) and Treg (p < 0.001) was found in cox regression analysis.

Conclusion: We showed that HLA class I and Treg both affect prognosis, exclusively in chemotherapy-treated patients. In mouse studies it has been shown that chemotherapy can selectively eliminate Treg, therefore possibly enabling Cytotoxic T-lymphocytes to kill tumor cells that have retained HLA class I expression. Therefore, we conclude that HLA class I and Treg could be applied in response prediction to chemotherapy in early breast cancer patients.

PP28

Prediction of response to neo-adjuvant radiotherapy in patients with locally advanced rectal cancer by means of sequential 18F-FDG-PET

M. De Ridder, H. Everaert, A. Horens, B. Engels, C. Vanhove, A. Sermeus, D. Debruyne, D. Verellen, D. Urbain, G. Storme. *UZ Brussel, Belgium*

Background: The current approach to curative treatment of locally advanced rectal cancer is comprised of surgery combined with neo-adjuvant (chemo)radiotherapy. Radiosensitivity of rectal cancer however is variable. Morphological imaging techniques are performing poorly in assessing the response because of their inability to differentiate residual neoplastic from scar tissue. The aim of this study was to investigate the potential of sequential 18F-FDG-PET(CT) in assessing the response of rectal cancer to neo-adjuvant radiotherapy (RT), and to determine which parameter(s) can be used as useful metabolic response indice(s).

Materials and Methods: Patients (pts) were treated by Tomotherapy: dose of 46 Gy to the presacral space and integrated boost to 55.2 Gy on the tumor, if circumferential resection margin was <2 mm on magnetic resonance imaging. Pts underwent total mesorectal excision within 6 w after completion of RT, and tumor regression was graded histologically.

18F-FDG-PET or PET/CT scans were acquired prior to and in the 5 w after the end of RT. Tumoral uptake of 18F-FDG was assessed semi-quantitatively using standardized uptake values (SUV). The percentage difference (Δ) between pre- and post-RT scans in SUVmax, SUVmean (average SUV of tumoral pixels with SUV $\geqslant$2.5) metabolic volume (MV, sum of tumor pixels with SUV $\geqslant$2.5) and the total glycolytic volume (tGV, MV × SUVmean) was investigated as possible metabolic response indices.

Results: 45 consecutive pts (34 male and 11 female; age 65.4$\pm$12.5) with histologically confirmed rectal adenocarcinoma (cT3/T4) were enrolled. Following neo-adjuvant RT, of the 45 pts 20 (44.4%) were classified as responders, while the remaining 25 (55.6%) were non-responders. Intense 18F-FDG uptake was seen in all tumors prior to neo-adjuvant RT: average SUVmax 12.9$\pm$6.0 (no significant different between responders and non-responders). When classifying pts according to histology significant differences in average ΔSUVmax (55.8% vs 37.4% decline, p = 0.023) and ΔSUVmean (40.1% vs 21.0%, p = 0.001) between responders and non-responders respectively were observed. For MV and tGV decreases were more prominent in responders (72.9% vs 62.7% and 80.2% vs 68.1%, respectively), but not significantly different from non-responders.

Conclusion: Sequential FDG-PET(CT) is a useful method to evaluate response of rectal cancer to neo-adjuvant RT. ΔSUVmax and ΔSUVmean are parameters that can be used as indices of metabolic response.

PP20

Clinical significance of the epidermal growth factor receptors (EGFR and HER-2) overexpression in esophageal squamous cell cancer

V. Delektorskaya, G. Chemeris, P. Kononec, A. Grigorchuk. *Russian Cancer Research Centre RAMS, Russian Federation*

Background: The present study was aimed to assess EGFR and HER-2 expression in esophageal squamous cell carcinoma (ESCC) and to correlate the results with clinic-pathological findings and prognosis.

Materials and Methods: The immunohistochemical staining of EGFR and HER-2 receptors were retrospectively investigated in biopsy specimens from 31 patients with T (2−3), N-any, and M-0 ESCC. The results were classified according to the Herceptest criteria (Dako): negative (0/1+) and positive (2+/3+).

Results: The EGFR expression was negative in 7/31 (22.6%) and positive in 24/31 (77.4%), of which 12 (38.7%) were 2+ and 12 (38.7%) were 3+.