metastatic sites was 37.8% lung, 11.8% lymph nodes, 11.8% CNS and 9.9% bone. The frequency of Krasmut subtypes were: G12C 44%, G12V 20%, G12A 16%, G12D 12%, G13D 4%, G13V 4%. EGFR mutation was present in 1 patient (4%). BRCA expression levels were 36% low, 4% intermediate, 0% high and 32% insufficient sample. RAP80 expression levels were 4% low, 24% intermediate, 12% high and 32% insufficient sample. For pts treated in first line with platinum based chemotherapy (21/25) the response rate (RR) was: Complete response 4%, Partial Response 12%, Stable Disease 9.5% and Progressive Disease 47.5%. Time to progression (TTP) was 6.6 m and Overall Survival (OS) was 12.5m. TTP and OS according to Krasmut were: G12C 10.1m/15.4m, G12V 5m/14.1m, G12A 2.3m/8.5m, G12D 9.1m/9.6m, G13D 3m/8.3m, G13V 3.2m/6.9m. Pts received a median of 2 lines of treatment (range 1−5) Seven pts (33.3%) were included in specific targeted studies for Krasmut pts beyond the second line. No differences were found in RR or TTP according to PS, gender smoking history, Krasmut subtype and BRCA1 or RAP80 levels. No differences were found in OS according to gender, smoking history, Krasmut subtype and BRCA1 or RAP80 levels except for PS ($p = 0.0033$).

Conclusions: Krasmut were more frequent in male, smokers and former smokers and pts with adenocarcinoma. PS was associated with differences in OS. No other variables were associated with differences in RR, TTP or OS. The small sample size could explain the lack of differences.

1435 POSTER

Prostate Cancer Prognosis by Real-time PCR Analysis of PITX2 Methylation

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Background: PITX2 is a bicoid-related transcription factor induced by the Wnt pathway and required for effective cell-type-specific proliferation during development. The potential of PITX2 gene promoter methylation and/or RNA expression for outcome prediction in breast, prostate and colorectal cancer patients has been reported. Accurate prognosis and selection of appropriate treatment for breast, prostate and colorectal cancer patients is a significant clinical need. Here we present the development of a methylation-specific *PITX2* real-time PCR assay based on formalin-fixed, paraffin-embedded (FFPE) tissue for prostate cancer prognosis.

Material and Methods: *PITX2* methylation status was assessed in FFPE tissue samples from 483 prostate cancers patients treated with radical prostatectomy (RP). Associations between *PITX2* methylation and biochemical recurrence (BCR) were assessed using log-rank test and Cox regression, controlling for prostate cancer features.

Results: In multivariate analysis, the prognostic value of *PITX2* methylation in prostate cancer was confirmed with a newly developed real-time PCR assay. Prostate cancer patients with a high methylation status as assessed with the new assay were at significantly higher risk for BCR compared to patients with low methylation status (HR = 2.7; 95% CI=1.83−3.98; p-value: <0.001). Concordance between the real-time PCR assay and the former Affymetrix GeneChip™ assay for PITX2 was demonstrated, with a correlation coefficient of 0.93 (p-value: <0.001).

Conclusion: This newly developed *PITX2* methylation real-time PCR assay has the potential to facilitate the management of prostate cancer patients by significantly adding to the prognostic information provided by standard clinicopathological analyses and improving the stratification of prostate cancer patients that have undergone radical prostatectomy into high- and low-risk for BCR. This tool may be of particular benefit for patients with non-aggressive prostate cancer if the prognostic information could be assessed at the time of prostate biopsy using biopsy tissue. Prostate cancer patients might then be stratified into those who would benefit from active disease surveillance and those who should undergo prostatectomy.

1436 POSTER

Spontaneous Bacterial Peritonitis in Cancer Has Atypical Clinical Presentation and Biological Markers

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Background: Spontaneous bacterial peritonitis (SBP) causes an inflammatory reaction, leading to an increase of polymorphonuclear neutrophil counts (PMN) in the ascitic fluid (AF). The threshold used to define a SBP is >250 PMN/mm^3. The peritoneal response linked to the presence of cancer can alter the clinical signs and confound the interpretation of biological markers in AF. The objective of this study was to analyze the clinical presentation and the biological markers of SBP in the context of cancer.

Methods: This was a retrospective study conducted in the emergency unit of a cancer hospital. The records of patients with SBP over a 7 years period were analyzed. The diagnosis of SBP was made in case of positive AF culture with a pathogenic microorganism (Infectious group IG n = 30). In a first instance, AF (n = 36) growing with skin flora microorganisms (coagulase negative staphylococci, viridans streptococci) were analysed apartEach patient was his own control by using data collected from a paracentesis prior to contracting SBP. This was possible for 14 patients with a pathogenic isolate and for 23 patients with skin flora organism. The rest of the control group included AF analyses without SBP (n = 26).

Results: There were no significant differences between the clinical and biological data of patients with skin flora organism positive AF and those of the control group. Before further analysis, these two groups were merged into one group, non infected group (NIG n = 99). The body temperature for 7 over 30 patients in the IG group was >38ºC compared to 3 over 99 patient in the NIG group ($p = 0.01$, Fisher's test). In the IG group, 23 over 30 had a temperature <38ºC. Diarrhoea was observed in 4 out of 30 IG patients versus 3 out of 99 NIG patients ($p = 0.05$) (Fisher'stest). Inflammatory parameters were higher in the IG vs. NIG group, respectively for CRP (mg/l): 173±114 vs. 97±97 ($p = 0.002$), and for PMN (cells/dl): 12.1±8.1 vs. 7.9±7.2 ($p = 0.01$). We observed more than one microorganism in the ascitic fluid of 11 out of 30 patients. PMN counts in ascitic fluid were statistically higher in IG than in NIG (1895±3900 vs. 5±128 (cells/mm^3), ($p = 0.001$)). It is important to point out that in 11 of the 21 IG patients; PNN was <250/mm^3.

Conclusion: Spontaneous ascitic infections have few clinical signs. Only 1/3 of the patients in our study presented with fever while half had a PNN level in the ascitic fluid less than the infection threshold. The only parameters favoring the presence of infection were elevated CRP and PNN in the case of SBP.

1437 POSTER

Gene Expression Signature TOPFOX Reflecting Chromosomal Instability Refines Prediction of Prognosis in Grade 2 Breast Cancer

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Purpose: To assess the ability of genes selected from those reflecting chromosomal instability to identify good and poor prognostic subsets of Grade 2 breast carcinomas.

Methods: We selected genes for splitting grade 2 tumours into low and high grade type groups by using public databases. Patients were diagnosed between 1999–2002 at the Budai MÁV Hospital. 187 formalin-fixed, paraffin-embedded breast cancer samples were included in the qPCR-based measurement of expression of AURKA, FOXM1, TOP2A and TPX2 genes. The expression of the genes were correlated to recurrence-free survival (RFS) and immunophenotypical characterization of tumours. 1509 samples were in silico analyzed for further validation of the selected genes.

Results: Grade 1 and 3 groups were used as training set for the selected genes. The 4-gene signature was able to split grade 2 carcinomas (n = 62) into a good and a poor prognosis group (RFS: 83.8±4.9 months and 69.4±8.2 months, respectively, $p = 0.016$). Furthermore, independent of grade, the identified signature containing only TOP2A and FOXM1 (TOPFOX) was able to separate ER+ tumours in an efficient manner ($p = 0.009$), which is further supported by validation in a dataset containing 1509 patients (p = 8.1E-8).

Conclusions: The selected genes with the appropriately selected control genes are able to separate the different prognostic subgroups independently from histological grade. Our results show the feasibility of the selection of a minimal set of genes for the development of a clinically applicable prognostic test.

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