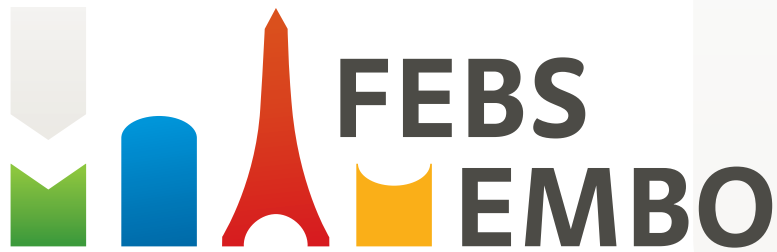

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according to the nonparametric Wilcoxon–Mann–Whitney test ($p < 0.05$) with Benjamini and Hochberg adjustment for p-values. Over one third of these compounds were identified only in the malignant ascites. The major significant differences between the malignant and control ascites were observed for fatty acids and their derivatives, which are known to be among the key components of intercellular signaling.

In summary this study extended our knowledge of the protein and metabolomic composition of the ovarian cancer ascites and revealed its specific features which were associated with the function of the ascitic fluid as a medium of interaction between the malignant cells and their environment.

Keywords: Ovarian cancer ascites, Proteomics, Metabolomics.

TUE-199
Proteomic and protein glycosylation changes associated with TGFBR2 deficiency in MSI colorectal cancer

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Members of the transforming growth factor (TGF)-signaling pathway are common targets for mutation in colon cancers. Deregulation of this pathway appears to play an important role in colon carcinogenesis by affecting TGF-mediated growth inhibition, apoptosis, and differentiation as well as other TGF-regulated processes. In particular, inactivating mutations of the TGF-ß-receptor type II (TGFBR2) occur in more than 90% of microsatellite unstable (MSI) colon cancers. In order to systematically analyze TGFBR2-deficiency-associated changes of the biochemical phenotype of MSI colon carcinoma cells we used the TGFBR2-deficient MSI colon carcinoma cell line HCT116 as a model system. Stable clones conferring doxycycline (dox)-inducible expression of a single copy wild type *TGFBR2* transgene were generated by recombinase-mediated cassette exchange (RCME). By applying a click-chemistry approach with azido-derivatized amino-acids or monosaccharides we specifically labeled newly synthesized proteins or post-translational glycan modifications after dox-induction as well as in uninduced cells and clicked a biotin residue to the metabolically labeled proteins or oligosaccharide chains. Finally we extracted the labeled proteins by streptavidine-coupled magnetic beads. Identification of the bound proteins was achieved by nano-HPLC-coupled Orbitrap mass spectrometry. A total of 76 proteins was found to be expressed in a TGFBR2-dependent manner: 40 individual proteins were only expressed in TGFBR2-deficient cells and 36 individual proteins were exclusively found in TGFBR2-proficient cells. For 19 proteins altered sialylation and for 21 proteins altered fucosylation was found.

Altogether this study, based on a combination of three technologies, i.e. RCME, click-chemistry and mass spectrometry, provides a versatile platform to analyze proteomic as well as posttranslational modifications caused by MSI-relevant target genes like TGFBR2. On the one hand this approach can help to systematically puzzle out the consequences of tumor-specific mutations in a major signalling pathway as exemplified by the TFGBR2 tumor suppressor, on the other hand this approach facilitates the identification of tumor markers that could be used for diagnostic and therapeutic applications.

Keywords: colon cancer, microsatellite instability, TGF-beta signalling.

TUE-201
Quantitative expression analysis of the apoptotic gene BCL2L12 in breast cancer: association with clinical and molecular prognostic parameters

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Introduction: Apoptosis is a highly orchestrated, genetically regulated form of cell death, the impairment of which is crucial in breast cancer (BC) development and progression. *BCL2L12*, a member of the *BCL2* family of apoptosis-related genes, has been studied in various malignancies, revealing its potential role as a tumor biomarker. It has been recently found that *BCL2L12* is subjected to alternative splicing, resulting in the generation of 13 alternatively spliced variants. The aim of this study was the quantification of *BCL2L12* splice variants 1 and 2 (v.1 and v.2) expression at the mRNA level and the assessment of their biomarker potential in BC.

Methods: Total RNA was extracted from 40 pairs of BC and normal tissues. Thereafter, RNA was reverse transcribed into first-strand cDNA, which in turn was used as template in a SYBR Green based Real-Time PCR assay. Relative quantification analysis was conducted using the comparative C_T (2^{-ddC_T}) method, and the associations of *BCL2L12* variants expression with various clinopathological parameters, were evaluated by statistical analysis.

Results: *BCL2L12* v.1 mRNA levels were found to be significantly ($p = 0.003$) higher in malignant compared to their matched non-cancerous breast tissues. Moreover, *BCL2L12* v.1 demonstrated increased expression in premenopausal women ($p = 0.026$) as well as in those with early TNM stage tumors ($p = 0.039$). Interestingly, significant *BCL2L12* v.1 upregulation ($p = 0.044$) was observed in triple negative BC. Regarding *BCL2L12* v.2, a negative correlation with patients' age was found (($r_s = -0.376$; $p = 0.017$), whereas increased *BCL2L12* v.2 expression levels were associated with advanced tumor grade ($p = 0.022$) and ER-negativity ($p = 0.01$).

Conclusion: Our preliminary results indicate a possible involvement of *BCL2L12* v.1 and v.2 in BC progression and suggest their potential as biomarker in this malignancy.

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Keywords: Apoptosis, Breast Cancer.

TUE-203
Redox role of STAT3 in cellular survival during oxidative stress

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Signal Transducer and Activator of Transcription 3 (STAT3) is a transcription factor that is essential for embryogenesis and is involved in the development and maintenance of several tissues,

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