polymorphisms in *XRCC1* and *ERCC2* leading to reduced DNA repair capacity may be of benefit in cancer chemotherapy and may prolong patient's survival.

Methods: Overall survival (OS) was evaluated in 303 Caucasians with primary lung cancer who received anticancer treatment that include first-line chemotherapy using the statistical methods of Kaplan–Meier curves and Cox proportional hazards model with hazard ratios (HRs). DNA isolated from peripheral blood was genotyped for *XRCC1* (*Arg*^{280} *His* and *Arg*^{399}*Gln*) and *ERCC2* (*Asp*^{312}*Asn*) by fluorescence-based melting curve (LightCycler) analysis and for *XRCC1* (*Arg*^{194}*Trp*) and *ERCC2* (*Lys*^{751}*Gln*) by PCR-RFLP.

Results: Among all lung cancer cases, only small cell lung cancer (SCLC) patients carrying the *XRCC1* ^{399}*Arg* allele had a reduced overall survival (HR 2.13, 95%CI 0.92–4.92) compared to the homozygous ^{399}*Gln* genotype. When compared to *XRCC1 Arg*^{280}*His* heterozygotes, ^{280}*Arg* homozygotes showed increased survival being significant only for SCLC patients (HR 0.31, CI 0.14–0.69). A significantly increased HR was found for *ERCC2* ^{751}*Gln* homozygous carriers (HR 3.05, CI 1.20–7.73) for SCLC but not for non-SCLC.

Conclusion: The survival of lung cancer patients receiving chemotherapy seems to be modified by certain repair gene polymorphisms notably in the subgroup of SCLC patients.

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P53. IN VITRO HISTOCULTURE OF COLORECTAL CARCINOMAS AS A MODEL SYSTEM FOR THE ASSESSMENT OF THERAPEUTIC APPROACHES

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Introduction: A histoculture experimental system of colon cancer was studied to evaluate the reliability and utility of new biological approaches. The three-dimensional growth pattern of the tissue, preserved by this technique is essential for observing the oncogenic properties, differentiated functions and cellular heterogeneity of the tumors. Colon cancer as one of the most common neoplastic diseases worldwide was chosen as a model for remedial testing with viruses with enhanced oncoselective activities, as parvovirus H-1. Paralleled in vitro testing of sensitivity to the oncolytic H-1 parvovirus, using experimental systems of both cell lines and organotipic cultures of colon cancer, will support a better prediction of the in vivo response of patient with this type of cancer.

Methods: Samples from 30 patients with primary untreated colorectal carcinomas were set in histoculture. This technique has been reported as a reliable system, in which tumours can be cultivated with high efficiency by the transfer of human tumour samples to collagen sponges. H-1 virus in the treated tissue samples and the colon cancer cell lines was detected by IHC and RT-PCR. Immunofluorescence was used to characterize the protein patterns of cellular E-cadherin and viral proteins. Tissue growth inhibition was determined by calculating glucose consumption rates.

Results: The analyses revealed significant differences in the response of the five different human colon cancer cell lines to H-1 wt parvovirus infectivity and killing abilities. Increased permissiveness of the colon cancer cells to virus killing was correlated to the lower expression pattern of E-cadherin. Higher virus toxicity was measured in colon cancer cells, over-transformed with SV40 large T-antigen. Growth inhibition assays performed in histocultures showed slight reduction on tissue viability after H-1 wt infection, compared to the stronger effects after 5-FU treatment. RT-PCR and IHC revealed the presence of viral transcripts and viral proteins in the samples, which showed reduced tissue metabolism after infection.

Conclusion: All examined colon cancer cell lines showed a heterogenic response to H-1 parvovirus infectivity. The genetic background of the cell lines showed that cells characterized as aneuploid exert better permissivness to virus infectivity. Straightforward correlation was observed between the E-cadherin expression pattern and sensitivity to virus infection. The weak effects observed after tissue treatment with H-1 wt parvovirus, are due to the intrinsic cellular heterogeneity of the tumor tissues and confirm the higher virus oncotropism, with selective killing of the tumor cells in the original samples, but not their normal counterparts.

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P54. EXPRESSION ALTERATIONS OF MOLECULAR MARKERS IN DIFFERENT TYPES OF NSCLC AS A SIGNIFICANT PROGNOSTIC FACTOR

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Background: The genetic alterations and expression rates of the molecular markers, associated with prognosis of patients with lung cancer (LC) were investigated. Biomarker expression levels were compared in groups of patients with different histological types and survival rates.

Methods: Tumor samples from 54 patients with NSCLC were analyzed in a retrospective study of paraffin-embedded tissues by immunohistochemistry and in fresh frozen biopsies by RT-PCR. The expression of MMP2, MMP9, b-catenin, E-cadherin, CAV1, Ki67 were evaluated.

Results: Normal membrane-bound E-cadherin expression was absent in 80% of the squamous cell LC, 69.2% adenocarcinomas, 85.7% bronchoalveolar carcinomas The normal membrane bound form of b-catenin was absent almost in all bronchoalveolar carcinomas, but it preserved partly in 40% cases of squamous cell LC and in 53.8% of adenocarcinomas. The MMP2 expression was common for squamous cell and for bronchoalveolar cancer (60–71%), but was absent in SCLC. There was no correlation between the frequency and intensity of expression of adhesion molecules and proliferation index. The expression of caveolin and RALGDS was also compared with clinical parameters. The prognostic significance of each marker and their complexes was analysed.

Conclusions: Abnormalities in adhesion molecules is common for different lung carcinomas. Frequency and intensity of expression varies depending on the histological type of NSCLC. Identification of tumor immunophenotype makes possible to obtain more data about metastasis potential, malignancy rate and prognosis. This molecular markers panel can be used for early detection of LC recurring and metastasis.

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P55. IN SITU MOLECULAR ASSESSMENT OF CD8+ T CELL REACTIVITY IN NSCLC

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Background: While in cancer from colon and ovary number and reactivity of tumor infiltrating lymphocytes (TILs) were associated with survival, in NSCLC, the clinical significance of TILs is unknown. While TILs demonstrated antigen specific Interferon (IFN)-γ secretion and cytotoxicity in vitro, their in situ activation status remains difficult to determine. Here, we examine molecular assessment of CD8+ T cell reactivity in NSCLC.
Methods: We determined CD8+ T cell counts in 19 patients with NSCLC by immunohisto-chemistry and assessed T-cell immune reactivity by measuring mRNA IFN-γ levels by quantitative RT-PCR (TaqMan) from corresponding tissue. CD8+ T cells were classified into two groups: Intra-tumoral (distributed in cancer cell nests and stroma) and peri-tumoral (presented along the invasive margin). Five hpf were evaluated per each localization (IT and PT, respectively). Distribution of CD8+ T cells was semi-quantitatively classified into: 0-none or mild; I-moderate; II-severe. The relationship between the median CD8+ T cell density/hpf and the CD8-normalized IFN-γ mRNA expression was tested (Spearman's correlation).
Results: Semi-quantitative analysis revealed significantly higher CD8+ T cell counts within the tumor compared to the invasive margin ($p < 0.001$). However, immune activation status of TILs represented as IFN-γ/CD8 ratio was higher in the peri-tumoral than in the intra-tumoral compartments ($p = .022$).
Conclusion: In human NSCLC, IFN-γ reactivity of CD8+ T cells is mostly attributed to the tumor–host interface and indicates an inadequate activation of TILs within the tumor. This methodology can be applied to a variety of experimental trials if tumor tissue is available.

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P56. UPREGULATION OF COX-2 EXPRESSION OCCURS ALREADY IN GASTROESOPHAGEAL REFLUX DISEASE BUT IS FURTHER INCREASED IN BARRETT'S ESOPHAGUS AND BARRETT'S CANCER

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Background: Cyclooxygenase-2 (COX-2) mRNA expression is known to be progressively increased in the metaplasia–dysplasia–adenocarcinoma (MDA) sequence of Barrett's cancer (BC) development. Much less however, is known about COX-2 mRNA expression in patients with gastroesophageal reflux disease (GERD).
Methods: Endoscopic biopsies from 3 patient groups were analyzed: 43 patients undergoing evaluation for GERD (20 GERD positive/23 GERD negative) by 24-h pH-monitoring, 20 patients with Barrett's esophagus (BE) without dysplasia and 47 with BC. COX-2 mRNA expression was determined by quantitative real-time RT-PCR (TaqMan™) assays. The Demeester composite score ($DS > 14.72$) was used to match COX-2 mRNA expression levels with the degree of acid exposure.
Results: Median COX-2 mRNA expression was significantly upregulated in Barrett's metaplastic epithelium compared to matched normal squamous epithelium (NE) in the BE ($p = 0.03$) and BC group ($p = 0.001$). COX-2 mRNA expression levels in NE did not differ significantly between the 3 study groups however, within the group of patients evaluated for GERD, specimens obtained from patients with a mean Deemester score >14.72 showed significantly upregulated COX-2 mRNA levels in the distal acid-exposed esophagus ($p = 0.01$).
Conclusion: Our findings suggest that the induction of increased COX-2 mRNA expression occurs already in GERD without the presence of Barrett's metaplasia. A field effect as shown for other genes could not be detected for COX-2 expression in squamous epithelium in GERD positive, BE or BC patient groups. Chemoprevention strategies using selective or non-selective COX-2 inhibitors might be useful in patients with GERD to potentially prevent the development of Barrett's metaplasia.

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P57. ASSOCIATION OF CYCLOOXYGENASE-2 EXPRESSION WITH DEVELOPMENT AND PROGRESSION OF BARRETT'S METAPLASIA–DYSPLASIA–CARCINOMA SEQUENCE AND THE ENVIRONMENTAL INFLAMMATORY REACTION

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Background: Epidemiological data assume a reduction of risk for developing an adenocarcinoma of the esophagus for individuals taking non-steroidal anti-inflammatory drugs. One of the inhibited enzymes, cyclooxygenase-2, is supposed to be involved in the pathogenesis of Barrett's cancer. We examined a possible association between COX-2 protein expression and the progression of Barrett's sequence and the type and degree of the environmental inflammatory reaction.
Methods: Squamous epithelium, metaplastic, low-grade and high-grade dysplastic lesions and tumor tissue of 49 resection specimens from patients with Barrett's adenocarcinoma were analyzed. Immunohistochemical staining was performed with a