BFB model for amplification in breast cancer. Fine mapping of borders of amplified regions, which including her2/neu, will open new goals for target therapy of advanced beast cancer.

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Prognostic value of CCN3 in osteosarcoma and Ewing's sarcoma

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Patients with osteosarcoma or Ewing's sarcoma, the two most common bone tumor, still suffer from the paucity of prognostic markers that could distinguish patients before therapy and drive treatment choices. Herein, we assessed the prognostic value of CCN1−3 genes, a group of genes involved in fundamental biological processes as well as in mesenchymal differentiation. Expression of CCN1−3 was detected by means of quantitative PCR in a series of newly diagnosed osteosarcoma or Ewing's sarcoma. In osteosarcoma, CCN1 and CCN2 expression was found statistically associated with genes involved in the commitment of mesenchymal stem cells toward osteoblasts and in the early phases of osteoblastic differentiation (RUNX family genes; cadherin 4, 11, and 13; jun and fos; collagen I and SPARC). CCN3 is highly expressed in osteosarcoma and its level of expression did not correlate with any specific osteoblastic differentiating genes. While neither differentiation genes nor CCN1 and 2 expression were statistically associated with survival, high expression of CCN3 significantly correlated with worse prognosis in osteosarcoma. CCN3 overexpression also showed a prognostic adverse relevance also in Ewing's sarcoma, either at gene and protein levels. Therefore, assessment of CCN3 expression levels at diagnosis may represent a useful molecular tool to early identify subgroups of patients with different prognosis either in osteosarcoma and in Ewing's sarcoma.

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Prognostic significance of p53 and Ki67 in Ewing's sarcoma tumours

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Background: Ewing's sarcoma (ES) is a heterogeneous neoplasm in which several genetic alterations involving cell cycle regulators have been described. Around 10% of ES suffer p53 alterations, which may be demonstrated by immunohistochemistry and/or mutational analysis. Many studies have demonstrated the prognostic significance of p53 in ES, but no large series of cases have been analyzed to validate its clinical use. Ki67 is a molecule that is detected in growing cells. Several papers have revealed the prognostic implication of Ki67 in sarcomas, but which needs to be confirmed in the case of ES. The aim of the present study is to evaluate the prognostic significance of p53 and Ki67 in a large series of ES.
Material and Methods: Paraffin-embedded material from 226 ES subtyped as follows: 66% classic ES, 10% large cell ES, 10% PNET, 3% clear cell ES, 3% atypical ES, 6% spindle cell ES and 1% hemangioendothelial ES. Seven tissue arrays (TA) were performed and immunohistochemical expression of p53 (clon DO7, DAKO) and Ki67 (MIB1, DAKO) was determined using a 1:50 dilution of each antibody.
Results: Follow-up was available from 132 patients with a median of 49 months (range: 1–306 months). 22% of cases expressed Ki67 in more than 5% of tumor cells. Expression of Ki67 was correlated with the progression of ES, being higher in recurrence (30%) and in metastasis (42%) than in primary tumors (20%) ($p = 0.042$). In the case of p53, 31% of ES expressed the protein but no relationship with progression was observed. Log rank test for progression-free (PFS) and overall survival (OS) showed the following results: Antibody: Ki67 ($\leqslant$5%, >5%), %PFS: 68 vs. 31, p: 0.001, %OS: 68 vs. 37, p: 0.009 Antibody: p53 (negative, positive), %PFS: 62 vs. 59, p: 0.366, %OS: 60 vs. 78, p: 0.040. In contrast to the expected, immunostaining of p53 was correlated with a better OS, suggesting that a mutational analysis of these cases should be performed in order to detect those with real mutant behaviour.
Conclusion: Ki67 immunostaining defines a subgroup of ES with a poor outcome and should be taken into consideration in the pathological staging of ES patients.
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Micronuclei in exfoliated bladder cells of gynecological cancer patients receiving pelvic radiotherapy

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Background: The micronucleus (MN) assay in human exfoliated cells has been widely used to detect the genotoxic effects of environmental mutagens, infectious agents and hereditary diseases. This study clarifies the usefulness of the MN assay in exfoliated bladder cells to show normal (not related to the cancer) tissue damage of pelvic radiotherapy.
Materials and Methods: We measured the MN yield in exfoliated bladder cells of 20 gynecological cancer patients received pelvic radiotherapy. These patients were non-smokers, had no urinary tract disease and previous chemotherapy or radiotherapy. They received pelvic irradiation with 2 Gy daily fractions for 5 weeks. Urine samples were taken from the patients before commencement of radiotherapy (0 Gy), 24 hours after completion of the first fraction (2 Gy) and at the end of the therapy (50 Gy). In addition, to determine whether exfoliated bladder cells could be used as a sign of a genomic instability in cancer patients, baseline MN yields of the patient group before the therapy were compared with the healthy control group.
Results: We have detected significant difference between results of three different time periods ($P < 0.01$). The yield of MN after radiation doses of 50 Gy (2.93 ± 2.29) has increased when compared with the 0 Gy (1.37 ± 1.13) ($P < 0.01$) and 2 Gy (2.1 ± 1.92) ($P < 0.05$). There was no significant difference between the MN frequencies of 0 Gy (1.37 ± 1.13) and the control group (1.29 ± 0.74).
Conclusion: Exfoliated bladder cells which can be taken non-invasively could be used to show normal tissue damage after cumulative doses of pelvic radiotherapy but it is not an indicator of a genomic instability in gynecological cancers.

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Malignant mesothelioma (MM): prognostic risk factors and immunohistochemical markers in correlation with pathological changes and prognosis

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Background: Malignant mesothelioma (MM) is known to be a fatal malignancy that is related to asbestos exposure. A number of clinical prognostic factors have been described in the last 20 years, including histological cell type, performance status and clinical stage. However, much of the data have been conflicting probably because many of the studies have been of small size from a single centre. We conducted a population based study in Nova Scotia, Canada to examine the potential prognostic factors, as well as the protein expression of EGFR, VEGFR, and SV40 in MM and their impact on patient's survival.
Methods: All cases of MM diagnosed in the province of NS between 1990–2005 were identified through the Nova Scotia Cancer Registry. Clinical and laboratory data, including known prognostic factors such as WBC, LDH, platelet count and hemoglobin level, were abstracted through a retrospective chart review. Tissue microarray (TMA) with immunohistochemical (IHC) staining for EGFR, VEGFR and SV40 was performed. Survival, with Kaplan Meier analysis, and a multi-factorial model will be performed to detect prognostic factors.