(region of interest) and the gain were constant during the entire exam. Other vascular parameters were assessed also: velocity (V), resistivity and pulsatility indexes (RI, PI) derived from flow velocity. The diagnosis of cancer was confirmed by pathological exam in all patients. We compared also the vascularity index with the tumoral stage.

Results: We found a significant correlation between the power Doppler vascularity index and the microvessel density. The resistivity index and pulsatility index were variable.

Conclusions: Vascularity index is an accurate parameter for assessment of tumoral vascularity. The vascularity index is correlated to the tumoral stage also. The results of our study are limited due to the small number of patients, extended studies being necessary in the future.

618 Poster

Investigation of the relationship between dna-dependent protein kinase and lymphatic metastasis in colorectal cancer

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Aim: To investigate DNA-dependent protein kinase (DNA-PK) expression, and its relationship with lymphatic metastasis in colorectal cancer.

Methods: Tumor tissues from 60 patients, divided into two groups according to lymphatic metastasis, were immunohistochemically stained to detect the DNA-PK expression including Ku70, Ku80 and PKcs proteins.

Results: Positivity of both Ku70 and Ku80 in colorectal cancer was negatively correlated with lymphatic metastasis with an r value of -0.57 and -0.38, respectively. Similar correlation was found between Ku expression, especially Ku70, and long-term survival. PKcs, however, displayed no significant correlation. Statistical analysis failed to detect any correlation between DNA-PK expression, and clinical characteristics, such as age, sex, tumor location, tumor thickness and distant metastasis ($p>0.05$).

Conclusions: DNA-PK expression, especially Ku70 expression, is negatively correlated with lymphatic metastasis, and the survival of patients with colorectal cancer. Ku70 expression may be a potential indicator for the preoperative evaluation, and prognosis in colorectal cancer.

619 Poster

Methodology matters - prognostic significance of HER2 protein expression versus HER2 gene amplification in metastatic breast cancer

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Background: After so many years of research, clinical value of HER2 (Human epidermal growth factor receptor 2) is unclear. Clinical use of HER2 status for prognosis of breast cancer patients remains controversial, mostly because of different testing methods used in different studies and consequently variability of results. There is a lack of studies regarding prognostic value of CISH especially in metastatic breast cancer (MBC) when risk evaluation is based on different parameters than for primary breast cancer. Aim of this study was to compare prognostic relevance of HER2 status in MBC tested by two different methods i.e. immuno-histochemistry (IHC) and chromogenic in situ hybridization (CISH).

Material and methods: In the same group of 107 MBC patients HER2 protein overexpression was determined by IHC and HER2 gene ampliication was determined by CISH in a primary tumor tissue.

Results: There was significant correlation ($p<<0.001$) between HER2 protein overexpression determined by IHC and HER2 gene amplification determined by CISH, beside the existence of discrepant results. However, there was a difference in prognostic value of compared methods during the course of metastatic disease. In a whole group of MBC patients there was no significant difference when patients are stratified by CISH or IHC results. There was significant difference in metastatic breast cancer survival between HER2 nonamplified and HER2 amplified cases in subgroups of patients determined by available clinicopathological parameters i.e. in a subgroup of patients older than 50 years, postmenopausal subgroup and node-positive subgroup. When patients are stratified by IHC results there was no significant difference in survival in these or any subgroups of patients.

Conclusion: These results indicate a discrepancy in the ability of two methods to predict patient's survival. CISH grading system in contrast to IHC grading, offers a real cut-off value for determination of different breast cancer prognostic subgroups. CISH seems to be more accurate and more informative than IHC in prediction of clinical outcome in metastatic breast cancer. Beside that, these results show that HER2, although as biomarker with limited significance in different subgroups of patients, has relevant prognostic value in metastatic breast cancer. In that context, our results confirm that methodology matters and those gene-based testing methods should be really accepted as a gold standard for assessment of HER2 status.

620 Poster

Utility of p53 gene expression for early diagnosis in oral leukoplakias

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Background: The last advances in cellular biology demonstrated the precise mechanisms regulating the cell cycle and show that abnormalities in cell proliferation are a very common manifestation in some cancers and precancerous lesions. Nevertheless tumor suppressor genes, like p53, and other proteins associated to the cell cycle also mediate in this sequence. Oral leukoplakia is a precancerous stage that constitutes a canzerisable lesion due to the genetic alterations that mediate in the evolution of lesion. Since p53 disturbs lead to a loss in cell cycle control, routine molecular study of p53 gene expression would contribute to an improved diagnosis and treatment of oral premalignant lesions. Objective: Study the utility of p53 gene expression as diagnosis factor in oral leukoplakias by means of Quantitative Real Time PCR (qPCR). Materials and Methods: Expression levels of p53 gene, in 24 unique freeze samples from 24 patients with leukoplakia, were measured. From each patient, 2 samples were obtained: opposed lateral oral mucosa and leukoplakia mucosa. As control, a pool of healthy human oral mucosa from healthy donors (n=4) was used. qPCR experiments were performed on a LightCycler 480 Instrument (Roche) using LightCycler 480 SYBR Green I Master (Roche). A constitutively expressed gene, HPRT, was used as internal control. Results: The expression levels of p53 were higher in opposed lateral oral mucosa and leukoplakia both from patient, with regard to the pool of healthy human oral mucosa from healthy donors. When comparing opposed lateral oral mucosa and leukoplakia from the same patient, 54.2% of samples showed higher p53 expression in opposed lateral oral mucosa than in leukoplakia. This could be explained by the "field cancerization" hypothesis in oral cavity, since when the field alteration occurs it is followed by progression of the lesions or the appearance of recurrences or second lesions. Conclusions: qPCR assays confirmed that p53 is up-regulated in premalignant oral epithelial lesions, indicating that p53 may contribute to carcinogenesis. On the other hand, although in other kind of tumors p53 over-expression is a late event, in oral cavity it can be observed in more initial phases of the precancerous lesion. Therefore p53 could represent an attractive diagnosis factor in oral leukoplakias. Support: S. Díaz Prado is beneficiary of an Isidro Parga Pondal contract from Xunta de Galicia (Spain).

621 Poster

Gene expression analysis in pheochromocytoma - searching for new pathways involved in the hereditary susceptibility and the malignant outcome

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Introduction: Phaeochromocytomas and paragangliomas are rare neuro-endocrine tumors that arise from adrenal and extra-adrenal chromaffin tissue respectively, usually causing secondary hypertension by oversecretion of catecholamines. Nowadays, it is widely accepted that 25-30% of patients carry a germline mutation in one of six susceptibility genes: SDHB, SDHC, SDHD, RET, VHL and NF1. Nevertheless, there are still some familial cases not associated with any predisposing gene. On the other hand, malignancy occurs in 15-40% of cases (depending on location and genetic alteration), and is defined as the presence of metastases, with no other clinical features useful for an early diagnosis.

Aim: On this basis, new strategies are needed in order to find new susceptibility genes responsible for the remaining familial cases. In addition, new molecular tools that help us to characterize those patients at risk of malignancy are needed in order to intensify the follow up.