Conclusions: This study reveals that the IL-1RN A2 allele seems to be involved in genetic susceptibility for the development of viral associated neoplasias. We assume that the mechanism trough which it increases the risk is by increasing the predisposition to shorter immune responses that predispose the host to develop easily viral infections. Therefore, oncogenic viruses can infect cells efficiently and promote cancer development.

106 Lung cancer risk and air pollution in an industrial region of Northern Spain: a hospital-based case-control study

T.G. Adonina[1], M.F. Lopez-Cima[1], J. García-Perez[2], B. Perez-Gómez[2], N. Aragones[2], G. Lopez-Abente[2], M. Pollán[2]. *[1]Universidad de Oviedo, Instituto Universitario de Oncologia, Oviedo-Asturias, Spain, [2]Instituto de Salud Carlos III, Centro Nacional de Epidemiología, Madrid, Spain*

Background: Asturias, an Autonomous Region in Northern Spain with a large industrial area, registers high lung cancer incidence and mortality. While this excess risk of lung cancer might be partially attributable to smoking habit and occupational exposure, the role of industrial and urban pollution also needs to be assessed. The objective of this abstract was to ascertain the possible effect of air pollution, both urban and industrial, on lung cancer risk in Asturias.
Material and Methods: This study will be undertaken within the wider context of the Asturian Lung Cancer (*Cáncer de Pulmón en Asturias – CAPUA*) study, a hospital-based case-control study conducted in Asturias with the aim of ascertaining the influence of environmental and genetic factors on the development of lung cancer. This analysis included 626 lung cancer patients and 626 controls matched individually by ethnicity, hospital, age, and sex. Distances from the respective participants' residential locations to industrial facilities and city centers were computed. Using logistic regression, odds ratios (ORs) and 95% confidence intervals (95% CIs) for categories of distance to urban and industrial pollution sources were calculated, with adjustment for sex, age, hospital area, tobacco consumption, family history of cancer, and occupation.
Results: Whereas individuals living near industries displayed an excess risk of lung cancer (OR = 1.49; 95% CI = 0.93–2.39), which attained statistical significance for small cell carcinomas (OR = 2.23; 95% CI = 1.01–4.92), residents in urban areas showed a statistically significant increased risk for adenocarcinomas (OR = 1.92; 95% CI = 1.09–3.38). In the Gijon health area, residents in the urban area registered a statistically significant increased risk of lung cancer (OR = 2.17; 95% CI = 1.25–3.76), whereas in the Aviles health area, no differences in risk were found by area of exposure.
Conclusions: This study provides further evidence that air pollution, both urban and industrial, is a moderate risk factor for lung cancer, which varies according to histologic type and health area.

107 LNA™ based universal RT microRNA PCR system – a new generation high throughput QPCR platform optimized for development microRNA based molecular diagnostic assays on clinical FFPE and blood serum and plasma

B. Nielsen[1], S.J. Nielsen[1], I.K. Dahlsveen[1], A. Baker[1]. *[1]Exiqon, Diagnostics, Vedbæk, Denmark*

Background: Using a Locked Nucleic Acid (LNA™) based miRNA detection technology we have developed a high throughput QPCR system for genome wide detection of miRNAs in clinical paraffin-embedded tissue as well as blood derived plasma or serum. The use of the LNA™ bases adds critical specificity and sensitivity creating a more robust system for more rapid assay development in the clinical and diagnostic assay development.
Material and Methods: Blood derived serum or plasma are important bio-fluids that potentially hold critical biomarker information about disease diagnosis and prognosis. We have developed the advantages of our PCR system to provide a truly sensitive miRNA genome wide screening technology from extremely small volumes of blood derived serum or plasma. In addition the system is ideally suited for screening laser captured and macro-dissected tissue specimens allowing us to build extremely accurate and sensitive miRNA expression profiles from critical tumour biopsies.
Results and Conclusion: We have used the PCR system to screen miRNAs in colorectal cancer patient plasma samples and their matching tumour samples. We have been able to identify miRNAs in both the blood derived plasma and tumours that are differentially expressed between patients and healthy controls.

108 Association between FAS-670A/G polymorphism and ovarian cancer development

L. Lima[1], D. Pereira[2], A.M. Gomes[1], D. Pinto[1], R. Medeiros[1]. *[1]Portuguese Institute of Oncology, Molecular Oncology Group, Porto, Portugal, [2]Portuguese Institute of Oncology, Oncology Department, Porto, Portugal*

Background: Apoptosis is an essential process in malignant cells elimination. One of the characteristics of malignant cells and of tumour development is tumoural cell evasion to apoptotic stimuli and alterations of the apoptotic pathways components.
FAS-670A/G polymorphism in the promoter region of *FAS* gene has been identified, it was proposed that *FAS-670* G allele may reduce Fas expression and might influence apoptosis activation. The aim of this study was evaluate if *FAS-670A/G* have a possible role in ovarian cancer development.
Methods: We performed Polymerase Chain Reaction – Restriction Fragment Length Polymorphism (PCR-RFLP) methodology, for *FAS* gene locus −670 genotyping. It was evaluated DNA samples from 428 women: 189 ovarian cancer patients and 239 healthy control female individuals.
Results: We found that the presence of GG genotype of *FAS-670* A/G represents a significant risk for development of grade III tumours (OR = 3.53; 95% confidence interval (CI): 1.30–9.58). Moreover, we found that individuals carrying *FAS-670* G allele had a higher risk of recurrence after first line chemotherapy with complete response (OR = 5.25; 95% CI: 1.51–18.2). Cumulatively, Kaplan–Meier function plots and probabilities analysis showed that *FAS-670* G allele carriers have a shorter recurrence free survival after first line chemotherapy with complete response (p = 0.017).
Conclusions: Our results indicate that *FAS-670A/G* may have an important role in ovarian cancer development; the study of this polymorphism could help selecting groups at progression risk.

109 Implementation of qPCR and sequencing for KRAS and EGFR mutation detection in Bulgarian patients with colorectal and lung cancer

S. Bichev[1], S. Hristova[2], Y. Slavova[3], R. Vajarova[1], D. Kachakova[4], R. Kaneva[4], I. Kremensky[1]. *[1]Medical University – Sofia, National Genetic Laboratory, Sofia, Bulgaria, [2]Medical University – Sofia, Pathoanatomy, Sofia, Bulgaria, [3]University Hospital of Lung Diseases, Pathomorphology, Sofia, Bulgaria, [4]Medical University – Sofia, Molecular Medicine Center, Sofia, Bulgaria*

Background: Colorectal and lung cancer are among the most common human malignancies both in the United States and Europe. New targeted therapies have been developed in the past decade, such as monoclonal antibodies against epidermal growth factor receptor (EGFR) or KRAS oncogene. Genetic alterations of the intracellular effectors involved in EGFR related signaling pathways may have an effect on response to this targeted therapy Recent data now suggests a differential response to anti-EGFR antibody therapy based on mutational status of a major oncogene called KRAS and 18−21st EGFR's exons for patients with CRS and non-small cell lung cancer (NSCLC) respectively. The aim of this study was to introduce reliable methods for identifying of KRAS/EGFR mutational status in patients with CRC/NSCLC.
Methods and Results: In both groups DNA was extracted from paraffin embedded tissues. Twenty colorectal cancer patients were screened for KRAS mutations by qPCR based on Scorpions technology. Our results showed that five of those patients had mutations in the 12th codon of KRAS oncogene Two patients carried mutation 12 Asp, mutations 12 Ala, 12 Val and 12 Ser were found in the other three patients respectively. No mutations in the 13th codon of KRAS oncogene were found. Eight NSCLC patients were screened for EGFR mutations by qPCR based on high resolution melting technology and subsequent sequencing of aberrant profiles. Among these patients we found only 2 with mutations – one with a deletion (2236−2253del18) and the other a SNP(G719C) in 19th exon of EGFR.
Conclusion: Our study showed that HRM is reliable method for screening of NSCLC patients, however aberrant profiles should be sequenced in order to establish the exact mutation. Scorpion technology used for detection of KRAS status proved to be successful in all 20 patients.

110 Gastric adenocarcinoma development in patients with atrophy or/and intestinal metaplasia: the role of COX-2 polymorphisms in a Northern Portuguese population

A.C. Pereira[1], H. Sousa[1], A.L. Pinto-Correia[1], A.L. Teixeira[1], M. Fragoso[2], L. Moreira-Dias[3], R. Medeiros[1], M. Dinis-Ribeiro[3]. *[1]Portuguese Institute of Oncology, Molecular Oncology GRP, Porto, Portugal, [2]Portuguese Institute of Oncology, Oncology Department, Porto, Portugal, [3]Portuguese Institute of Oncology, Gastroenterology Department, Porto, Portugal*

Background: COX-2 overexpression observed in 69% of gastric cancers (GC) and precancerous tissues is closely intertwined with key mechanisms of gastric carcinogenesis, namely inhibition of apoptosis, tumour growth, angiogenesis, invasion and metastasis. Genetic variations that modify6 the levels of COX-2 protein would be anticipated to have a substantial influence on disease phenotype. Hence, with this study we aimed at understanding the contribution of two functionally expected *COX-2* polymorphisms (−1195A>G and 8473T>C) in the development and progression of gastric lesions.
Material and Methods: A hospital-based case-control study was developed that gathered 134 patients diagnosed with gastric lesions (94 with GC and 40 with atrophy and/or intestinal metaplasia (AIM)) and 255 healthy individuals all from the Northern region of Portugal and recruited at Portuguese Institute