> 50 years), by histology (intestinal vs diffuse type) and by gastric site of disease (cardial vs body and pylorus neoplasms) of the pts.

Results: We found 4 cases of CFS (of which only in one case a HNPCC was suspected). Among the 1502 relatives of the other 77 pts there were 101 neoplasms: of these, 22 were GC, 12 breast cancer, 9 HCC. No significative differences in the number of affected relatives was detected when the sample was stratified by age (p: 0.70) and by histology (p: 0.95), while the number of affected relatives was higher for pts with a cardial neoplasm (p: 0.05).

Conclusion: Genetics of GC remains largely unknown. Despite the reduction of GC incidence, cardial tumor is increasing and an inherited predisposition could play an important role in its aetiology.

740 PUBLICATION

Absence of point mutations on serine 17 of MDM2 in human primary tumors

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Purpose: Studies *in vitro* have demonstrated that the mutations of the Serina 17 of Mdm2 protein, blokcs its phosphorilation for a serin-treonin kinase that regulates the interaction between Mdm2 and p53. The present study investigates the occurrence of mutations at this corresponding Mdm2 gene position, somaticaly in human tumors and in germline in patients with multiple primary tumors, as a possible mechanism for which the tumoral cells can escape to this regulation.

Methods: DNA extracted from tissue samples provenient of 192 cases of different tumor types: 70 breast carcinomas, 14 bladder tumors, 18 colon cancers, 60 testicle tumors and 30 samples of peripheral mononuclear blood cells of patientes with three primary different tumors, were analyzed by PCR-SSCP method and electrophoresed on polyacrylamide gels. To corroborate the PCR-SSCP results, twenty tumor DNA and five blood DNA samples were selected randomly and also checked by direct sequence of the third exon of Mdm2, independently of the normal pattern of SSCP.

Results: In none of the cases studied, tumor and blood samples, electroforetic mobility shifts of bands after SSCP were observed. No mutations at this position (Ser-17) in the twenty-five cases sequenced, were observed.

Conclusion: Mutations of Mdm2 gene, corresponding at Ser-17, implicated in phosphorilation process of Mdm2, were not demonstrated in human tumors, somaticaly neither at germline level. This fact suggest that mutations at this position of Mdm2 gene is not a pathogenic mechanism of tumorigenesis in some common type of human cancers.

741 PUBLICATION

Study of L-MYC polymorphism in elderly tumour-free individuals, healthy donors, and cancer patients

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Purpose: The earlier reports provided evidence that S allele of L-MYC oncogene may be associated with tumour-resistant genetic constitution. The aim of the study was to assess the involvement of L-MYC polymorphism in the cancer tolerance and susceptibility.

Methods: L-MYC alleles were identified by PCR in 184 elderly tumour-free individuals, 122 healthy middle-aged donors (HD) as well as in 95 breast cancer (BC), 63 colorectal cancer (CC) and 58 lung cancer (LC) patients.

Results: Contrary to previous publications, L:S allele frequencies ratio in elderly donors (ED) did not significantly differ from that in HD (0.49:0.51 and 0.54:0.46, respectively). However, S allele was slightly overrepresented among elderly smokers as compared to middle-aged ones (55% vs. 44%; P = 0.059; OR = 1.57 (0.98–2.50)), that implies it may be linked with smoking-tolerant genetic constitution. Whereas CC and LC were strikingly similar to the controls, specific features were observed in the BC patients. Occurrence of S allele in BC cohort (57%) was significantly higher than in middle-aged healthy females (41%; P = 0.016; OR = 1.92 (1.13–3.25)) and elderly non-affected women (47%; P = 0.050; OR = 1.54 (1.00–2.37)).

Conclusions: 1) S allele of L-MYC indicates an increased risk of breast cancer development; 2) the same allele may be associated with better longevity among smokers.

742 PUBLICATION

DCC and p53 protein expression in early stages of gastric cancer

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Purpose: Oncogenes and tumor suppressor genes may be involved in the pathogenesis and the progression of gastric cancer (GC). We investigated the expression of the p53 and the DCC proteins in the early stages of the disease.

Methods: An immunohistochemical analysis for p53 and DCC was performed on consecutive tumor tissue samples from patients (pts) with stage pT1-2 GC. DCC positivity expresses a normal gene function and its staining is reported an "all or nothing" phenomenon. Nuclear accumulation of p53 is commonly related to gene point mutations and a cut-off value of 30% was selected for positivity.

Results: Thirty-eight consecutive cases of GC were analyzed. All the pts underwent radical surgery with a median time of follow-up of 60 months. Disease stage was pT1 in 23 cases and pT2 in 15 cases. Lymphnode metastases were present in 17 cases. DCC positivity was found in 33/38 cases (87%) and p53 positivity in 23/38 cases (60%). A significative higher number of p53 positive cases was found among pT2 cases (11/15; 73%). Preliminary data on 9 relapsed pts showed a high frequency of p53 positivity (7/9).

Conclusions: The detction of wild-type DCC protein in the majority of cases suggests that mutations of this gene are not early events in the genesis of GC. On the contrary, p53 gene mutations with accumulation of its abnormal protein may be related to GC development and invasiveness.

743 PUBLICATION

Identification of HLA class II in patients with endometrial adenocarcinoma (EA)

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Purpose: We determined the distribution of HLA class II alleles in patients (pts) with EA comparing with healthy control group to find the correlation between the phenotype frequency of HLA class II alleles and early risk of developing of EA in North-West Russian population.

Methods: We typed by PCR-SSP technique (HLA-DRB1*01–16, DQB1*0201–0608, DQA1*0101–0601 alleles) of 37 pts with EA and 78 healthy subjects.

Results: The phenotype frequencies of the DRB1*03 and DQB1*0601 alleles were increased in pts with EA (29.7% and 16.2%) compared with healthy subjects (12.8% and 5.1%), respectively; x2 = 4.81 and 3.89, $p < 0.05$. The phenotype frequencies of the DRB1*01, DRB1*04 and DQB1*0301 were decreased in pts with EA (13.5%, 5.4% and 10.8%) compared with healthy subjects (32.1%, 26.9% and 37.2%), respectively; x2 = 4.47, 7.26 and 8.53, $p < 0.01$. In group of patients with EA there was no alleles of HLA-DQA1*0401, but x2-test was not significant (3.003, $p < 0.1$) compare with control group.

Conclusion: We suppose that increased phenotype frequencies of HLA-DRB1*03 and DQB1*0601 alleles are correlated with early risk of developing of EA in North-West Russian population.