found. All affected workers were operators and had a long term direct professional contact with lubricating agent N80.

The aims: The purpose of this work was to estimate the possibility of determination of localization of carcinogenically dangerous production by data of Belorussian cancer registry.

Materials and methods: Skin cancer in two close settled cities Polotsk and Novopolotsk and whole Belorussian urban population was estimated by data of Belorussian Cancer Registry for 1990-2006. Standardized incidence ratios (SIRs) were calculated using the Belorussian urban population incidence rates to generate expected numbers. We have used in the study GIS methodology to make the Atlas of skin cancer SIR time (1978-2005) distribution by 117 regions of Belarus.

The results: We have designed some criteria for primary identification of occupational risk factors in small towns based on data of Population Cancer Registry. There are high numbers of cancer cases with specific localization and morphology, younger mean age of patients and plurality of tumors. Since 1990 to 2006 it was established 956 cases of skin cancer (C44) in Polotsk, 856 cases in Novopolotsk and 61586 in Belarus. According to Atlas of Skin cancer Standardized Incidence Ratios distribution Polotsk region seems to have high skin cancer risk in compare with other Belorussian areas. The proportions of C44.6 localization were 6,5% in Polotsk, 4,3% in Novopolotsk and 3,9% in Belarus. But in the same time among C44.6 cases the proportions of squamous cell carcinoma were 66% in Polotsk, 32% in Novopolotsk and 20% in Belarus. The next feature is the number of plural primary malignant tumors (10 double and 4 triple of metachronous tumors C44.6 in Polotsk against 1 of double tumors in Novopolotsk). The mean age of diseased of carcinoma C44.6 was 55,0 in Polotsk and 62,7 in Novopolotsk and 68,7 years in Belarus. SIR of C44.6 for Polotsk (SIR=2,18; 95%CI=1,67-2,82) and Novopolotsk (SIR=1,58; 95%CI=1,11-2,18) were significantly higher than in whole population. Thus we can conclude that presence of significant professional carcinogenic factor in small city could be discovered in population based descriptive epidemiological study.

169 Poster

Mouse mammary tumor virus (MMTV)-related sequences in the juvenile acute myeloid leukemia patients

E. Smirnova[1], A. Lushnikova[1], A. Parokonnaya[2], L. Lubchenko[2], E. Polevaya[2]

[1]Blokhin Cancer Research Center, Carcinogenesis Institute, Moscow, Russian Federation; [2] Blokhin Cancer Research Center, Clinical Oncology Institute, Moscow, Russian Federation

Background: MMTV-homologous sequences were found earlier in DNA samples from tumor tissue and lymphoid cells of sporadic/familial breast cancer (BC) and Non-Hodgkin's lymphomas + BC patients. Two female BC patients in our cancer-register had child suffered with acute leukemia (AL). We have analyzed a primary patients with AL to verify this observation. Material and Methods: Peripheral blood and bone marrow DNA samples obtained from 11 primary patients with acute myeloid leukemia (AML) and 6 ones with acute lymphoblastic leukemia (ALL) were analyzed by PCR using specific primers for gp52-coding area of the env MMTV gene and Sag-coding area of 3'LTR MMTV. PCR products of 665 bp and 725 bp were cloned in pGEM-T vector and sequenced. RT PCR using primers for the env MMTV gene was performed to evaluate MMTV-homologous sequence expression. Results: 4 bone marrow DNA samples from 11 patients (3 boys of 9, 11,13 years old and 1 girl of 15 years old) were the env /LTR MMTV-positive, one boy has mother with BC and young healthy brother. While five ALL patients (3 - 11 years old) were MMTV-negative by PCR. Sequencing of the env MMTV and 3'LTR –related cloned PCR products has found 93-94% homology to the exogenous env MMTV gene (C3H starin and Mus musculus MMTV), and 92% homology to SAG protein gene of Mus musculus MMTV. The sequence transcripts were revealed by RT PCR. ORF finder has shown one Frame of 567 bp long in gp 52-coding area of the env MMTV sequence and one Frame of 563 bp long in Sag-coding sequence. BLAST analysis puts the sequences into tree clusters between endogenous MMTV RNA env gene / right LTR (Mtv 17) and Mus musculus mammary gland cDNA branches. Conclusions: MMTV-homologous sequences were firstly revealed in 4 from 11 juvenile patients with AML. It indicates that MMTV-related virus might involves both in lymphomas and in leukemia in human by infection of dendritic and/or pluripotent hemopoetic stem cells. A possible ways of MMTV infection in AML patients are under discussion.

170 Poster

Glutathione-S-transferase T1, M1 and P1 polymorphisms as risk factors for early onset lung cancer

M. Timofeeva[1], S. Kropp[2], W. Sauter[3], A. Rosenberger[4], T. Illig[3], H. Dienemann[5], H. Bickeböller[4], J. Chang-Claude[2], A. Risch[1], H.E. Wichmann[3]

[1]German Cancer Research Center, Division of Toxicology and Cancer Risk Factors, Heidelberg, Germany; [2] German Cancer Research Center, Division of Clinical Epidemiology, Heidelberg, Germany; [3] Helmholtz Zentrum München, Institute of Epidemiology, Neuherberg, Germany; [4] University of Göttingen, Department of Genetic Epidemiology, Göttingen, Germany; [5] Thoraxklinik, -, Heidelberg, Germany

Lung cancer (LC), the leading cause of cancer death worldwide, is considered the result of complex interactions between environmental - predominantly smoking - and genetic factors. It is supposed that a particularly strong genetic component exists in the group of individuals with early onset LC. Glutathione-S-transferases (GSTs) are among the central enzymes involved in cellular detoxification.

A case-control study was carried out to identify GST genetic polymorphisms that might modify the risk of developing early onset LC. 638 Caucasian patients under the age of 51 with confirmed primary LC and 1300 cancer free control individuals, matched by age and sex, were included in this analysis. Overall, 5 SNPs in the GSTP1 gene and deletion polymorphisms in GSTM1 and GSTT1 were analysed. Genotyping of the GSTP1 polymorphisms was carried out using MALDI-TOF (matrix assisted laser desorption/ionization time-of-flight) mass spectrometry. A new semi quantitative real-time multiplex PCR assay on the LightCycler 480 was established for genotyping GSTM1 and GSTT1 copy numbers.

Conditional logistic regression analysis adjusted by smoking was applied to assess polymorphism-associated ORs. The GSTP1 SNP rs1138272 homozygous variant genotype was associated with an increased risk of LC overall (OR 3.14; 95% CI 1.01-8.96, p=0.032). For GSTP1 SNP rs4891 an increased risk of LC associated with the homozygote variant genotype was observed in the group of heavy smokers (>21 packyears) (OR 1.76; 95% CI 1.05-2.84, p=0.032). Interestingly, for GSTT1 an effect was only observed in the group of heavy smoking women, where carriers of at least one null allele showed an increased risk of LC (OR 2.33; 95% CI 1.31-4.14, p=0.004). However, all these findings were not significant after Bonferroni correction for multiple testing. An effect of GSTP1 SNP rs1695 was detected only among individuals with GSTT1 null genotype (OR 3.36; 95% CI 1.36-8.32 p=0.009), however, gene-gene interaction was not significant (p=0.07).

Our results do not support a main effect of GSTP1, GSTM1 and GSTT1 genotypes with regard to LC. However, further studies, including gene-gene interaction analysis, will be necessary. To the authors' knowledge the current study is the first investigation of GSTT1 and GSTM1 deletion polymorphisms as risk factors for early-onset LC, employing a method that distinguishes between homozygous wild-type and heterozygous individuals.

171 Poster

Melanocortin receptor 1 variants and melanoma risk - a study on two European populations

D. Scherer[1], A. Figl[1], E. Nagore[2], D. Schadendorf[3], K. Hemminki[1], R. Kumar[1]

[1]Deutsches Krebsforschungszentrum, Molecular Genetic Epidemiology, Heidelberg, Germany; [2] Valencia Institute for Oncology, Department of Dermatology, Valencia, Spain; [3] University Medical Centre, Skin Cancer Unit, Mannheim, Germany

The G-protein coupled Melanocortin receptor 1 (MC1R) is a pivotal component of melanin synthesis in melanocytes. The gene encoding MC1R is highly polymorphic and many variants are associated with an increased risk of melanoma. At least five variants are strongly associated with high risk phenotypes of red hair and fair skin (RHC alleles; D84E, R142H, R151C, R160W and D294H) in Caucasians.

We investigated two European populations, German and Spanish, for the effect of MC1R variants on risk of malignant melanoma and on disease outcome. 1298 melanoma cases (595 German and 703 Spanish cases) and 1582 healthy controls (1038 German and 544 Spanish controls) were genotyped by direct sequencing. The risk of any variant in the German population (odds ratio OR 1.59, 95% confidence interval CI 1.24-2.05) was comparable to the risk observed in the Spanish population (OR 1.84, 95% CI 1.42-2.40). Carriers of two variants were at twice the risk than carriers of only one polymorphism indicating a gene dosage effect of this risk factor.

Despite similarities in the risk associated with MC1R variants, we also observed subtle differences in the two populations. RHC variants were more frequent in German than in Spanish population. However, an association between RHC variants and increased risk of melanoma was found in both populations (German: OR 2.40, 95% CI 1.81-3.19, Spanish: