estimated for each individual on the diet questionnaire that was reported to be consumed. Odds ratios (OR) and 95% confidence intervals (CI) were computed using unconditional logistic regression. The each nutrients intake amounts were categorized by quartiles based on the distribution among controls.

Results: Intakes of total fat, saturated fat, monounsaturated fat, trans-fat and cholesterol were positively associated with the risk of RCC; the ORs for the highest versus the lowest quartile were 1.67 (95% CI, 1.21-2.32), 1.53 (95% CI, 1.14-2.05) and 1.46 (95% CI, 1.05-1.97), 1.31 (95% CI, 1.04-1.65) and 1.48 (95% CI, 1.16-1.89), respectively. The positive association was apparently stronger in women, overweight or obese, and never smokers. An increased risk was also observed with increasing intake of sucrose. High fiber intake was inversely associated with RCC risk, the OR for the highest versus the lowest quartile were 0.69 (95% CI, 0.53-0.92). No association was found with intake of total protein and polyunsaturated fat, n-3 and n-6 polyunsaturated fatty acids and total carbohydrates.

Conclusion: Findings suggested that nutrition may play a role in the risk of RCC. A diet low in fat and rich in fiber could favourably affect the risk of RCC.

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Gene expression analysis of formalin-fixed, paraffin-embedded breast cancer tissues using the multiplex branched DNA assay

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Formalin-fixed, paraffin-embedded (FFPE) tumor tissue specimens represent the largest tissue archive where also the patient's clinical record is available. There is a growing interest to use RNA from FFPE tumor specimens to perform gene expression analyses to predict prognosis and response to treatment. The branched DNA (bDNA) assay measures mRNA directly from crude cell lysates and thus avoids variations introduced by RNA isolation, reverse transcription and amplification procedures. A modified version of the bDNA assay quantifies RNA directly from FFPE tissues specimens. The multiplex bDNA assay combines the bDNA assay with the xMAP (multi-analyte profiling) beads allowing simultaneous quantification of multiple RNA targets. The aim of the study was to investigate the molecular classification of breast cancer samples by quantifying the expression of selected genes directly from FFPE tissue, using the multiplex bDNA technology.

We used the 1.0 multiplex bDNA assay to measure the gene expression of 69 genes directly from 20 FFPE breast cancer samples. The genes were chosen from the list of genes able to discriminate between the 5 breast cancer subgroups (Sørlie et al Proc Natl Acad Sci , 2001). The genes were divided into 3 panels with PPIB, RPL19 and RPS3 as housekeeper genes. All the five breast cancer subgroups were represented in the FFPE samples. We also analyzed isolated total-RNA from fresh frozen tissue from 9 of the 20 samples.

The comparison between total RNA and FFPE on the bDNA technology showed that 42% of the genes had correlation >0.5. Hierarchical clustering of the FFPE samples based on the 69 genes was able to divide the samples reasonably well into their subgroups. Most of the luminal A samples clustered together, 2/3 samples for both basal-like and ERBB2+ samples clustered together in a main subcluster, and all luminal B and normal-like samples clustered together in a main subcluster. Hierarchical clustering of the FFPE samples, using only the genes with a correlation >0.6 between FFPE and total-RNA, showed that all the samples within the subgroups ERBB2+, normal-like and basal-like clustered together in a main subcluster, 5/8 luminal A samples clustered together and 3/4 luminal B samples clustered together in a main subcluster.

We conclude that the bDNA technology is able to quantify the expression of genes directly from FFPE tissues, and shows potential use in classifying breast cancer samples into their respective subgroups.

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Genetic polymorphisms in the promoters of IL-6 and IL-10 in CIN and cervical cancer patients

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Introduction. Cell-mediated immunity is important in controlling both HPV infection and HPV –associated carcinogenesis. It was suggested that the cytokine response to HPV infection may potentially affect the disease process. Single nucleotide polymorphisms (SNP) in the promoters of IL-10 and IL-6 genes have been associated with different cytokine production and susceptibility to a number of diseases. The aim of this case-control study was to compare the IL-10 (-1082 G→A) and IL-6 (-174 G→C) polymorphisms in patients with cervical intraepithelial neoplasia (CIN) or cancer (CC) and the healthy controls. We would like to assess whether these polymorphisms increase the risk of cervical cancer in Russian patients.

Methods. Genomic DNA was isolated from the paraffin-embedded tissue from 130 CC patients and 45 patients with CIN I-III. The control DNA was extracted from peripheral blood from 144 females without any cancer, autoimmune or infectious diseases. Polymorphisms of IL-10 and IL-6 were studied in RFLP-PCR and the allele-specific PCR respectively. The Fisher's exact test was used to calculate statistical significance.

Results. We observed the increase of IL-10(-1082AA) low-secretor genotype frequency in CC patients versus control (p=0.012) and versus CIN patients (p=0.036). CC patients demonstrated the significant decrease of the high-secretor genotype IL-6 (-174CG) compared to the control (p=0.038).

Conclusions. These data suggest that the genetically determined ability to produce the different levels of IL-10 and IL-6 cytokines may be associated with cervical carcinogenesis.

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Cancer mortality in patients with schizophrenia - 11-year cohort study

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Schizophrenia is associated with a rate of premature mortality 2 to 3 fold higher than in the general population. The role of cancer in this excess mortality remains unclear, previous incidence or mortality studies having found contradictory results.

The authors initiated in 1993 a large prospective study in a cohort of 3470 patients with schizophrenia to determine mortality rates and specific causes of death. Standardized mortality ratios were calculated, adjusting for age and sex relative to a representative sample of the French general population.

During the eleven years follow-up, 476 (14%) patients died, corresponding to a mortality rate near 4-fold higher than in the general population. Cancer was the second cause of mortality (n=74), with a global SMR of 1.5 (95% confidence interval [95% CI], 1.2-1.9). For all cancers, the SMRs were 1.4 (NS) in men and 1.9 (95% CI, 1.4-2.8) in women. In men, lung cancer was the most frequent localization (n=23, 50%), with a SMR of 2.2 (95% CI, 1.6-3.3). In women, breast cancer was the most frequent localization (n=11, 39%), with a SMR of 2.8 (95% CI, 1.6-4.9). There were two significant baseline predictors of death by lung cancer in the final logistic regression model: duration of smoking and age ≥ 38 years old.

The results of the current study demonstrate an increased risk of mortality by cancer in patients with schizophrenia, especially in women for breast cancer and in men, for lung cancer. These results seem to be consistent with the lack of medical care in schizophrenia.

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Polymorphisms in Fibroblast growth factor receptor 2(FGFR2) and susceptibility to breast cancer in Chinese women

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Background: FGFR2 belongs to the FGFR family which plays an important role in cell growth, invasiveness, motility and angiogenesis. Studies showed that FGF and FGFR expression is ER dependent and significantly correlated with an antiapoptotic role in human breast cancer. Recently, several single nucleotide polymorphisms (SNPs) of FGFR2 were identified as novel breast cancer susceptibility loci by whole genome association studies. In this study, we test the hypothesis that polymorphisms of FGFR2 may interact with estrogen related factors to contribute to breast cancer susceptibility in Chinese women.

Materials and methods: we genotyped three FGFR2 polymorphisms (rs2981582, rs1219648 and rs2420946) in a case-control study of 1,049 breast cancer patients and 1,073 cancer-free controls by using the SNPstream 12-plex genotyping platform.

Results: We found that the three SNPs were all associated with significantly increased breast cancer risk in a dose-dependent manner. Jointly, compared with subjects carrying '0-2 risk loci', the '3 risk loci' carriers had a 1.36-fold increased risk of breast cancer (adjusted OR =