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demethylation induced by 5-aza-2′-deoxycytidine or genetic double knock-out of DNMT1 and DNMT3B which led to demethylation of the promoter and strong reactivation of NPAS4 expression. NPAS4 was further found to be up-regulated after Ultra-Violet (UV) light irradiation and Adriamycin drug treatment and may be an indirect target of the TP53 tumor suppressor, suggesting a role in the DNA-Damage Response pathway. Ectopic expression of NPAS4 in silenced cell lines elicits a strong inhibitory effect on cell clonogenicity, proliferation and migration.

Conclusions: Taken together, our data show that NPAS4 could be one of the candidate TSGs responsible for the tumor suppressive function of 11q13. Characterization of the mechanism by which NPAS4 exerts tumor-suppressive effects is on-going.

534 Epigenetic Changes in Tumour Tissue and Plasma DNA Samples From Breast Cancer Patients

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Background: Breast cancer is recognized as the most common malignancy among women that is caused by progressive accumulation of genetic and epigenetic abnormalities. Many tumour suppressor genes are inactivated by DNA hypermethylation of promoter sequences, which could be utilized for identification of new cancer epigenetic biomarkers.

Patients and Methods: To investigate the relation between DNA methylation profiles and breast cancer progression, we analysed DNA methylation in 5 genes (*RASSF1A, CDH1, TIMP3, ESR1, and SYK)* using quantitative multiplex methylation-specific PCR in paraffin-embedded tumour tissues, blood cells and plasma samples from 71 breast cancer patients. The associations between methylation profiles and regular clinico-pathological parameters were analysed by Student's t-test or ANOVA and Mann–Whitney U test or Kruskal–Wallis H test depending on data distribution. Statistical analyses were performed by SPSS 15.0 software.

Results and Discussion: DNA methylation was found in tumour tissues from 85.5% (59/69), 7.1% (5/70), 15.7% (11/70), 8.6% (6/70) and 10% (3/30) of evaluated patients in *RASSF1A, CDH1, TIMP3, ESR1, and SYK* genes, respectively. However, promoter hypermethylation (methylation level more than 20%) was detected in cancers of 55 *(RASSF1A),* 6 *(TIMP3)* and 1 *(ESR1)* patients. In the most frequently methylated *RASSF1A* gene the simultaneous finding of DNA methylation presence in tumour tissues and plasma samples were identified in 23 patients (39%). In less frequently methylated genes *CDH1, TIMP3* and *ESR1,* this correlation was found in 1, 4 and 1 patients, respectively. In all five genes, genomic DNA isolated from patient's peripheral blood was methylated very rarely in the range from 0.01 to 0.53% except one case with 1.34%. In the group of patients with *RASSF1A* methylation we found statistically significant difference between those with absence or presence oestrogen expression ($p = 0.007$) and different IHC subtype ($p = 0.041$). Hormonal negative patients presented significantly lower DNA methylation that could indicate the possible hormonal influence on DNA methylation process.

Conclusion: High level of DNA methylation in *RASSF1A* gene was presented in tumour tissues of almost 80% breast cancer patients and more than one third of them were methylated also in matched plasma samples. Clinical utility of cell-free DNA from plasma for testing of cancer specific methylation profiles need to be more deeply evaluate in larger study.

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535 Investigation of P53 Gene Codon72 Polymorphism in Colon Cancer

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Introduction: This study has been performed to determine the allele frequencies and distribution of genotypes of p53 gene codon 72 polymorphism in Turkish colon cancer patients and healthy controls.

Material and Method: Genomic DNA was extracted from 103 persons (56 with colon cancer and 47 controls) in the study. PCR-RFLP technique was used to analyze p53 codon 72 polymorphism. Products were assessed with UV transilluminator by being exposed to agarose gel electrophoresis.

Results and Discussion: According to genotype distribution and allele frequencies of p53 gene codon 72 polymorphism there was no significant difference between groups.

Conclusion: Consequently, in this study, we may assert that the polymorphism of p53 gene codon 72 polymorphism cannot be considered as a genetic marker for identifying colon cancer in Turkish population.

536 The Relationship Between Colon Cancer and Methylenetetrahydrofolate Reductase (MTHFR) C677T Polymorphism

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Introduction: This study has been performed to determine methylenetetrahydrofolate reductase (MTHFR) gene C677T polymorphism in Turkish colon cancer patients and healthy controls.

Material and Method: Genomic DNA was extracted from 78 persons (39 with colon cancer and 39 controls) in the study. PCR-RFLP technique was used to analyze methylenetetrahydrofolate reductase gene C677T polymorphism. Products were assessed with UV transilluminator by being exposed to agarose gel electrophoresis.

Results and Discussion: According to genotype distribution and allele frequencies of MTHFR gene C677T polymorphism there was no significant ($p > 0.05$) difference between groups.

Conclusion: Consequently, in this study, we may assert that the polymorphism of methylenetetrahydrofolate reductase gene C677T polymorphism cannot be considered as a genetic marker for identifying colon cancer in Turkish population.

537 Analysis of the Codon 72 Polymorphism of P53 Gene in Patients With Multinodular Goiter to Develop Thyroid Cancer

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Introduction: In this study it was aimed at determining whether or not p53 gene codon 72 polymorphism is a genetic marker of thyroid cancer development in multinodular goiter patients.

Material and Method: Genomic DNA was extracted from 90 persons (42 with multinodular goiter and 48 healthy controls) in the study. DNA was amplified with specific primers by PCR and RFLP technique was used to analyze p53 gene codon 72 polymorphism genotypes. PCR products were assessed with UV transilluminator by being exposed to agarose gel electrophoresis.

Results and Discussion: According to genotype distribution and allele frequencies of p53 gene codon 72 polymorphism there was no significant difference between groups.

Conclusion: As a result of our study we may assert that p53 gene codon polymorphisms cannot be considered as a genetic marker to develop thyroid cancer in Turkish population with multinodular goiter.

538 P53 Gene Codon72 Polymorphism and Endometriosis – Risk Factors of Cancer

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Introduction: In this study it was aimed to determine genotype distribution and allele frequencies of p53 gene codon 72 polymorphism in Turkish endometriosis patients.

Material and Method: Genomic DNA was extracted from 60 women (30 with endometriosis and 30 controls) in the study. PCR-RFLP technique was used to analyze p53 codon 72 polymorphism. Products were assessed with UV transilluminator by being exposed to agarose gel electrophoresis.

Results and Discussion: According to genotype distribution and allele frequencies of p53 gene codon 72 polymorphism there was no significant difference between groups.

Conclusion: As a result of our study we may assert that p53 gene codon 72 polymorphism and endometriosis cannot be considered as risk factors for cancer development.