

POSTER PRESENTATION ABSTRACTS

PP-01

EVALUATION OF ANTIPROLIFERATIVE EFFECTS OF SODIUM DICHOROACETATE ON LUNG ADENOCARCINOMA

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OBJECTIVES: Cancer cells alter their metabolism to proliferate and metastasize by consuming high level of glucose and generate energy via aerobic glycolysis by yielding 2 ATPs and lactate and this is known as Warburg effect which is actually mitochondrial dysfunction due to suppression of Pyruvate dehydrogenase(PDH) by Pyruvate Dehydrogenase Kinase(PDK) which prevents delivery of pyruvate into mitochondria. Dichloroacetate(DCA) is a metabolic mediator for inhibiting PDK and reactivating PDH which encodes by PDHA1 gene. The aim of this study is to see the effect of sodium dichloroacetate(NaDCA) on cell viability and associate PDK1 and PDHA1 genes with cell viability in lung adenocarcinoma.

MATERIAL&METHODS: The human lung adenocarcinoma A549 cell line was cultured and treated with 5mM, 10mM, 50mM, 100mM of NaDCA. The cell viability was analyzed after 24-and 48-hours incubation. Apoptosis was detected by AnnexinV staining. RNAs were extracted from cells for qRT-PCR.

RESULTS: Different doses were not significantly effective at 24 hours. 10mM, 50mM, and 100mM of NaDCA significantly decreased cell viability at 48 hours. According to results of AnnexinV staining, cells treated with different doses of NaDCA induced apoptosis, especially at 48hours, treatment with 100mM of NaDCA led to 40.5% of apoptotic population. According to qRT-PCR analysis, PDK1 gene expression decreased with the treatment of increased doses of NaDCA at 24hours. Also, increased doses of NaDCA increased PDHA1 gene expression at 48 hours gradually.

CONCLUSIONS: In this study, the apoptosis inducing effect of NaDCA had been correlated with the decreased PDK1 and increased PDHA1 gene expression. This study demonstrates that defining PDK as a potential target is ideal for lung adenocarcinoma.

Keywords: Lung adenocarcinoma, sodium dichloroacetate, Warburg effect, apoptosis

PP-02

EFFECTS OF RANOLAZINE AND ELECLAZINE ON GLIOBLASTOMA CELL LINES

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OBJECTIVES: The potential involvement of voltage-gated sodium channel (VGSC) activity in glioma progression was studied. In particular, anti-invasive effects of the VGSC persistent current blockers were determined.

MATERIAL&METHODS: The human glioma cell lines U87, LN229 and LN18 were maintained in RPMI medium with 10% added foetal bovine serum (FBS) under normoxia or hypoxia (1% O₂, 48h). Eleclazine (with 0.15% DMSO as supplementary solvent) was used at a working concentration of 5-15 μ M. Ranolazine and tetrodotoxin (TTX), dissolved directly in RPMI medium, were used at concentrations of 5-10 μ M and 1 μ M, respectively. Cell viability was determined by trypan blue dye exclusion assay. Cell proliferation was quantified colorimetrically. Cell invasion along a chemokine (FBS) gradient was determined using Boyden chamber assays incorporating Matrigel-coated transwell filters. A pan-VGSC antibody was used to study VGSC expression. Each experiment was carried out 3-7 times.

RESULTS: All cells expressed VGSC protein. Further results were obtained for the U87 cell line as the main model. Under eleclazine (15 μ M), ranolazine (10 μ M) and TTX (1 μ M) treatments, cell viability remained at 100%. Ranolazine (10 μ M) had no effect on proliferation and invasion. Eleclazine (15 μ M) decreased proliferative activity via non-VGSC mediated mechanism (at least, partially) in both normoxia and hypoxia. Surprisingly, however, it significantly increased invasiveness by 64% (normoxia) and 31% (hypoxia). Hypoxia by itself did not affect the invasiveness.

CONCLUSIONS: (1) Glioma cell proliferation and invasiveness are controlled differently. (2) It is possible to regulate cancer progression without cell killing. (3) Further experiments are needed to determine effects of (i) more acute hypoxia and (ii) lower concentrations eleclazine.

Keywords: Eleclazine, Glioma, Invasion, Proliferation, Ranolazine, U87

PP-03

IS THERE ANY CO-CHANGES BETWEEN VOLTAGE-GATED NA+ CHANNEL SCN5A AND CTNNB1 GENES IN COLORECTAL CANCER?

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OBJECTIVES: New evidence suggests that ion channels play important roles in cell proliferation, migration, apoptosis and differentiation. NaV1.5 encoded by the SCN5a gene. Also, mutations or polymorphisms in CTNNB1 (gene encoding b-catenin; mostly mutations in exon 3) can lead to aberrant activation of Wnt/b-catenin signaling at the onset of various types of malignancies. The aim of this study was to assess relation between the SCN5A gene and CTNNB1 alteration in the patients with colorectal cancer and compared their tumor and normal tissues.

MATERIAL&METHODS: A total of 30 paraffin-embedded colorectal cancer and normal tissue specimens were used. Ten-micrometer-thick tissue sections were placed on a glass slide. DNA was extracted from the tissues with extraction buffer at 55°C over night. The tubes were boiled to inactivate the proteinase K. The SCN5A exon 18 and CTNNB1 genotypes were determined by PCR amplification. PCR products of SCN5A exon 18 were digested with restriction enzyme BseRI. SSCP is used for CTNNB1 exon 3 to observe any difference between the 2 groups. The gel was stained with silver staining method.

RESULTS: In our study no significant differences were found in the CTNNB1 exon 3 and SCN5A exon 18, between the tumor group and normal groups, also any association with two sides.

CONCLUSIONS: Adhesion involve continuous modulation of cell motility, ion channels play major roles. We need urgently much more work with large sample sizes are required for the association Na+ channels with adhesion molecules.

Keywords: CTNNB1, SCN5A, Colorectal cancer, SSCP, RFLP

PP-04

EFFECTS OF PACLITAXEL ON INTRACELLULAR CALCIUM AND POTASSIUM AND TRANSMEMBRANE POTENTIAL

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OBJECTIVES: Paclitaxel (PTX) is a chemotherapeutic agent commonly used in breast cancer. We investigated its effect on cytosolic calcium and potassium levels and their impact on transmembrane potential.

MATERIAL&METHODS: Estrogen positive MCF-7 (ATCC HTB- 22) and triple negative MDA-MB-231 (ATCC HTB-26) cell lines were used. IC50 values were determined by trypan blue exclusion and used throughout. Intracellular calcium (Ca²⁺) was determined with Fura-2-AM, intracellular K⁺ was determined with PBFI-AM and membrane potential was determined with DiBAC4(3) for 24 hours by fluorescent spectrophotometer. Statistical analysis was performed using one way ANOVA and p value < 0.05 was accepted as significant.

RESULTS: Effect of PTX was cell specific. Kinetic measurement showed that Ca²⁺ increased by 20% from the onset PTX application till 24 hours in MCF-7 cells but had no effect on K⁺ levels. An increased depolarization was seen till 24th hour where a hyperpolarization was detected. On the contrary PTX increased K⁺ levels up to 240% of control while Ca²⁺ increase was only 13% in MDA-MB231 cells. Membrane potential of MDA-MB231 cell line did not differ with respect to control cells throughout.

CONCLUSIONS: These results are a consequence of differential ion channel expression in malignant cells and they also indicate that to elucidate the impact of ion channels and intracellular concentrations of ions not only K⁺ and Ca²⁺ but intracellular Na⁺ and Cl⁻ levels must also be considered.

Keywords: Paclitaxel, intracellular potassium, transmembrane potential, intracellular calcium

PP-05

THE ACCURACY OF MTT PROLIFERATION ASSAY IN STUDIES INVOLVING ANTI-METASTATIC DRUG AND HYPOXIC MICROENVIRONMENT

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OBJECTIVES: Simply, cancer develops and forms tumours by losing control on proliferation because of mutations and epigenetic changes. Following this primary tumorigenesis, cells spread to secondary sites (i.e. metastasis) which involves invasion and migration. In order to stop metastasis, which is the main cause of death from cancer, drugs targeting this metastatic cascade is widely used in medical research. In addition, microenvironmental factors, such as O₂ level, is important in cancer development and metastatic cell behaviour. One of the most widely used technique to measure cell growth is colorimetric 3-[4, 5-dimethylthiazol-2-yl]-2, 5-diphenyltetrazolium (MTT) assay. In the present study, we investigated possible effect of anti-metastatic drug treatments and hypoxic microenvironment (1% O₂) on the MTT proliferation assay accuracy.

MATERIAL&METHODS: In this study, MDA-MB-231, triple negative breast cancer cell line was used. Eleclazine (5?M & 10?M) is used as potential anti-metastatic drug. Cells were incubated in hypoxic (1% O₂) or normoxic (18% O₂) environment. MTT proliferation assay was performed with three biological repeats for every condition and standard curve was generated for each treatment. For statistical analysis, ANOVA (one-way) test and post-hoc Tuckey test were performed.

RESULTS: There was no significant difference between the calibration curves of different treatments.

CONCLUSIONS: It was concluded that Eleclazine, and the hypoxic microenvironment conditions did not affect the accuracy of the assay and the standard curves did not deviate significantly. MTT therefore, can be a good measurement for proliferation activity of the cells under these conditions.

Keywords: Anti-metastatic drug, breast cancer, Eleclazine, hypoxia, MTT proliferation assay,

PP-06

ANTI-PROLIFERATIVE EFFECT OF THE {MESOBUTHUS GIBBOSUS} VENOM PEPTIDE ON HUMAN BREAST CANCER CELL LINES

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OBJECTIVES: Incidence and mortality rates of breast cancer(hBCa) cases are expected to increase approximately %50 by 2040. Although the 5-year survival rate is significantly higher than before, targeted therapy approach is still too specific. Therefore, a drug candidate that can be widely used in hBCa treatment is still needed. Animal venoms consist of several biologically active peptides, capable of specifically binding to ion channels and their anti-cancer activity had been shown. Moreover, it was shown that Kv1.3 expression appear in hBCa tissue and cells. In light of all, we aimed to show the anti-proliferative effect of the previously determined {Mesobuthus gibbosus} peptide, which was predicted as Kv 1.3, on hBca cell lines.

MATERIAL&METHODS: Venom milking was performed by electrical stimulation. Venom peptides were separated by RP-HPLC. The study was done with the fraction, molecular weight and sequence of which previously established in our lab. Sequence alignment and homology search was done with standard protein-BLAST tool. MDA-MB-231 and MCF-7 cell lines were used. The effects on cell viability and population were determined with NR and SRB assay, respectively. Morphological evaluation was done after PAP and Giemsa staining. Data was analyzed with GraphPad Prism8.

RESULTS: The highest tolerated dose was determined with viability assay. IC50 of the peptide for 24 hours were determined as 2.88 and 6.39 nM for MDA-MB-231 and MCF-7, respectively. Morphological effects of the peptide were also shown in consistence with these results.

CONCLUSIONS: The anti-proliferative effect of Kv channel inhibiting peptide, purified from scorpion venom, has been demonstrated on breast cancer cell lines

Keywords: venom, peptide, voltage gated potassium channel, breast cancer

PP-07

ROLE OF SELENIUM ON MPP+ NEUROTOXICITY IN SH-SY5Y NEUROBLASTOMA CELLS: FOCUS ON TRPV1 CHANNELS

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OBJECTIVES: Selenium, co-factor of most powerful intracellular antioxidant glutathione peroxidase enzyme, is one of trace elements that found in the body. The SH-SY5Y human neuroblastoma cell line is frequently used for in vitro model of Parkinson's disease. The 1-methyl-4-phenylpyridinium (MPP+) is a toxic metabolite and breakdown of mitochondrial complex-1 by its activity is known that induce Parkinson's pathology in SH-SY5Y cell line through an increasing the cellular redox level and decreasing cell viability. The TRPV1 channels are oxidative stress-sensitive and calcium-permeable non-selective cation channels that widely expressed in neuronal cells. Hence, we aimed to investigate that the role of selenium supplementation and TRPV1 channel activity on MPP+ induced neurotoxicity in SH-SY5Y cells.

MATERIAL&METHODS: For this aim, we grouped cells as 1- Control, 2- Selenium, 3- MPP and 4- MPP + Selenium. After all incubations, different cellular functions such as Wright-Giemsa staining for assessment of apoptosis and calcium signaling (fura-2) for TRPV1 mediated calcium influx were evaluated in study groups.

RESULTS: Intracellular calcium concentration was statistically lower in MPP group comparing to control. However, selenium treatment alters that level to control. It is determined that low concentration of selenium contributes to cell viability and it modulates MPP+ induced apoptosis.

CONCLUSIONS: We observed novel effects of selenium on the regulation of calcium signaling via TRPV1. Selenium treatment can be useful for the inhibition of neurodegeneration induced by MPP+. Further studies are needed to illuminate role of TRPV1 channels in molecular mechanisms of MPP induced apoptosis in neuronal cells.

Keywords: TRPV1 channels, SH-SY5Y neuroblastoma cells, apoptosis.

PP-08

EXPRESSION LEVELS OF MIR-423-5P AND MIR-664B-5P IN PATIENTS WITH FAMILIAL AND SPORADIC OVARIAN CARCINOMA

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OBJECTIVES: miRNAs play an important role in the early diagnosis of ovarian cancer, prognosis and chemotherapy sensitivity. Our study was aimed to validate and investigate the expression of miR-423-5p and miR-664b-5p, among the miRNAs found to be important for ovarian cancer etiology in our previous study in the large cohorts of the peripheral blood of familial and sporadic ovarian cancer patients (150 cases) and healthy individuals (100 cases)

MATERIAL&METHODS: Expression analysis was performed using the Real-Time PCR and the results were statistically evaluated with the SPSS v21.0.

RESULTS: When the expression results of ovarian cancer patients were evaluated, it was found that the expression of miR-423-5p increased by 2.35 times and miR-664b-5p expression increased 2.47 times in ovarian cancer patients compared to the healthy control group. In the subgroup of ovarian cancer patients in comparison with the control group, the miR-423-5p expression level was higher in patients both ovarian and breast cancer diagnosis although the level of miR-423-5p was found as decreased in the patients with diagnosed both ovarian and endometrial carcinoma. In the subgroup of ovarian cancer patients in comparison with the control group, the miR-664b-5p expression level was 1.95 fold higher in patients both ovarian and breast cancer diagnosis although the level of miR-664b-5p was found 0.27 fold decreased in the patients with diagnosed both ovarian and endometrial carcinoma.

CONCLUSIONS: The increased expression level of both miR-423-5p and miR-664b-5p suggests that they may be a possible biomarker for ovarian carcinoma. The decreased miR-664b-5p expression might be a biomarker for BRCA associated cancers.

Keywords: Ovarian cancer, miRNA, BRCA mutation

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PP-09

THE INVESTIGATION OF EXPRESSION LEVELS OF MIR-16-5P, MIR-17-5P, MIR-638 IN PATIENTS WITH OVARIAN CANCER

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OBJECTIVES: Ovarian cancer is one of the most lethal gynecological malignancy among women. Many miRNAs have been determined to act as oncogenes, tumor suppressors, and even modulators of cancer stem cells and metastasis. Based on the findings obtained from the microarray study previously, we conclude that the miR-16-5p, miR-17-5p, miR-638 might be important in the etiology of ovarian cancer and, should be validated in large patients cohorts with ovarian cancer and healthy control group. The aim of this study was to validate and determine whether three molecules, miR-16-5p, miR-17-5p, miR-638, are any biomarker in the early diagnosis and prognosis of patients with high-risk ovarian cancer.

MATERIAL&METHODS: In the study, peripheral blood samples of 142 patients with ovarian cancer and 97 healthy controls which were ethnicity, age and gender matched were used. For gene expression analysis, Real-Time PCR methods were performed.

RESULTS: miRNA gene expression levels increased more than 2 times in the patient groups compared to healthy controls and statistically significant ($p < 0.05$). The p value obtained for each miRNA was determined as miR-16-5p, $p < 0.001$; miR-17-5p, $p < 0.001$, miR-638, $p = 0.005$. In addition, we compared the clinical data of patients with miRNAs; There was a significant difference between the smoking status of the patients and the increased expression level of miR-17-5p ($p = 0.007$). In addition, miR-638 was expressed at significantly higher levels in distant metastasis-positive patients than in distant metastasis-negative patients ($p = 0.03$).

CONCLUSIONS: The findings suggest that these miRNAs were associated with metastasis. miR-16-5p, miR-17-5p, and miR-638 may be potential biomarkers to detect ovarian cancer and indicate its progression.

Keywords: Ovarian cancer, miR-16-5p, miR-17-5p, miR-638, Biomarkers

PP-10

INVESTIGATION OF MUTATIONS OF DICER1 AND BAFF GENES IN B-CELL NON-HODGKIN'S LYMPHOMA

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OBJECTIVES: B-cell Non-Hodgkin's lymphoma (B-NHL) is one of the increasing cancer species over the world. DICER1 gene is a member of ribonuclease type III family and it plays a crucial role in biogenesis of miRNAs that regulates the gene expression in posttranscriptional level. In addition, studies have showed that the germline mutations in DICER1 exon 11 may be hazardous because they result in frame shift and exon 25 mutations play role in biogenesis of miRNA. BAFF is expressed by immune system cells such as monocytes, macrophages, dendritic cells, a subtype of T-lymphocytes and B-lymphocytes. Studies, that has been done till now, show high levels BAFF gene expression in malignant B-cells of patients with B-NHL.

MATERIAL&METHODS: In our study, DICER1 c.3473A>G (rs3742330) and BAFF c.-871C>T (rs9514828) single nucleotide polymorphisms in DNA materials, that were isolated from peripheral blood samples of 60 patients that were diagnosed B-cell non-Hodgkin's lymphoma and 30 healthy people matched with patients by age, sex and ethnicity, were examined with PCR-RFLP method.

RESULTS: The detection of mutation existence in exon11 and 25 in DICER1 gene was examined by SANGER sequencing analysis. Chi-Square and Fisher tests were used for evaluation of the results between control and patient groups. No significant results were found between the two groups ($p > 0, 05$).

CONCLUSIONS: In our study, the presence of mutations and polymorphisms related to DICER1 and BAFF genes was not found in patients with B cell non-Hodgkin lymphoma. It is thought that the disease may be related to other factors in the patient group in our study.

Keywords: B cell non-Hodgkin's lymphoma, DICER1, BAFF, Mutations, SNP

PP-11

FREQUENCY OF BRCA1/2 AND OTHER GENE VARIATIONS IN PATIENTS WITH BREAST CANCER IN OUR CENTER

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OBJECTIVES: One of the major risk factor of developing Hereditary Breast and Ovarian Cancer Syndrome (HBOC) is, occurrence mutation in BRCA1 and BRCA2 genes. The risk for breast cancer in the general population is about 12%, but for women with a BRCA1 gene variation it can be between 46%-87%, and between 38%-84% for women with a BRCA2 variation. The risk for ovarian cancer in the general population is about 1%-2%, but about 39%-63% with BRCA1 gene variations and 16.5%-27% with BRCA2 variations. In addition to BRCA1 and BRCA2, other genes, such as TP53, PTEN, CDH1, ATM, CHEK2 or PALB2, can play an important role of developing HBOC Syndrome.

MATERIAL&METHODS: From 1 January 2019 to 1 August 2019, 43 patients aged between 22 and 60, with prediagnosis HBOC, referred to Istanbul Medipol University, Genetic Diagnosis Center (MEDIGEN) to be tested for Breast and Ovarian Cancer Next Generation Sequencing (NGS) test panel which include 23 genes related with HBOC.

RESULTS: All BRCA1 and BRCA2 mutations were classified as pathogenic in 6 patients while other HBOC related gene variants classified as likely pathogenic in one patient and variant of uncertain significance (VUS) in 8 patients.

CONCLUSIONS: In conclusion, the possibility of variation in other genes should be kept in mind in addition to BRCA1 and BRCA2 genes in cases with HBOC. However, more data sharing and functional studies are needed to determine the pathogenicity of variants of unknown clinical significance.

Keywords: Breast cancer, HBOC syndrome, BRCA1 gene, BRCA2 gene

PP-12

ANTI-PROLIFERATIVE EFFECTS OF THE {MESOBUTHUS GIBBOSUS} VENOM PEPTIDES ON HUMAN BREAST CANCER CELL LINES

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OBJECTIVES: Incidence and mortality rates of breast cancer (hBCa) cases are expected to increase approximately %50 by 2040. Although the 5-year survival rate is significantly higher than before, targeted therapy approach remains too specific. Therefore, a drug candidate that can be widely used in hBCa treatment is needed. Animal venoms consist of several biologically active peptides, capable of specifically binding to ion channels and their anti-cancer activity had been shown. Moreover, Kykrk15 channel dysregulation appears in hBCa tissue and cells. In light of all, we aimed to show the anti-proliferative effect of the five most abundant {Mesobuthus gibbosus} Kykrk15 channel blocker peptides on hBCa cell lines.

MATERIAL&METHODS: Venom milking was performed by electrical stimulation. Venom peptides were separated by RP-HPLC. The study was done using the first most prevalent fractions of Kykrk15 channel blockers in scorpion venom, which are known to appear between 20-30 minutes of chromatogram. The effects on cell viability and population of MDA-MB-231 and MCF-7 cell lines were determined with NR and SRB assay, respectively. Morphological evaluation followed PAP staining. Data was analyzed with GraphPad Prism8.

RESULTS: The highest tolerated doses were determined. Subsequently, IC50 of the peptides for 24 hours were determined as 23.980, 51.100, 1.048, 0.362, 0.139 µg/ml for MDA-MB-231 and N/A, N/A, 0.393, 0.005, 0.005 µg/ml for MCF-7. Morphological effects of the peptide were also observed as in consistence with these results.

CONCLUSIONS: The anti-proliferative effects of three Kykrk15channel inhibiting peptides, have been demonstrated on hBCa cell lines. MCF-7 was shown to be more sensitive to the effects of these peptides than MDA-MB-231.

Keywords: venom, peptide, potassium channel, breast cancer

PP-13**A NOVEL SPLICE SITE MUTATION IN PALB2 GENE: A PATIENT WITH TESTICULAR TUMOR**H. Betül Gerik Çelebi¹, Fethi Sırrı Çam²¹Balıkesir Atatürk Hospital, Medical Genetics, Balıkesir, Turkey²Manisa Celal Bayar University, Medical Genetics, Manisa, Turkey

OBJECTIVES: Partner and localizer of BRCA2 (PALB2) gene mapped to the 16p12.2 chromosomal location and may play a role in tumor suppression. Because of this, it is related to Hereditary cancer-predisposing syndrome in Clinvar. PALB2 gene has an important role in homologous recombination repair (HRR) by recruiting BRCA2 and RAD51 to DNA breaks.

MATERIAL&METHODS: DNA was isolated from blood with standard protocols. Trusight one sequencing was applied in a patient with testicular tumor and Sanger Sequencing was performed on patient with right breast mass (Breast Imaging Reporting and Data System score of 2) and two healthy individuals. Study of other living cancer patients was planned.

RESULTS: A 36-year-old male patient who was treated for testicular tumor. When the family history was questioned, it was learned that the patient had relatives with thyroid cancer, larynx cancer, prostate cancer, breast cancer, colon cancer, lung cancer, stomach cancer and leukemia. Trusight one sequence analysis was revealed a heterozygous mutation in PALB2 gene NM_024675.3: c.2587-1G>C; (rs761214886). While we examined some members of the family for the mutation, patient with right breast mass was found heterozygous and two healthy individuals was not present.

CONCLUSIONS: In this study a novel PALB2 mutation was reported. According to in silico analysis softwares this mutation affect splicing and therefore it could be the cause of cancer. Studies on the role of PALB2 gene in cancer development are ongoing. Changes in the PALB2 gene may play a role in the emergence of different types of cancer other than breast cancer.

Keywords: novel, PALB2, testicular tumor

PP-14**HIGH EXPRESSION LEVEL OF MIR-1260 FAMILY IN THE PERIPHERAL BLOOD OF PATIENTS WITH OVARIAN CANCER**Arash Adamnejad Ghafour¹, Mukaddes Avsar¹, Seref Bugra Tuncer¹, Busra Kurt¹, Seda Kilic¹, Ozge Sukruoglu Erdogan¹, Gozde Kuru¹, Betül Celik¹, Demet Akdeniz Odemis¹, Pınar Saip², Hülya Yazici¹¹Department of Cancer Genetics, Istanbul Faculty of Medicine, Oncology Institute, Istanbul University, Istanbul, Turkey.²Department of Medical Oncology, Istanbul Faculty of Medicine, Oncology Institute, Istanbul University, Istanbul, Turkey

OBJECTIVES: According to TÜİK-Turkish statistics, every year around 2790 OvarianCancer cases have been reported in Turkey. In order to have effective treatment of OvarianCancer as well as to follow the treatment process and to diagnose in early stage, there is need for disease-specific and sensitive biomarkers. This study aims to determine whether miR1260a and miR1260b molecules can be non-invasive biomarkers for sporadic and familial OvarianCancer cases compared with healthy controls.

MATERIAL&METHODS: The expression levels of miR1260a and miR1260b were investigated in 150 patients with familial and sporadic OvarianCancer, and 100 healthy controls matched with patients for age, gender, ethnicity.

RESULTS: It was seen that there was a statistically significant difference (p = 0.000) for expression levels of both miRNAs between the ovarian cancer patients and the healthy control group. According to healthy controls, it was found that the expression of miR-1260a and miR-1260b in OvarianCancer patients increased between 16.1-43.21 fold. STRING analysis was performed to understand the interactions of these molecules with other genes. It was found that miR-1260a has relationship with the ribosomal protein family known to have effect on the cellular stage of translation and miR-1260b is associated with the proteins CHEK2 and CDK4.

CONCLUSIONS: The significant expression of miR-1260 and miR-1260b in peripheral blood lymphocytes of patients with ovarian cancer compared to healthy controls was shown first. The miR-1260 and miR-1260b molecules may be responsible for the etiology of ovarian cancer. It is thought that miR1260 and miR1260b molecules may be used as non-invasive biomarkers for diagnosis and prognosis of OvarianCancer.

Keywords: Ovarian cancer, miR-1260 family, prognosis, diagnosis, Biomarkers

PP-15**DEVELOPMENT OF A COLON PDX MODEL TO ANALYZE THE EFFECT OF A POINT MUTATION IN METABOLISM**Esra Bulut Atalay¹, Ender Ellidokuz², Ralph Meuwissen³, Hülya Ayar Kayalı^{3,4}¹Dokuz Eylül University, İzmir International Biomedicine And Genome Institute, İzmir²Dokuz Eylül Research Hospital, Department Of Gastroenterology, İzmir, Turkey³İzmir Biomedicine And Genome Center, İzmir, Turkey⁴Dokuz Eylül University, Department Of Chemistry, İzmir, Turkey

OBJECTIVES: The aim of this study was to develop a patient-based xenograft (PDX) model by transplanting biopsy samples from colon cancer patients into NOD-SCID (non-congenital diabetic severe combined immunodeficiency) mice by heterotopic methods.

MATERIAL&METHODS: Experiments were performed after receiving patient informed consent and approval from Dokuz Eylül University Clinical Research Ethics Committee and İzmir Biomedicine and Genom Center Animal Experiments Ethics Local Committee. Human colon biopsy samples (5-20 mm³) were excised from 6 patients during colonoscopy from Dokuz Eylül Research and Application Hospital. Immediately, biopsy samples divided into small pieces were suspended in Matrigel (1: 1) and injected into the subcutaneous layer on the backs of NOD-SCID mice. When the tumor size reached above 1 cm, the tumor was surgically removed.

RESULTS: The tumor has grown successfully within 9 weeks after transplantation. Tumor tissue removed from the mouse will be used for RNA-seq, Western Blot, and qPCR assays. Thus, the effects of target point mutation on metabolism will be investigated in detail.

CONCLUSIONS: With PDX models, tissue samples taken in small amounts from human are amplified to a larger tumor mass. Furthermore, since human tissue is used, the tumor tissue obtained from the mouse is very similar to that of human in molecular character. This will provide more reliable data for point mutation studies.

Keywords: Colon Cancer, NOD-SCID Mice, PDX model, Point Mutation.