Saffari S[1*], Iranpour M[2], Ghaedi H[2], Omrani MD[2]

Islamic azad university tehran north branch
sanasaffari@gmail.com

Background and objective: Diabetes mellitus (DM) is metabolic syndrome with high level of fasting blood sugar (FBS). Type 2 diabetes mellitus (T2DM) has been started in late age .The association between long non-coding RNAs (LncRNAs) and human diseases has been showed in many studies. Two LncRNA genes (ANRIL & PVT1) have been played an important roles in metabolic pathway and for this reason the aim of this study was to evaluate the expression of these two genes in peripheral blood sample of diabetic patients according to clinical and paraclinical data.
Materials and methods: 75 peripheral blood samples of T2DM patients and 75 peripheral blood samples of non-diabetic people has been collected in CBC tubes with EDTA. Then total RNA was extracted and cDNA was synthesized. The expression of two genes (PVT1 & ANRIL) in T2DM patients compared to non-diabetic people was evaluated by Real-time PCR assay.
Result: The expression of both genes examined in this study was significantly increased in T2DM patients compared to non-diabetic people.
Discussion and conclusion: Due to significant overexpression of studied genes, they may be involved in process of T2DM. Also it is possible to use them as candidate genes for the diagnosis of diabetes pathogenesis.
Keywords: ANRIL, PVT1, LncRNA, Type 2 diabetes mellitus

P-319: The study two SNP of GRIN1 gene associated with addiction to heroin and methamphetamine

sahraei M[1], Hamta A[2]

1. Department of Biology, Faculty of Basic Sciences, Arak University, Arak, Iran
2. Department of Faculty of Sciences. Arak Univ.Arak.IRAN.
sahraeimaryam@gmail.com

Introduction: Glutamate increases the probability of drug relapse. N-methyl-D-aspartate receptor (GRIN1) is a glutamate ionotropic receptor and is found in mammals' brain. This study sought to investigate the association between rs11146020, rs1126442 and addiction to heroin and methamphetamine in Iranian male.
Materials and methods: 90 males addicted to heroin and methamphetamine and 100 healthy male were the participants of the study. Genomic DNA extracted from the blood, and then PCR-RFLP and T-ARMS PCR were respectively used to determine the rs1126442 and rs11146020 polymorphism genotype.
Results: Two SNP studied in the development of heroin and methamphetamine addiction which, in the study is not a contributing factor, because was no association between rs1126442 and rs11146020 polymorphism. The genotype frequencies of CC, GC and GG at the rs 11246020 polymorphism were 57%, 30%, and 3% in the patient, respectively. The genotype frequencies of AA, GA and GG at the rs1126442 were respectively 52%, 28%, and 10% in the patient. The results obtained from the analysis of rs1126442 and rs 11146020 polymorphism showed a significant association between the two polymorphisms with marital status and educational level and showed no association with job status.
Conclusion: The results of the study indicated that neither of the two polymorphism in GRIN1 gene had not showed significant association in the control samples and addicted person.
Keywords: rs1126442, rs11146020, GRIN1, heroin, methamphetamine

P-320: Bioinformatics and experimental analysis of lncRNAs associated with prostate cancer

Sajadi R[1], safari M[2], Tabatabaiefar MA[3]

1. MSc. Student of Human Genetics, Department of Genetics and Molecular Biology, School of medicine, Isfahan University of Medical Sciences, Isfahan, Iran
2. PhD Student of Medical Genetics, Department of Medical Genetics, Faculty of medicine, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Genetics and Molecular Biology, School of medicine, Isfahan University of Medical Sciences, Isfahan, Iran
Roshan.s_89@yahoo.com

Introduction: Prostate cancer is the second leading cause of cancer death in men. Clinicians use clinical criteria as well as PSA to detect prostate cancer. Currently based on clinical stage, serum level of PSA and histological grade are decided to guide treatment. For personalized medicine approach, it is necessary to define collection of molecular lesions in prostate cancer and determine the effect of these on disease aggressiveness and effective therapies against individual molecular lesions. Recently, increasing evidence has suggested that a number of lncRNAs have important and diverse functions. Therefore, it is no surprise that lncRNAs are becoming a large class of novel molecules for disease diagnosis and therapy. the purpose of this study was to predict lncRNAs associated with prostate cancer and also Evaluating their expression experimentally.
Materials and method: We predicted several of lncRNAs associated with prostate cancer such as ZNF518A, ZNRD1-AS1, LINC00641, JPX, LINC00094,..
This prediction result from different method based on the genes, miRNAs and pathways interaction databases and bioinformatics analysis. We evaluated expression of two example of them in different cell line such as DU145, LNCaP, PC3 using qRT-PCR.
Result: Expression study indicated the subset of lncRNAs that were differentially expressed in the cell lines.
Discussion and conclusion: Due to the difference in expression in different cell lines, we can conclude that each of these markers may have different roles in the prostate tumorgenesis mechanism.
Keywords: prostate cancer, long non coding RNA, bioinformatics analysis

P-321: Cytotoxic Effects of Auraptene in Mouse Colon Adenocarcinoma Cells

Salary H[1], M. Matin M[1,2*], B. Rassouli F[1,2*], Iranshahi M[3]

1. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2. Cell and Molecular Biotechnology Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Pharmacognosy and Biotechnology, Biotechnology Research Center, Faculty of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
behnam3260@um.ac.ir

Colon adenocarcinoma is a growing public health concern with increasing rate of incidence in developing countries. Al-

though screening methods and therapeutic options have been improved, patients with colon cancer still suffer from disease recurrence. Auraptene (AUR) is the most abundant prenyloxycoumarin identified in nature with wide range of pharmacological properties. Beside antioxidantive, antigenotoxic and antimicrobial effects, AUR induces cancer chemopreventive effects in animal models. Since research in the field of colon cancer is focused on introduction of more effective anticancer agents, the goal of present study was to determine cytotoxic effects of AUR in mouse colon adenocarcinoma cells (CT26 cell line). In this regard, AUR was first synthesized by a reaction between 7-hydroxycoumarin and transgeranyl bromide, its purification was carried out by column chromatography, and its structure was confirmed by nuclear magnetic resonance spectroscopy. Then, CT26 cells, as well as mouse normal fibroblasts (NIH/3T3 cell line), were treated with increasing concentrations of AUR for 24, 48 and 72 hours, and viability of cells was evaluated by MTT assay. Result of this study indicated that the IC50 values of AUR in CT26 and NIH/3T3 cells were >30 Âµg/ml and<20 Âµg/ml, respectively. To determine whether AUR has synergic effects with ionizing radiation, our plan is to examine viability of CT26 cells upon AUR treatment (in concentrations less than its IC50) and radiation exposure. In case AUR improves efficacy of radiotherapy, it could be considered as an effective coumarin derivative for future in vivo experiments.

Keywords: Colon adenocarcinoma, Auraptene, Cytotoxicity

P-322: Premature ovarian failure (POI) in correlation to FRAXA premutation: a study on 41 women in Saram Hospital

Samadpour S[1], Abdi H[1], Rojhannezhad M[2], Rezaei s[1], Pouladi A[1,3], Salimi M[1], Younesi B[1], karimian M[1], Karimzad Hagh J[1]

1. Sarem medical genetics department, Sarem women hospital, Tehran, Iran
2. molecular genetics department , Tarbiat Modares University, Tehran, Iran
sanazsamadpoor@yahoo.com

Sarem cell Research center, Sarem medical genetics department, Sarem woman hospital, Tehran, Iran3Fragile X-associated primary ovarian insufficiency (FXPOI) is one of the fragile X-associated disorders. Women with the fragile-X premutation are at risk for primary ovarian insufficiency (POI), which includes cessation of menses prior to the age of 40 years. For unknown reasons, the premutation leads to the overproduction of abnormal FMR1 mRNA that contains the expanded repeat region. Women with POI not only experience loss of normal fertility but are also at increased risk for osteoporosis and cardiac disease and have higher rates of mortality. Thus, women who have a fragile X premutation face the increased health risks related to POI and FXTAS as well as the risk that their children will inherit the unstable repeat as either the pre- or full mutation. About 1% of women in the general population experience POI. In comparison, approximately 20% of women who are carriers of fragile X syndrome experience POI. A total of 41 women <42 years old affected by premature ovarian insufficiency were evaluated for fragile X (FRAXA) permutation in Sarem Women Hospital during year 1396. The CGG sizing was performed using the Asuragen (Austin, TX) AmplideX FMR1 PCR Kit. The FRAXA premutation was only detected in one out of 41, indicating of only about 2.5% of tested women with POI. However, the results of our small tested group donâ€™t consist the results of published literature. In a big cohort study the further testing of POI women must be performed and collated.

Keywords: FXPOI, POI, POF, Premutation, FRXA, FMR1, Asuragen

P-323: The relationship between IL-10 and TNF-α gene polymorphism and therapy resistance to platelet transfusion and recombinant factor VII administration in Glanzmann Thrombasthenia

Sarani H[1], Keramati MR[1], Hassanian SM[2] , Avan A[3], Sohrabi T[1], zafari Z[1], Moradi Zarmehri A[4], Naderi M[5]

1. Cancer molecular pathology research center, Mashhad University of Medical Sciences, Mashhad, Iran.
2. Metabolic Syndrome Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
3. Cancer Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
4. Mashhad University of Medical Sciences, Mashhad, Iran.
5. Genetic Research Center in Non-Communicable Disease, Zahedan University of Medical Sciences, Zahedan, Iran.
hosna.sarani@gmail.com

Background: Resistance to platelet and recombinant factor VII administration in patients with Glanzmann Thrombasthenia is a major problem causing bleeding, morbidity and mortality. There is no data on the risk factors for therapeutic resistance in Glanzmann Thrombasthenia. IL-10 and TNF-α play an important role in immune responses. Recent studies have shown that some of cytokine gene polymorphisms can produce different level of cytokines, altering severity of immune responses and therefore create therapeutic resistance. In this study, probably for the first time, the relationship between immune regulator genes in the development of resistance to therapy in Glanzmann Thrombasthenia patients is investigated.
Method: this study was performed in Mashhad University of Medical Sciences in collaborative with Thalassemia and Hemophilia Center in Zahedan, Iran in 2017. Blood samples were collected from 15 therapy resistant Glanzmann Thrombasthenia patients and 15 therapy non-resistant patients as a control group. DNA was extracted and IL-10 and TNF-? gene polymorphism was analyzed by Taqman Realtime PCR Based Method. Results were analyzed by SPSS (V 11.5).
Results: all patients in therapy resistant group had the IL-10 polymorphism at -1082 position (rs1800896) with G/G genotype that was significantly more frequent than the non- resistant group. However, we did not find any difference in the frequencies of TNF-? polymorphisms between two groups.
Conclusion: IL-10 gene polymorphism, was a risk factor for inhibitor formation and therapeutic resistance in Glanzmann Thrombasthenia patients. However, TNF-? polymorphism was not associated with the development of therapeutic re

Keywords: Glanzmann, Thrombasthenia, therapy resistance, recombinant factor VII, IL-10, TNF-α

P-324: Association of FBXO40 rs527341033 Polymorphism and Susceptibility to Autism in Northern Iran

Sarkar Lotfabadi A*, Ramezani S, Mashayekhi F, mirzanejad L, Shahangian S Sh, Bidabadi E

Department of biology, Faculty of Sciences, University of Guilan, Rasht, Iran
alireza96lotfabadi@gmail.com