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of FOXP3 and CTLA4 genes.
Conclusion: The Results of our study showed that FOXP3 and CTLA4 genes promoting in AITD and T1D patients and NFATC2 regulating expression of mentioned genes.
Keywords: Type 1 Diabetes, Autoimmune Thyroid Disease, Gene Expression, Bioinformatics Analysis and Transcription Factor

P-58: In silico study of anti-CCHFV effect of lactoferrin from different origin

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Crimean-Congo haemorrhagic fever (CCHF) is a mortal viral infection. Human beings become infected through tick bites, or by contact with blood or tissues from viraemic livestock. Recent studies suggest that ribavirin is effective against CCHF, although the efficaciousness of ribavirin in the treatment of CCHF has not yet been demonstrated conclusively. The protective effects of lactoferrin (LF) against common viral infections have been demonstrated in several studies. This glycoprotein is one of the innate immune system components with broad range of antimicrobial activates comprising antiviral, antibacterial, antifungal and anti-cancer actions. LF prevents entry of virus in the host cell, either by blocking cellular receptors, or by direct binding to the virus protein. A comprehensive study comparing anti-CCHFV properties of LFs derived from different origins has not been yet conducted. In the current study, in silico evaluation of antiviral effects of LF from different species against CCHFV was evaluated by a protein-protein docking approach. The crystal structures of human, horse, cattle, goat, buffalo and camel LF were retrieved from the uniprot, and the protein structure of sheep and zebo cattle LF were predicted. The crystal structures of CCHF virus envelopment polyprotein Gn and Gc were retrieved from the protein data bank, then the pdb files prepared for docking calculation. Autodock 4.2.6 was used for protein docking. Results showed that the N- and C-lobe fragments and the full-length of LF had effective anti CCHFV activities. Buffalo LF showed the highest binding energy among studied species and the lowest energy belonged to cattle LF.
Keywords: Lactoferrin, antivirus, in silico, CCHF, buffalo

P-59: Identification of differentially expressed miRNAs and RNAs by using The Cancer Genome Atlas (TCGA) miRNA set

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In order to extraction of the differentially expressed genes (DEGs), several data set of the colorectal polyp and non-polyp sample miRNA expressions were downloaded from TCGA database. In total, 379 of 1883 miRNAs were differentially expressed in 459 Polyp and 5 non-polyp samples compared with normal samples.
The raw data were analysis by statistical R software. The data had been normalized by Deseq package and PCA plot had drawn also by Deseq package. Finally by machine learning differentially expressed microRNAs between polyps and non-polyps has been done. After analysis data, top 10 of microRNAs had best p-value were chosen for pathway analysis.
Pathway analysis was done by DIANA software. Results from analysis these pathways show that microRNAs up regulated are more involved to progressing of polyps to colorectal cancer and microRNAs down regulated not to progressing of polyps to colorectal cancer.
Keywords: bioinformatics, polyp, colorectal cancer, biomarker

P-60: The Possible Role of Long Noncoding RNA as Novel Player in Type 2 Diabetes

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Type 2 diabetes mellitus (T2DM) is a chronic disease with increasing rate of prevalence in the world that causes substantial public health and economic burden.
Although more than 20 genetic susceptibility loci have been reported for type 2 diabetes (T2D), most reported variants have small to moderate effects and account for only a small proportion of the heritability of T2D, suggesting that the majority of inter-person genetic variation in this disease remains to be determined, So finding genetic variants plays an important role and provides a lot of data. Since non coding region is likely to have a significant effect on pathogenicity and susceptibility of diabetic and cardiovascular diseases, then it is useful to study the involved lncRNAs.
Materials and methods: Analysis of RNA-Seq data has revealed there are three lncRNAs (PVT1, H19, CDKN2B-AS1) that are associated with diabetes. Among these lncRNAs, PVT1 was selected and assessment its functional and regulatory role was done by bioinformatics.
Conclusion: PVT1 bioinformatics analysis has shown there is association between variants (rs2720709, A>G) in the plasmacytoma variant translocation 1 gene (PVT1) and end-stage renal disease (ESRD) attributed to both type 1 and type 2 diabetes and the SNP has key role in both pathogenicity and gene regulation. PVT1 fullfills its role by modulating the function of some transcription factors such as c-Myc, P53, YY1.
Keywords: Type 2 diabetes mellitus (T2DM), lncRNAs, RNA-Seq

P-61: In silico analysis targeting of the genes involved in Notch signaling pathway by hsa-miR-3163

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