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Day 1

Saturday 28 Jan 2017

15:00 – 16:30

Hall A		
Cancer Surveillance		
Chair: Dr. Gholamreza Roshandel, **Co-Chairs:** Dr. Seyyed Mahmoud Tara, Dr. Kazem Zendehdel, Dr. Abbas Rezaeianzaeh, Dr. Roya Dolatkhah, Dr. Azin Nahvijou,		
15:00 – 15:20	Azin Nahvijou	*"History & Challenges of PBCR in Iran"*
15:20 – 15:40	Gholamreza Roshandel	*"The National Cancer Registry Program of Iran"*
15:40 – 16:00	Abbas Rezaieianzadeh	*"Cancer incidence in Fars Province in 1394: A Population-based Approach"*
16:00 – 16:20	Roya Dolatkhah	*" East Azerbaijan Population Based Cancer Registry during 2015-2016: Preliminary Report."*
16:20 – 16:40	Seyyed Mahmoud Tara	*"Electronic Medical Records and Opportunities for Improvement of PBCR in Iran"*
16:40 - 17:00	Azam Majidi	*"Cancer Registry in West Asia, Opportunities and Future Directions"*

Hall B		
Food, Nutrition and Cancer		
Chair: Dr. Ahmad Esmaillzadeh, **Co-Chairs:** Dr. Leila Azadbakht, Dr. Rasoul Dinarvand, Dr. Abolghasem Djazayeri, Dr. Hedayat Hoseini, Dr. Hamed Pouraram		
15:00 – 15:15	Ahmad Ismailzadeh	*"Nutritional Factors Determining Gastric Cancer in Iran"*
15:15 – 15:30	Leila Azadbakht	*"Dietary Acid load and Cancers"*
15:30 – 15:45	Azita Hekmatdoost	*"Nuts Consumption and the Risk of Gastric Cancers"*
15:45 – 16:00	Hamed Pouraram	*"Exposure to Pesticides and Risk of Cancers "*
16:00 – 16:15	Hossein Imani	*"The Association between Supplement Intake & Risk of Cancer"*

Methylation Status of E6 Gene Promoter in High-Risk and Low-Risk Papilloma Viruses

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Background: Cervical cancer is one of the most important causes of death in women worldwide. Methylation of the cytosine carbon 5 is one of the most important epigenetic mechanisms for gene expression control among prokaryotes. Methylation status of DNA may be evaluated using the BSP technique, in which the DNA sample treated with sodium bisulfate is subjected to PCR and then sequencing. DNA methylation results in changes in conformation of chromatin and chromatin-like structures, leading to gene expression suppression in papilloma virus type 16 which is a major viral factors for cervical cancer. As changes in methylation pattern cause disorders, it was hypothesized that samples of high- and low-risk papilloma viruses may differ in their genome methylation, and thus it may be possible to determine their methylation pattern.

Methods: In this study, we used the MethPrimer and Methyl Primer Express v1.0 software to prepare primers for the E6 gene promoter of types 12, 16, and 18, as well as the HeLa cell as positive control. Methylation status was assessed through BSP technique.

Results: The product of PCR was run on agarose gel. After confirmation, the gel was cut and clones, and the cloned segments were sequenced for assessing the cytosine methylation status of the gene promoter. We observed different promoter methylation patterns between high- and low-risk papilloma viruses.

Conclusion: Considering the difference in methylation pattern of these two types, it is possible that the difference in methylation pattern, and ultimately gene expression, may be the cause of cervical cancer related to high-risk papilloma virus.

Keywords: methylation, cancer, papilloma virus, PCR

High Throughput Design, Synthesis, and *ex vivo* and *in vivo* Evaluation of Anticarcinogenic Properties of New Drug-like Compounds using Novel Chemoinformatic Methods

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Background: According to previous studies, cancer constitutes the second most common cause of mortality in the world, claiming more than 11 million lives per year. It is estimated that cancer-related deaths will exceed an annual 16 million by the year 2020. Similarly, reports of the 9 million cancer-related deaths in 2015 which will rise to approximately 11.4 million in 2030 indicate the growing rate of cancer on the global scale.

As current therapies for cancer often cause collateral damage and death to normal cells, extensive research is being conducted to discover and introduce new anti-cancer compounds or optimize compounds currently used in chemotherapy with enhanced anticarcinogenic properties and diminished adverse effects, using novel bioinformatics and chemoinformatics methods.

Methods: Methods based on virtual screening (VS) using pharmacophore similarity and targeting strategies in addition to *de novo* ligand synthesis alongside docking-based synthesis are among the most commonly utilized *in silico* techniques which are employed in the present study.

Based on the items mentioned above, the present study aims to create a database of cellular and molecular targets involved in cancer development and progression, *de novo*

design of novel compounds with anticarcinogenic properties using this database, synthesis of the selected compounds designed, and eventually, *in vitro* and *in vivo* evaluation of the new synthesized compounds.

Finally, it may be anticipated that target *in silico* design of new anticancer compounds based on cellular and molecular targets involved in tumor initiation and progression, and synthesizing compounds selected from the designed substances will be an effective step towards providing new drug-like compounds with maximal anticarcinogenic properties and minimal side effects, and introduce a promising hope for efficient pharmaceutical treatment of cancers.

In this step, we have created two databases of cellular and molecular targets, with identified crystallography structures, involved in development and progression of malignancies, as well as a database of ligands and chemical and pharmaceutical structures related to these cellular/molecular targets, and used docking screening to study the interactions of the proteins in the database of cellular/molecular targets with ligands and chemical/pharmaceutical structures in order to evaluate their anticancer properties with bioassay tests.

Keywords: cancer, chemoinformatics, bioinformatics, drug design

Developing Recombinant Single Chain Antibodies against Epitopes of ErbB2 and ErbB3 Receptors for Controlling and Treating Breast Cancer

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Background: The ErbB family of receptors play a key role in growth and expansion of different types of cancer. Developing therapeutic methods for breast cancer based on identifying mechanisms of gene expression and regulation, and function of signaling pathways involved in carcinogenesis has resulted in Background of the recombinant antibody Trastuzumab (Herceptin) against ErbB2. Nevertheless, tumoral cells use different methods such as signal transmission via other components of these receptors, to counter the effects of these drugs and develop resistance against them. Therefore, this study aims to break the biologic resistance of breast cancer cells, produce monoclonal antibodies, and simultaneously block signal transmission via ErbB2 and ErbB3 receptors.

Methods: In this study, after producing stable ErbB2 and ErbB3 and evaluating the baseline expression of these receptors on the surface of some popular cell lines in breast cancer, and with help of genetic engineering on the surface of VERO cell line, monoclonal antibodies against ErbB2 and ErbB3 were produced using Tomlinson commercial library and the Subtractive phage display technique. The efficiency of the produced antibodies was evaluated using cell proliferation inhibition and Phage-ELISA techniques.

Results: With cloning, ErbB2 and ErbB3 receptors were stably expressed on the surface of VERO cells. Panning with the Tomlinson phage library on the surface of the engineered VERO cells indicated that antibodies obtained in the third cycle of the Fingerprinting test have a more homogeneous pattern as well as greater affinity for the receptor on the Phage-ELISA test. The selected clones were used for production and purification of phage-free antibodies and we produced these antibodies. These clones have the specific ability to bind to SKBR3.

Conclusion: The findings indicate a suppression of cancerous cell growth when exposed to the produced antibodies. The effect of simultaneous inhibition of signal transmission via ErbB2 and ErbB3 receptors by the antibodies produced in this study indicated that these antibodies may be effective in breaking the resistance of breast cancer cells against HER2 receptor blocker (Trastuzumab).

Keywords: breast cancer, ErbB2, ErbB3, phage display, stable cell line

Docetaxel Differentially Alters the Expression Level of mir-21 and Let-7a in Gastric Cancer Cell Lines

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Background: MicroRNAs are noncoding RNAs which play critical roles in carcinogenesis. Mir-21 and Let-7a are oncomir and tumor suppressor miRNAs, respectively which are involved in tumorigenesis of gastric cancer. Here, we aimed to study the alterations in expression of these miRNAs