Short Talk – 01

Breaking Barriers in Cancer Treatment: Unleashing the Power of Drug Repurposing

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Cancer is a major global cause of death, with a projected 29 million diagnoses by 2040. Despite advancements in technology, the introduction of new drugs into clinical practice is experiencing significant delays. Additional clinical assessment is essential for determining dosage, ensuring safety, and evaluating effectiveness. Developing new cancer therapies traditionally requires a lengthy process including regulatory requirements, approval procedures, and commercial considerations. Thus, a promising alternative approach called “drug repurposing” has emerged to tackle this challenge. It involves discovering new therapeutic uses for known compounds or identifying novel targets for existing drugs. Leveraging existing knowledge provides improved efficiency, reduced time and financial investment, and a lower risk of failure.

Viewing diseases as networks of interconnected molecular pathways have paved the way for exploring the combined effects of multiple drugs. Combining repurposed drugs with chemotherapeutic agents has shown intriguing results, particularly in cases where standard anti-cancer monotherapy has limitations in terms of safety and tolerability. Drug combinations target various oncologic pathways simultaneously, leading to enhanced therapeutic efficacy and decreased likelihood of drug resistance development. The synergy achieved by combining drugs with different targets or signaling pathways allows for lower drug concentrations, further optimizing treatment outcomes.

This study discusses the significance of drug repurposing in cancer treatment and highlights recent advancements. We provide a comprehensive perspective on the role of drug repurposing in addressing the challenges of cancer therapy. Ultimately, drug repurposing holds great promise for improving patient outcomes and accelerating the success rate of drug discovery and development in oncology.

Keywords: Drug discovery and development, drug repurposing, combinatory therapy, synergism, cancer

Short Talk – 02

An Overview of Tumor Agnostic Therapies Through the Hippo Signaling Pathway

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Tumor agnostic therapy means drug therapy that can be used in the treatment of all cancers, regardless of the type of tissue in which the cancer develops. This treatment is used when the tumor has a specific molecular alteration targeted by the drug or when the drug is predicted to work. If the cancer type has the specific molecular alteration that the drug targets, tumor agnostic therapy will work. The Hippo signaling pathway is evolutionarily conserved and is generally described as a pathway that regulates and controls growth. In most studies on the Hippo signaling pathway, it has been reported that the main task of this pathway is the control of organ development, stem cell function, regeneration and tumor suppression. However, some studies report that this pathway may also play a role in tumor initiation and progression in different types of cancer. Targeting the YAP1 protein, one of the most important components of this pathway, has recently been shown as an important treatment option. Today, drug repurposing through FDA-approved molecules and virtual activity scanning of libraries containing non-FDA-approved commercial molecules/compounds are frequently preferred methods. There are very few studies in the literature within the scope of the Hippo signaling pathway and tumor agnostic approach. As it had been reported that YAP1 expression can be used as a tumor agnostic predictive biomarker, in this presentation, a novel compound targeting the Hippo signaling pathway YAP1 protein in different cancer types and how these studies will progress in the future will be discussed.

Short Talk – 03

Anti-Cancer and Anti-Stemness Action of Nonsteroidal Anti-Inflammatory Agents: A Special Focus on Hepatocellular Carcinoma

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Inflammation is strongly linked to cancer and plays a crucial role in the development and progression of tumors. Chronic inflammation is characterized by the infiltration of certain immune cells, tissue damage, fibrosis, elevated angiogenesis and is also linked to genomic damage, suppression of programmed cell death (apoptosis). Although nonsteroidal anti-inflammatory drugs (NSAIDs) have been used for many years in the treatment of acute and chronic conditions characterized by pain and inflammation, recent clinical investigations have shed light on the therapeutic potential of NSAIDs in cancer treatment. Numerous preclinical and clinical studies have documented that NSAIDs can have anti-cancer activities in many cancer types. Moreover, combining chemotherapeutic drugs with NSAIDs can greatly improve prognosis of patients and may be beneficial as adjuvants to conventional therapeutic approaches.

Liver cancer, in particular hepatocellular carcinoma (HCC) is one of the leading causes of cancer-related mortality worldwide and poses a significant challenge in terms of therapeutic options due to diagnosis at advanced stage, tumor heterogeneity and activation of resistance mechanisms. The vast majority of HCCs develop as a result of chronic inflammation where inflammation-mediated events such as production and release of cytokines, reactive oxygen species and the activation of inflammatory pathways takes place. This study focuses on current literature emphasizing the potential of NSAIDs as anti-cancer agents, and their mechanism of action with a special focus on HCC. Moreover, we discuss recent findings from our laboratory on novel and well-known NSAIDs against HCC cells and liver cancer stem cells.

Keywords: Nonsteroidal anti-inflammatory drugs (NSAIDs), hepatocellular carcinoma (HCC), liver cancer stem cells

Short Talk – 04

The Role and Importance of Biobanks Dedicated to Cancer Research

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The development of efficient therapies against cancer necessitates better understanding of cancer molecular mechanisms and quicker translation of laboratory findings to clinical implications. To facilitate an effective cancer research; tumor tissue samples, blood and other body fluids are greatly required to be collected and stored accordingly. Biobanks, therefore, are at the cornerstone of cancer research since they allow obtaining a sufficient number of high quality samples, archiving them, allow re-usability of the sample without re-sampling over the years. The importance of biobanks in cancer research continuously growing since they provide high quality annotated bio-sample which can be used for biomarker discovery and validity, drug screening, identifying molecular mechanisms. Biobanks are also very critical for personalized medicine because biobanks and omics technology are very closely related. Biobanks assures harmonization to provide interoperability, so that, larger research projects with sufficient number of samples (even for rare cancers) collected from different biobanks can be conducted and duplications in research is reduced. The multidisciplinary work between different steakholders requires the adoption of common standards for each biobanking step. Biobanks are very important for facilitating logistics and infrastructure where biological samples and associated information are collected, processed, stored with quality assurance. Since biobanks works with human samples; ethical, legal and social (ELSI) issues are major topics to be considered. To sum up, the aim of this short talk is to understand the biobanking role in cancer research, discuss biobanking processes and challenges, indicate implications to overcome challenges and to long term sustainability in oncology research.

Keywords: Biobank, Bio-sample, Bio-repository, Cancer research, personalized medicine

Short Talk – 05

Cancer Resistance to therapy: Is there a way out?

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Introduction and Aim: Cancer hallmarks are indisputable and the key question here is; how malignant-cells acquire and coordinate together numerous modifications for a unique purpose of sustained growth? If the philosophy of cancerous behavior is not grasped; it will be difficult to find the real therapeutic target(s) needed to stop cancer growth. In clinics today, cancer resistance to different treatment modalities has been linked to a subpopulation of cells named cancer stem-cells (CSCs).

Materials and Methods: This work is based on the analysis of cancer hallmarks looking for insights as to the nature of cancer stem-cells. Two questions remain to be answered: (1) Are biomarkers currently used to identify CSCs proper to cancer stem-cells themselves or shared with other cell types? (2) How CSCs could rise?

Results: To efficiently target cancer stem-cells; we need to understand: (i) What shapes their molecular identity; (ii) This means we need to find biomarkers proper to cancer stem-cells that are not shared with other cell types; (iii) This leads to understand the molecular event that gives rise to cancer stem-cells. The protein model for cancer genesis may lead us into that direction.

Conclusion: There should be a clear-cut difference between cancer and non-cancer cells. Genetic instability is a hallmark of cancer therefore using various combinations of DNA mutation-based biomarkers as targets for cancer therapy has not resulted in cancer cure as patients hope for. The protein model offers a fresh perspective on the nature of CSCs and could pave the way for innovative cancer treatment and prevention.

Keywords: cancer hallmarks, cancer resistance, cancer stem-cells, cancer biomarkers, protein model for cancer genesis.

Short Talk – 06

How to Target Tumor Heterogeneity to Overcome Drug Resistance?

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With the development of targeted and personalized medicine, the genetic heterogeneity observed in cancer cells has gained importance especially in terms of therapy resistance and disease recurrence. Tumors are formed as a result of mutations in a single gene in a single progenitor cell. Subsequent mutations and waves of clonal expansion in the offspring of this cell lead to the development of daughter cells with a cancer-specific growth advantage. Genetic instability, which allows for sequential selection of more aggressive subspecies and is most easily acquired cytogenetically, leads to highly individualized human malignancies, karyotypic and biological. Thus, each patient's cancer may require specific individual treatment, and even this treatment may not result in the emergence of a treatment-resistant variant subtype.

Tumors may spontaneously become drug resistant or develop resistance to chemotherapy during treatment. Acquired resistance is one of the biggest obstacles to anticancer therapies. Certain mutations that occur in clones within a heterogeneous population activates drug resistance mechanisms by leading to various results such as inhibited drug transport, target change, and metabolic changes. It has been determined that resistance to chemotherapy causes treatment failure in more than 90% of patients with metastatic cancer, and it is thought that resistant micrometastatic tumor cells may reduce the effectiveness of chemotherapy in adjuvant therapy. In the future, it is anticipated that the power to predict tumor and patient response to cytotoxic drugs and to modulate this response with targeted therapies will allow the selection of the best combined therapy for each patient.

Keywords: tumor heterogeneity, drug resistance, anticancer therapy, targeted therapy

Short Talk – 07

Recent Advances in Researching Cancer Types Using 3D Bioprinting

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Introduction and Aim: Cancer is a type of disease of which the incidence is increasing significantly day by day. Pre- and post-clinical research for cancer prevention and treatment continues rapidly. Limitations in in vivo and in vitro methods and ethical concerns have led researchers to find alternative methods for cancer modelling. The printing of various human tissues using three-dimensional (3D) bioprinters has also been an important step for cancer research. In this study, it is aimed to summarise new approaches in the use of 3D bioprinting in cancer by scanning the current literature.

Materials and Methods: Using the keywords "3D bioprinting" and "cancer", studies in which 3D Bioprinting was used in cancer research between 2016 and 2023 in a variety of databases (PUBMED, JSTOR, IEEE Xplore, Science Direct, DOAJ) were scanned.

Results: To date, there are current studies in which 3D bioprinting has been used in mimicking the microenvironment and modelling of most cancer types such as melanoma, glioblastoma, breast, lung, colorectal, etc. and in drug trials for the disease.

Conclusion: In order to understand and treat cancer by using 3D bioprinting, the priority is to maximise the similarity of the designed tissue with the target tissue. Therefore, it is recommended to focus on mimicking the targeted cancer model with maximum similarity.

Short Talk – 08

Determination of Intestinal Microbiota in Pediatric Patients who Underwent Allogenic Stem Cell Transplantation Before and After Transplantation

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Introduction and Aim: Allogeneic hematopoietic stem cell transplantation (allo-HSCT) is a curative treatment option (1,2). Preparation regimens and high-dose antibiotic use before allo-HSCT cause dysbiosis in the intestinal microbiota. In this study, it was aimed to determine the intestinal microbiota before and after allo-HSCT in 10 pediatric patients diagnosed with acute leukemia, thalassemia, aplastic anemia and primary immunodeficiencies and to investigate its relationship with the development of acute gastrointestinal-GVHD.

Material and Method: Gut microbiome were sequenced by 16S metagenomic analysis from the fecal DNA of patients.

Results: In children with malign and non-malign hematological diseases, Bifidobacterium and Bacteroides were found to be dominant in the pre-transplant microbiome. In patients with Primary Immunodeficiencies, in addition to Bifidobacterium, Actinobacteriota were found to be high. While dysbiosis was found in 2/3 of the patients in the hematological malignant patient group before allo-HSCT, dysbiosis was not found in the patients with Primary Immunodeficiencies. The fact that the patients had dysbiosis without any treatment in the study shows that the pathogenesis of the disease may be related to dysbiosis and at least, the dysbiosis status in these patients is not dependent on the preparatory regimens.

In the post-transplant microbiota analyzes, Bifidobacterium genus was seen predominantly. Actinobacterium and Firmicutes were observed the most, respectively. Acute gastrointestinal-GVHD did not develop in 2 patients with dysbiosis in the intestinal microbiota, while GVHD developed in 2 patients without dysbiosis.

Conclusion: It was concluded that studies with a larger patient population are needed in order to associate the gut microbiota with gastrointestinal-GVHD in patients undergoing allo-HSCT.

Keywords: Graft Versus Host Disease, Microbiota, Dysbiosis

Short Talk – 09

The Expression Analysis of Specific Genes in Ovarian Cancer

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Introduction and aim: Due to a lack of diagnostic and prognostic biomarkers, ovarian cancer (OC), the most lethal gynecologic malignancy, is frequently diagnosed at an advanced stage. Therefore, identification of OC specific biological markers is a vital step for diagnosis and treatment response. Our goal is to examine functional gene sets which are possibly markers for ovarian cancer and their expression profiles in OC patients. We also aim to determine the potential of the genes which could be possible therapeutic targets for OC patients.

Materials and methods: By using qRT-PCR, the expression profiles of seven genes (FOS, FOSL2, JUN, MMP-2, MMP-9, TIMP-2, and VEGFA) were identified. The tumor-free control group consisted of total abdominal hysterectomy (n=1) and bilateral salpingo-oophorectomy (n=9) patients who underwent gynecologic procedures. High-grade serous OC epithelial samples (n=10) were used for the experiment group.

Results: According to the qRT-PCR data, there is an increased expression of FOS (p=0.0089), MMP-9 (p=0.0029), VEGFA (p=0.0434) and decreased expression of FOSL2 (p=0.0271), JUN (p=0.0041), TIMP-2 (p=0.0062).

Conclusion: In conclusion, the data may produce new insights regarding OC pathogenesis and treatment. The candidate genes may improve individualized diagnosis and therapy for OC in the future.

Keywords: Ovarian cancer, gene expression, biomarker

Short Talk – 10

Antioxidant and Anti-growth Properties of Selected Anatolian Plant Species: Exploring the Potential of Heracleum humile, Doronicum reticulatum, Centaurea drabifolia, and Senecio olympicus

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Introduction and Aim: Plants are increasingly acknowledged as potential sources of novel compounds for public health challenges like cancer. Yet, only a small proportion of higher plants have undergone biological investigation. The Anatolian region, notable for its vast floristic diversity, hosts over 12,000 vascular plant species with an endemism rate surpassing 30% [1]. This study investigated the anti-growth and antioxidant properties of four plant species native to the Anatolian region: Heracleum humile, Doronicum reticulatum, Centaurea drabifolia, and Senecio olympicus.

Materials and Methods: Plant materials were collected, authenticated, and extracted using a Soxhlet apparatus. The growth inhibitory activities of the extracts were evaluated in human breast cancer cell lines MCF-7 and MDA-MB-231, and the nonmalignant immortalized human breast cell line MCF-10A, using the sulforhodamine B (SRB) assay. Antioxidant capacities were assessed via DPPH and CUPRAC assays.

Results: The study revealed that the extract of C. drabifolia showed strong cytotoxic properties. In contrast, D. reticulatum exhibited selective toxicity and demonstrated the most significant antioxidant activity among the species assessed.

Conclusion: These findings contribute to our understanding of the therapeutic potential of these indigenous plant species in addressing various public health issues, including cancer.

Keywords: cytotoxicity, antioxidant, Heracleum humile, Doronicum reticulatum, Centaurea drabifolia, Senecio olympicus.

Short Talk – 11

Cracking the Code of Drug Discovery: Technology's Impact on Novel Therapeutics

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The pursuit of novel therapeutic agents to combat a wide spectrum of diseases remains an enduring imperative in pharmaceutical research.

Historically, drug discovery relied on costly and time-consuming experimental methods. However, the integration of computational chemistry, molecular simulations, and data-driven approaches has revolutionized the landscape, significantly expediting the identification of potential drug candidates, shaped by advanced methodologies including molecular docking, computer-aided drug discovery, molecular mechanics energy calculations, virtual screening, shape screening, and data mining, now integral components of pharmaceutical research. These techniques constitute an indispensable toolset, fostering innovation and precision in the quest for therapeutic solutions. Researchers can now predict molecular interactions and evaluate drug candidates with unprecedented precision. The integration of artificial intelligence (AI) is transformative, with machine learning algorithms navigating vast datasets to pinpoint drug targets and anticipate interactions. The dynamic nature of drug discovery is underscored by perpetual innovation and technology's role in drug development, streamlining the identification and optimization of small molecules to combat diseases. Looking ahead, the anticipation of delivering targeted treatments for various diseases is vested in future small molecule drug candidates. Supported by computational modeling, molecular simulations, and AI-driven insights, these candidates have the potential to redefine therapeutic approaches, offering target-specific solutions with minimized side effects.

In conclusion, drug discovery is undergoing a profound redefinition, shaped by the synergy among computational chemistry, molecular simulations, data mining, and cutting-edge technologies. This abstract offers a glimpse into the promising future of pharmaceutical research, where innovation and technology converge to address pressing healthcare challenges.

Keywords: Computer-aided drug discovery, computational biology, artificial intelligence, target-specificity, molecular simulations, small molecules.