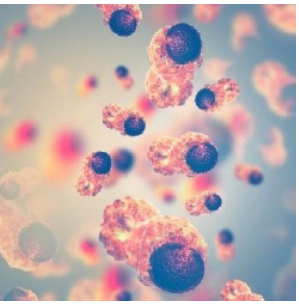
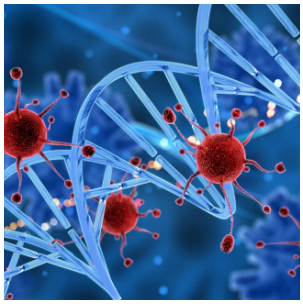
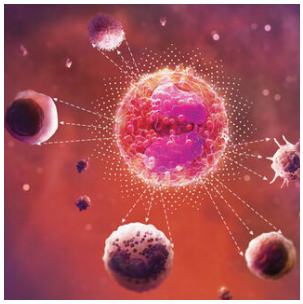
Accepted Abstracts

Surgical Pathology 2022



4th WORLD CONGRESS ON

SURGICAL PATHOLOGY AND ONCOLOGY RESEARCH

OCTOBER 17, 2022 | WEBINAR

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Hsa-miR-181a-5p, hsa-miR-182-5p and hsa-miR-26a-5p as potential biomarkers for BCR-ABL1 among adult chronic myeloid leukemia treated with tyrosine kinase inhibitors at the molecular response

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Tyrosine kinase inhibitors (TKIs) as first-line therapy for Chronic Myeloid Leukemia (CML) show a high success rate. However, a low number of patients with long-term treatment-free remission (TFR) were observed. Molecular relapse after imatinib discontinuation occurred at 50% at 24months, with 80% occurrence within the first 6months. One of the reasons for relapse is untimely TKIs discontinuation caused by large errors from estimates at very low-level or undetectable disease, thus warranting new biomarkers for CML. Methods: Next Generation Sequencing (NGS) was used to identify microRNAs (miRNAs) at the molecular response in CML adult patients receiving TKIs treatment. A total of 86 samples were collected, 30 from CML patients responsive and 28 from non-responsive to imatinib therapy and 28 from blood donors. NGS was conducted whereby 18 miRNAs were selected and validated by real-time RT-qPCR in triplicate.

Results

Hsa-miR-181a-5p was expressed significantly (p-value<0.05) with 2.14 and 2.33-fold down-regulation in both patient groups, respectively meanwhile hsa-miR-182-5p and hsa-miR-26a-5p were significant only in the non-responsive group with 2.08 and 2.39 fold up-regulation. The down-regulation was consistent with decreased amounts of BCR-ABL1 in patients taking TKIs regardless of molecular responses. The up-regulation was consistent with the substantial presence of BCR-ABL1 in CML patients treated with TKIs at the molecular response. Conclusions: Therefore, these miRNAs have potential as new therapeutic biomarkers for BCR-ABL1 status in adult CML patients treated with TKIs at molecular responses. These could improve current approaches and require further analysis to look for targets of these miRNAs in CML.

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Heterogeneity of circulating tumour cell neoplastic subpopulations interrogated by single-cell transcriptomics Heterogeneity of circulating tumour cell neoplastic subpopulations interrogated by single-cell transcriptomics

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Fatal metastasis occurs when circulating tumor cells (CTCs) disperse through the blood to initiate a new tumor at specific sites distant from the primary or metastatic tumor. CTCs have been classically defined as nucleated cells positive for epithelial-cell adhesion molecule and select cytokeratins (EpCAM+/CK+/DAPI+), while negative for the common lymphocyte marker CD45 ("classic" CTCs). The enumeration of these CTCs has also allowed the estimation of the overall metastatic burden of breast cancer (mBC) patients, however challenges regarding CTC heterogeneity and metastatic propensities persist and further CTC decryption could improve therapy effectiveness. To this end, we applied a four-pronged experimental approach consisting of interrogating peripheral blood mononuclear cells isolated from blood of mBC patients. We combined: 1) the use of multi-parametric flow cytometry sorting Lin+ (CD45+) and Lin- cell populations from the same patient, 2) the performance of RNASeq of Lin+/Lin- cell populations from 66 mBC patients of distinct subtypes, 3) employing 10x Genomics Chromium platform for the unbiased and comprehensive transcriptional profiling of Lin+/Lin- cell populations on a cell-by-cell basis and from distinct mBC patients and 4) the capture and analysis of "classic" CTCs using the RareCyteTM Cytefinder II platform. Of relevance, single-cell transcriptomic analyses of Lin- vs. Lin+ cell populations isolated from blood of mBC patients identified a unique and heterogeneous cluster of neoplastic cells including not only those expressing EpCAM/CK ("classic" CTCs) but also ones possessing an array of genes not previously associated with CTCs. This study put forward notions that the identification of these genes and their interactions will promote novel areas of analysis by dissecting properties underlying CTC survival, proliferation and cross-talks with immune system cells. It improves upon abilities to measure and interfere with CTC states and plasticity and functionalities of CTC subsets to identify vulnerabilities and interfere with CTC states for impactful therapeutic interventions.

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1. Molecular Interplay between Dormant Bone Marrow-Resident Cells (BMRCs) and CTCs in Breast Cancer.
2. Application of liquid biopsy for prognostic status of cancers and drug response
3. PMN-MDSCs enhance CTC metastatic properties through reciprocal interactions via ROS/Notch/Nodal Nodal signaling.

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Artificial Intelligence (AI) in biomedical engineering

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Artificial intelligence (AI) refers to the simulation of human intelligence in machines that are programmed to think like humans and mimic their actions. Recent advances and applications of artificial intelligence (AI) in medicine via emphasizing this research area with novel biomaterials technology have shown great interest in medical applications. The way AI rapidly processes large amounts of information and arrives at likely causes for symptoms can drastically reduce the diagnosis-treatment-recovery cycle for many patients. The present seminar is divided into two parts; in the first part I will discuss the basic principle of the AI technology. In the second part, I will discuss the recent applications of AI technology in healthcare. I will further show some of our recent project in which AI technology has been used in biomedical engineering including in cancer, diabetes, biosensor and tissue engineering.

Recent Publications

1. Hosseinkhani, H, Biomedical Engineering: Materials, Technology, Applications. 2022, John Wiley & Sons, ISBN: 9783527347469.

2. Domb, A.J.; Sharifzadeh, G.; Nahum, V.; Hosseinkhani, H. Safety Evaluation of Nanotechnology Products. Pharmaceutics, 2021, 13, 1615.

3. Khalaji, S.; Ebrahimi, N.G.; Hosseinkhani, H. Enhancement of biocompatibility of PVA/HTCC blend polymer with collagen for skin care application. International Journal of Polymeric Materials and Polymeric Biomaterials, 2021, 70, 459-468.

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A Rare presentation of T Cell lymphoma of Intestine

Mithlesh Kumar Parkar, Avishesh Singh and R K Chandrakar
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Intestinal lymphoma is a rare type of intraepithelial T cell lymphoma that characteristically involves the jejunum or ileum. It occurs in two subtypes:1. Enteropathy associated T-cell lymphoma (EATL) 2. Monomorphic CD56+ (NCAM1) Intestinal T cell lymphoma.

More common in Patients with Celiac disease, Age >50 years and Mean age of presentation is 64 years with M: F-3:1.

It is a rare type of T cell lymphoma in gastrointestinal tract. Incidence occurs less than 5% of total lymphoma and small intestine is the most common site of involvement. Immuno-histochemically the tumour cells are CD3+, CD4- &CD20-. The differential diagnosis includes MAL Tomas, GIST and B cell lymphoma. The most common type of lymphoma is a lymphomas involving the GIT are of B cell origin. We are here reported a case of T- cell lymphoma arising in small intestine with normal histology since these lymphomas are commonly encountered in patient with celiac diseases.

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How will penetrating the mutual coexistence between malaria & tumour improve our system of drug discovery?

Rahali Lawali
Usman Danfodiyo University Teaching Hospital, Nigeria

The true picture of our Global healthcare system raises the following questions at stake:

-Why the number of human diseases keeps on increasing, despite the current advancement in sconce and technology?

-When will malaria and tumor be listed among the eradicated and outdated diseases?

-Are the systems upon which diseases were operating more powerful than the collective efforts of the modern researchers?

The analysis of the numerical cascade of the two diseases deducted using a Lexical-Counting Method through the application of a Multidisciplinary Computational Formula reveals that malaria & tumour are in a mutual coexistence. This enables the author to make the following positive assumptions: The eradication of the two diseases can be achieved using the numerical cascade of any of the disease, especially the one having a vector, thus requiring a pair of eradication measures targeting both the Microbe & the Insect responsible for the disease. It can be achieved simply by designing a pathological module that will bridge the gap between malaria & tumour.

Recent Publications

1. Lawali, R. The Computerization Of Pain Management In Line With Pain Scoring System(Abstract) In Proceeding Of The 7th International Conference On Pain Research And Management, 11-13, 2018, Zurich, Switzerland DOI: 10.4172/2167-0846-Ci-021

2. Lawali,R.(2018): The Computerization Of Pain Management In Line With Pain Scoring System(Ebook) Amazon KDP

3. Lawali, R.(2018): The Computerization Of Pain Management In Line With Pain Scoring System(Paperback) Scholar's Press.

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