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KEYNOTE LECTURES' ABSTRACTS

Update on the National Cancer Institute (NCI) Human Tumor Atlas Network (HTAN)

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Critical steps in a cancer development and progression include the initiation and development of precancerous lesions, followed by local expansion and transition to tumor, invasive tumor, distant metastasis, and therapeutic resistant tumor. The process involves complex dynamic interactions between cells within the tumor ecosystem. Innovative single-cell genomics technologies and spatial multiplex in situ methods now provide an opportunity to interrogate this complexity at unprecedented resolution. The Human Tumor Atlas Network (HTAN), part of the National Cancer Institute (NCI) Cancer Moonshot Initiative, is establishing a clinical, experimental, computational, and organizational framework to generate a comprehensive and community accessible three-dimensional atlases of cancer transitions for a diverse set of tumor types. This project complements both, ongoing efforts to create healthy organs atlases and previous large-scale cancer genomics approaches which focused on bulk sequencing at a single point in time. Atlases based on single-cell multiparametric longitudinal analysis of the tumor ecosystem, integrated with clinicopathological information and clinical outcomes should help identify prognostic biomarkers and features as well as targets for preventive and therapeutic intervention relevant for specific cell types, cell states, and their molecular and cellular dynamic interactions through those transitions. Tumor atlases should have a profound impact on our understanding of cancer biology including tumor trajectory, have the potential to improve cancer early detection, prevention, diagnosis, prognosis, the discovery of new therapeutic targets and the development of new therapies for personalized precision medicine of cancer patients and those at high risk for developing cancer.

So far the HTAN:

- Establishment of biospecimen acquisition and clinical warehouse.
 - Harmonization of clinical and biospecimen metadata among all HTAN centers and with MCL.
- Establishment of methodology for processing fresh tissue, single cell RNA and DNA sequencing, MIBI, CODEX and other technological platforms.
 - Is identifying cell type-specific transcriptional changes.
- Is identifying unique cell populations that vary by precursor lesion type and shifts in cell populations during progression.
- Begun Identifying molecular changes in the development and transition from pre-cancer to invasive cancer; molecular signatures revealing new biology.
- Developed infrastructure (e.g., QC methods, data upload and sharing, image viewer, virtual biorepository of reference specimens).

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The power of metabolomics in biomarker research

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Metabolomics as a holistic analysis of metabolites provides functional insights into biological systems. Both in health and disease it goes beyond genetic coding further to the impact of life style, environment and interventions on metabolic pathways. Metabolomics provides dynamic description signatures useful for the risk stratification, early diagnostics, therapy monitoring or theranostics.

Examples for the applications of metabolomics in analyses of biomarkers in tumor biology, diabetes and endometriosis will be discussed.

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Advancing Biomarker Research through Biobanking in Europe and beyond – from community engagement to cross-country collaborations

Jens K. Habermann
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BBMRI-ERIC stands for “Biobanking and BioMolecular resources Research Infrastructure – European Research Infrastructure Consortium” (www.bbmri-eric.eu). Currently, 23 European countries and the World Health Organisation’s International Agency for Research on Cancer constitute with its National Nodes and affiliated biobanks BBMRI-ERIC as a research infrastructure, providing services and connecting biobanks across Europe. BBMRI-ERIC’s mission is to facilitate access to sample and data as well as to biomedical resources to foster biomarker research and personalized medicine. This is facilitated through services and advancements in the areas of Ethical, Legal and Societal Issues (ELSI), Quality Management (QM), Information Technology (IT), Biobank Development (BBD), Public Affairs (PA), and Outreach, Education & Communications (OEC). This presentation will highlight BBMRI-ERIC’s (i) access opportunities to over 600 biobanks in our biobank Directory hosting more than 2,500 collections with estimated >100,000,000 samples and associated data, (ii) how this is facilitated by current and prospect IT solutions, (iii) how quality measures are implemented and further developed, (iv) how our ELSI experts across Europe support research and guide on matters ranging from data protection to incidental findings, and (v) how we position our community’s services and research together with our stakeholders and partners in the overall EU research landscape in order to advance and implement personalized medicine. Hereby, the newly started 15 Mio. € EU funded project canSERV will be highlighted allowing various opportunities for benefits and interactions within the wider biomarker research community addressing cancer.

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Early cancer detection by dogs

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Identification of malignancies at an early stage increases dramatically the overall survival rates, reduces the need for long painful treatments and saves a great deal of money to the healthcare system. Creating an EASY and affordable cancer screening test will encourage a paradigm shift and adoption of more strict routine checks. In order to deliver this revolutionary screening solution, SpotitEarly has combined canine intelligence (CI) with artificial intelligence (AI), resulting in a new kind of test kit that will completely change the customer experience regarding cancer screening.

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