CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
RP160622

Project Title:
Computational live cell histology

Award Mechanism:
Individual Investigator Research Awards for Computational Biology

Principal Investigator:
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Entity:
The University of Texas Southwestern Medical Center

Lay Summary:

We rapidly gain genomic information of cancers, but tumors from different patients and even from different cells of the same tumor can exhibit vast genetic differences. This applies especially to melanoma, a deadly form of skin cancer, where diagnosis and definition of a robust treatment strategy based on the genomic profile is impossible. At the level of cells, however, heterogeneous genomic profiles seem to invoke universal programs to invade, survive and colonize distant organs. This supports the hypothesis that diverse oncogenic backgrounds converge to a few key functions that confer metastatic efficiency. Quantitative live cell histology is designed to identify cellular behaviors that are shared by groups of cancer cells with metastatic potential. Based on patient-derived melanoma models, we established a high-throughput live cell imaging assay and propose here to develop a novel analytical pipeline to encode a tumor as a distribution of dynamic cellular behaviors. The approach is inspired by a recent break-through in Artificial Intelligence, which demonstrated computer software that autonomously identifies image contents based on unstructured information inaccessible to a human observer. Our algorithm will derive a tumor morphodynamic profile from the spatiotemporal variation in image texture cancer cells generate in label free light microscopy. The profile will predict the risk of stage III tumors harvested by lymph node needle biopsy to advance to deadly stage IV metastases allowing early targeted treatment. The profile can also serve the systematic analysis of single and combination drug cocktails in their ability to suppress specific prometastatic behavior and allow the mapping of primary tumor samples into a reference space of drug action that will support personalized prescription of chemotherapy. Once established for melanoma the paradigm of using unstructured data of dynamic cell behavior can be transferred to other cancers with somatic mutations.