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Recent whole-genome sequencing efforts have expanded on the traditional histologically-driven subtypes to further stratify cases according to the presence/absence of specific somatic mutations in oncogenes integral to cancer initiation, progression and metastasis. The development of 'targeted therapeutics' intended to specifically short-circuit regulatory pathways has led to the successful development of efficacious compounds, but only in patients that harbor the targeted mutation. Tissue confirmation is required for targeted therapy prescription. In this era of molecularly based therapeutics, it may be valuable if somatic driver mutations could be correlated to imaging parameters in order to uncover a molecular profile-imaging signature. Radiogenomics/radioproteomics or radiology imaging based phenotypes—patterns—could be used to predict the molecular subtype of cancers. Functional, morphological and molecular imaging techniques are routinely used to visualize, characterize, and measure biological processes at the cellular, subcellular, and molecular levels in living subjects. Developing a noninvasive means for identifying the molecular subtype of cancer cases that bypasses or complements the need for tissue acquisition and assay and that can be performed in the clinic at the time of diagnosis would have the potential to be transformational in the accessibility of personalized cancer medicine.

In daily clinical practice tissue confirmation of driver mutations is required for targeted therapy prescription. Consequently, patients with contraindicated, failed or indeterminate biopsies do not receive potentially beneficial targeted therapies. Non-invasive driver mutation correlation methods could:

integrate non-invasive real-time data into the clinic and on the other hand add an additional layer of imaging information (besides standard staging) into the portfolio of clinical data necessary to guide therapeutics and prognosis. This will allow us to better stratify patient treatments and ultimately improve survival. Achieving patient specific personalized medicine by integrating multiple features provided from imaging, pathology and clinical biomarkers; as well as developing complementary synergistic systems between clinical, biochemical, imaging and cellular/subcellular (molecular/gene) biomarkers is essential.

The goal would not be to replace tissue characterization but to complement it in cases where:

1. Poor overall performance status, significant co-morbidities or the presence of de novo disease or recurrences in anatomic locations that cannot be or are high risk to be accessed—vascular proximity.

2. Inaccessible or necrotic, fibrotic or in inflammatory regions of the tumor.

3. Incomplete sampling of the tumor.

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