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MOSAIC: A Metric of Spatial Anatomical Intratumoral Genetic Complexity

Stanford scientists have developed a novel method that quantifies spatial anatomical genetic heterogeneity within a patient's tumor.

Cancers such as lymphoma can exhibit significant intra-patient spatial genetic heterogeneity, characterized by distinct mutational profiles across different disease sites. Comprehensive assessment of tumor heterogeneity remains a major clinical challenge, as single-site biopsies underrepresent systemic clonal diversity, while multi-region tissue sampling carries safety risks due to the burden of repeated invasive procedures. Circulating tumor DNA (ctDNA) can offer a more comprehensive, whole-patient snapshot of tumor-derived mutations, but it is limited in spatial resolution. Consequently, there is an urgent need for minimally invasive tools that provide comprehensive, spatially resolved genetic insights.

The Alizadeh lab at Stanford developed a novel method, Metric of Spatial Anatomical Intra-tumoral genetic Complexity (MOSAIC), which quantitively assess anatomic heterogeneity using liquid biopsy for a comprehensive assessment of spatially discordant tumor mutations, while anchoring to sequencing of a specific tumor lesion to provide spatial resolution. Quantitatively evaluating the differences in ctDNA and tissue biopsy can capture clinically relevant subclones and heterogeneity missed by conventional methods. This robust measure of anatomic heterogeneity has implications for resistance to chemotherapy, tumor biology, and has potential as a biomarker for treatment selection.

Stage of Research
Proof of concept

Applications

- A prognostic and predictive biomarker assay for anatomic genetic heterogeneity
- A biomarker to predict favorable response to specific targeted therapies

Advantages

- Provides a more comprehensive picture of spatial tumor heterogeneity
- Enables rapid longitudinal tracking of treatment response

Innovators

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