Predicting the Future: Translating Single-Cell Biology into Clinically Actionable Protein Biomarkers in CML

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This talk highlights how single-cell transcriptomic insights at the time of chronic phase diagnosis are being translated into clinically robust protein-based tests to forecast clinical outcomes at both extremes of the CML disease spectrum: patients who are at very high-risk of future blast crisis transformation, and those who will achieve durable treatment free remissions following TKI cessation. These insights, gained from multi-modal single cell studies on pre-treatment blood and bone marrow samples, highlight how pretreatment biology in the hematopoietic stem and progenitor cell and immune compartments cells are powerful determinant of both : 1. Primary TKI responses and blast crisis transformation; and 2. The likelihood of achieving durable treatment free remissions following TKI cessation. These tools are now ready for prospective validation studies and integration into routine pathology workflows. By bridging high-resolution biology to practical readouts, our approach aims to enable precision stratification, earlier intervention, and treatment optimization, including informing TKI selection and duration. Attendees will gain translational strategies, assay design principles, and a clear roadmap for validating truly predictive CML management.