Check for updates





Blood 142 (2023) 527-529

The 65th ASH Annual Meeting Abstracts

ORAL ABSTRACTS

621.LYMPHOMAS: TRANSLATIONAL-MOLECULAR AND GENETIC

A Personalized Whole Genome-Informed Assay Targeting Single Mutant in Circulating Tumor DNA Can Identify MRD and Predict Relapse in DLBCL

Reid W. Merryman, MD¹, Justin Rhoades², Kan Xiong², Katherine Antel, MDPhD^{3,4}, Hyun Hwan An⁵, Robert A. Redd, MS⁶, Mikaela M. McDonough, BS⁵, Lillian Guerrero³, Andela Crnjac², Sainetra Sridhar², Timothy Blewett², Ju Chen², Parastoo B. Dahi, MD⁷, Yago Nieto, MD PhD⁸, Yi-Bin Chen, MDMS⁹, Alex F. Herrera, MD⁹, Robin M. Joyce, MD¹⁰, Philippe Armand, MD PhD¹¹, Mark Alan Murakami, MDMA,MMSc⁵, Viktor Adalsteinsson²

¹Brigham and Women's Hospital, Boston, MA

²Broad Institute, Boston, MA

³Dana-Farber Cancer Institute, BOSTON, MA

⁴ Institute of Infectious Disease and Molecular Medicine, University of Cape Town, Cape Town, South Africa

⁵Dana-Farber Cancer Institute, Boston, MA

⁶Department of Data Science, Dana-Farber Cancer Institute, Boston, MA

⁷Adult Bone Marrow Transplant Service, Department of Medicine, Memorial Sloan Kettering Cancer Center, New York, NY

⁸Department of Stem Cell Transplantation and Cellular Therapy, The University of Texas MD Anderson Cancer Center, Houston, TX

⁹City of Hope, Duarte, CA

¹⁰ Massachusetts General Hospital, Boston, MA

¹¹ Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA

Introduction: Minimal residual disease (MRD) detected by circulating tumor DNA (ctDNA) has emerged as a promising biomarker in diffuse large B-cell lymphoma (DLBCL). MAESTRO (minor-allele-enriched sequencing through recognition oligonucleotides) was recently developed to aid the detection of low-frequency mutations by enriching for mutant alleles using probes preferentially capturing single-nucleotide variants. We have extended this application - termed MAESTRO-Pool - to analyze personalized MRD variant detection within a cohort-level single assay. We demonstrate high sensitivity to detect MRD using MAESTRO-Pool and the detection of emergent mutations using targeted sequencing of the same samples.

Methods: Fifty-nine plasma specimens from 9 patients with relapsed/refractory (R/R) DLBCL treated on a phase II trial (NCT02362997) of post-autologous stem cell transplant (ASCT) pembrolizumab maintenance were tested. Cases were selected based on the availability of genomic DNA from tumor tissue, patient-matched germline DNA, and serial post-ASCT plasma samples (\geq 3 time points). MAESTRO probes were designed to target patient tumor-specific somatic variants using results of baseline tumor-normal whole genome sequencing. Probes were then pooled into an integrated, cohort-level as-say (MAESTRO-Pool). Serial samples were compared with an orthogonal, whole-genome, tumor-informed MRD test which does not use mutation enrichment (MRD Tracker; Parsons, HA et al. *Clin Cancer Res* **26**, 2556-2564 (2020)) for sensitivity and specificity of variant detection. In addition, sensitivity to detect MRD and predict relapse was compared to that observed with immunoglobulin locus high-throughput sequencing (IgHTS). Additional baits were designed to capture single nucleotide variants (SNVs) previously reported in R/R DLBCL (63 loci in 12 genes), enabling detection of treatment-emergent mutations not identified in baseline tumor specimens.

Results: Tumor-normal WGS revealed a median of 433 somatic SNVs per tumor (range 81-1653). The pooled assay comprised 6044 SNV-specific probes. MRD identification was similar for MAESTRO-Pool and MRD Tracker. Among 59 samples, a discrepant MRD call was observed for a single sample where ctDNA was detected at 4 ppm using MRD Tracker, but not detected using MAESTRO-Pool (limit of detection [LoD] 16 ppm). Estimated tumor fractions using MRD Tracker and MAESTRO-Pool were concordant. Even with reduced sequencing requirements of MAESTRO-Pool, we observed a similar median limit of detection (LoD) for MAESTRO-Pool (median 30 ppm, range 1-18,243) and MRD Tracker (median 40 ppm, range 1-4,727 ppm).

MAESTRO-Pool identified ctDNA prior to recurrence for all 5 patients who relapsed, including at the earliest available post-ASCT timepoint for 4 of 5 relapsing patients. The time from ctDNA detection to clinical relapse (lead time) was the same or

ORAL ABSTRACTS

Session 621

longer for each patient using MAESTRO-Pool (median 178 days, range 69-518) compared to IgHTS (median 44 days, range not detected to 518 days) (p=0.37) (Fig.1a). MAESTRO-POOL was associated with improved sensitivity compared to IgHTS (MAESTRO-Pool sensitivity of 90.5% for samples with matched IgHTS results versus IgHTS sensitivity of 61.9%, p=0.006). Superior sensitivity was primarily driven by MAESTRO-Pool's improved detection of low-frequency (<1000 ppm) mutant alleles. In addition to tracking molecular tumor burden, we identified several de novo mutations in relapsing patients using targeted sequencing of the same samples. Notably, plasma from a patient who progressed at 18.5 months post-ASCT (DL-015) manifested an emergent CREBBP R1446H mutation not detected in the baseline tumor whose allele frequency steadily increased from 0.048% one week after ASCT to 30.533% at relapse (Fig 1b).

Conclusion: In this pilot study, MAESTRO-Pool enabled ultrasensitive detection and quantification of MRD with superior sensitivity compared to IgHTS. Complementary targeted sequencing also characterized genetic evolution, including detection of treatment-emergent mutations. Our results support the incorporation of ctDNA testing using MAESTRO-Pool in future prospective trials in DLBCL.

Disclosures Merryman: Genentech/Roche: Research Funding; BMS: Membership on an entity's Board of Directors or advisory committees, Research Funding; Alphasights: Membership on an entity's Board of Directors or advisory committees; Epizyme: Membership on an entity's Board of Directors or advisory committees; Genmab: Membership on an entity's Board of Directors or advisory committees, Research Funding; Intellia: Membership on an entity's Board of Directors or advisory committees; Seattle Genetics: Membership on an entity's Board of Directors or advisory committees; Abbvie: Membership on an entity's Board of Directors or advisory committees; Merck: Research Funding; Adaptive Biotechnology: Membership on an entity's Board of Directors or advisory committees. Nieto: Affimed: Research Funding; Secura Bio: Research Funding; Astra Zeneca: Research Funding. Herrera: Adicet Bio: Consultancy; Caribou Biosciences: Consultancy; Takeda: Consultancy; Tubulis GmbH: Consultancy; Pfizer: Consultancy; Merck: Consultancy, Research Funding; Genmab: Consultancy; Allogene Therapeutics: Consultancy; Seattle Genetics: Consultancy, Research Funding; ADC Therapeutics: Consultancy, Research Funding; AbbVie: Consultancy; BMS: Consultancy, Other: Travel/Accommodations/Expenses, Research Funding; Regeneron: Consultancy; Karyopharm Therapeutics: Consultancy; AstraZeneca/MedImmune: Consultancy; Kite, a Gilead Company: Research Funding; Genentech/Roche: Consultancy, Research Funding; Gilead Sciences: Research Funding; AstraZeneca: Research Funding. Armand: MSD: Consultancy, Research Funding; Affimed Therapeutics: Research Funding; Enterome: Consultancy; Xencor: Consultancy; Regeneron: Consultancy; Tessa Therapeutics: Consultancy; Kite - a Gilead company: Research Funding; ATB Therapeutics: Consultancy; Genentech/Roche: Consultancy, Research Funding; Foresight Diagnostics: Consultancy; ADC Therapeutics: Consultancy; GenMab: Consultancy; AstraZeneca: Consultancy, Research Funding; IGM: Research Funding; Adaptive Biotechnologies: Research Funding; Bristol Myers Squibb: Consultancy, Research Funding; Merck: Consultancy, Honoraria, Research Funding. Murakami: Novartis AG: Membership on an entity's Board of Directors or advisory committees; imCORE (Genentech/Roche): Research Funding. Adalsteinsson: Exact Sciences: Current equity holder in private company.



Fig 1A. Swimmer's plot showing MAESTRO-POOL MRD results along with matched ClonoSEQ results when available. **Fig 1B**. Patient vignette of tumor response dynamics shows the emergence of *de novo* mutations not present at baseline by MRD Tracker.

Figure 1

https://doi.org/10.1182/blood-2023-189962

Session 621