Multi-omics characterization of T-cell populations at the single-cell level utilizing sensitive dCODE Dextramer® and BD® AbSeq on the BD Rhapsody™ Single-Cell Analysis system

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Background

This study aimed to detect and characterize disease-specific CD4+ T cells within thousands of PBMC by combining two technologies: dCODE Dextramer® (Immudex) and single-cell multi-omics analysis using BD Rhapsody™ Single-Cell analysis system.

Workflow approach

dCODE Dextramer®(RiO) reagents are designed to be compatible with BD's Rhapsody Single Cell analysis system. Each reagent has a unique DNA barcode specific for the MHC-peptide displayed on the dCODE Dextramer and the barcode can be amplified and sequenced simultaneously with targeted mRNA from a single cell.

1. PBMCs stimulated with two peptide antigens (EBV and Tetanus toxoid) were stained with a panel of dCODE Dextramer® (DRB1*0101/EBV, DRB1*0101/TT and DRB1*0101 / DRB1*0101/negative control peptide)
2. Stained Cell sample was captured as single-cells by BD Rhapsody Single-cell analysis system
3. Upon cell lysis, polyadenylated mRNA and dCODE Dextramer® sequences from the same cell were captured and cDNA synthesized
4. mRNA and dCODE DNA libraries were amplified by PCR, sequenced, followed by data analysis using SeqGeq

Results

EBV-specific T cells were identified in PBMC samples and no specific cells were detected by the negative control Dextramer (**Fig.1**). Frequency of TT-specific T cells was very low, though detectable (**Fig.2**).

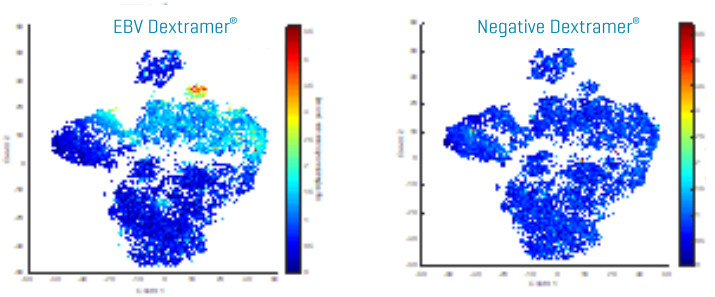

Fig.1 T-SNE plots showing detection of EBV dCODE Dextramer ® +cells

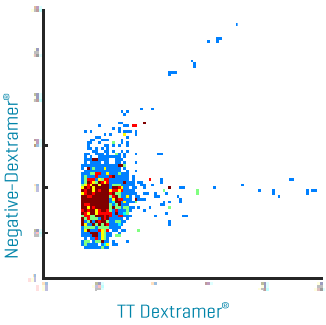

Fig.2. Detected rare TT Dextramer® + cells (dot-plot)

Differential gene expression analysis was seen between Dextramer EBV+ population *vs.* EBV-Negative and showed concordance with activated T cells.

Conclusions

- dCODE Dextramer® is compatible with BD Rhapsody™ Single-Cell Analysis workflow
- All dCODE Dextramer® used to stain cells were detected in sequencing experiments and antigen-specific T cell detection results further verified by conventional FACS
- Distinct cell populations with even low frequencies T cells could be identified in donor sample and their gene expression profile mapped at single cell level
- High-resolution T-cell profiling has broad implications in immune-oncology, autoimmunity and infectious disease