

Digital spatial profiling and antigen-dependent phenotypic analysis of IL15-engineered tumor-infiltrating lymphocytes (cytoTIL15[™] therapy) in an allogeneic melanoma PDX model

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Background

cytoTIL15[™] therapy is an IL2-independent, engineered TIL product which allows pharmacological control of membrane-bound IL15 (mbIL15). We have previously shown that cytoTIL15 TILs demonstrate enhanced persistence and anti-tumor efficacy in a human allogeneic melanoma PDX model, utilizing the melanoma associated antigen, MART-1, as a model system based on conserved antigen reactivity. Here we use digital spatial profiling and single cell sequencing to characterize the RNA expression profile and phenotypic markers of tumor infiltrating immune cells as well as tumor cells in this model and compare the results to unengineered, IL2-dependent TIL.



cytoTIL15 therapy contains TILs engineered with mbIL15 under the control of a carbonic-anhydrase-2 drug responsive domain, regulated by the ligand acetazolamide (ACZ). cytoTIL15 cells were generated from human melanomas through a proprietary rapid expansion process. Expanded TILs were phenotyped and assayed for in vitro polyfunctionality, cytotoxicity, and frequency of tumorassociated antigen-specific TCR. *In vivo* phenotype and anti-tumor functionality was examined through adoptive transfer of TILs into NSG mice bearing subcutaneous, HLA-matched, patient-derived-xenograft (PDX) tumors expressing conserved melanoma-associated antigen (MAA) MART-1, in IACUC approved animal studies. Tumors, spleen, bone marrow, and blood were harvested 14-21 days following adoptive cell transfer and assessed by flow cytometry, GeoMx[®] (NanoString) digital spatial profiling, and single cell sequencing to characterize the TIL and the tumor microenvironment (TME).



Figure 1. Schema of PDX Model and cytoTIL15 treatment. Left to Right: Melanoma patient-derived xenograft (PDX) tissue was serially passaged as 100 mg fragments implanted subcutaneously onto the flanks of female NSG mice. Animals were randomized 13-days following PDX-implant, and ACT with 10⁶ conventional TILs or cytoTIL15 was performed 14-days following PDX-implant. Unengineered TIL and cytoTIL15 were generated from two different HLA-matched, allogeneic donors. After adoptive cell transfer, animals received either IL2, ACZ, or vehicle dosing. At time points 14-21 days following adoptive cell transfer, tissues (tumor, cardiac blood, bone marrow) were harvested and assessed for downstream readouts. Assays included flow cytometry from individual fresh tissue cell suspensions, single cell RNA sequencing from pooled tumor suspensions, and GeoMx® digital spatial profiling from embedded and immunofluorescent stained tissue sections Sequencing data was processed, normalized, and analyzed (for differential gene expression) using standard R packages: tidyverse, edgeR, limma, Seurat. All gene annotations were based on the GRCh38 reference genome and Ensembl 105 gene models.



REP and IL15 engineering expands MART-1-reactive TILs



.15 expand in REP and enrich for MART1-specific TILs. Left: Two HLA-matched melanom Middle: At the end of REP, unengineered and cytoTIL15 cells were assessed for the frequency of MART-1 specific TCR by tetramer staining. 1 target: effector ratio with rested TILs, with and without 80 ug/mL HLA ABC blocking reagent. After 24 h co-culture, supernatant was assessed for IFNy content by MSD



Figure 4. cytoTIL15 demonstrate enhanced infiltration and accumulation. Left. Subcutaneous PDX tumors were harvested 20-days following ACT with unengineered TILs (+IL2) or cytoTIL15 therapy. Tumors were formalin-fixed and paraffin-embedded, and immunofluorescence was performed to identify the TILs (CD3+, red color) infiltrating the tissue. Right Top: 14-days following ACT, PDX tumors, cardiac blood, and bone marrow were harvested, processed into single cell suspension, and stained and assessed via flow cytometry. Staining for the fraction of cells positive for anti-human CD3 and negative for anti-mouse CD45 revealed significant tumor infiltration by all TILs, and improved trafficking and accumulation into blood and bone marrow by cytoTIL15 therapy + ACZ. Right Bottom: Flow cytometry was also used to evaluate the fraction of transduced TILs (IL15+) staining positive with MART-1 TCR tetramer; MAA-reactive TILs enriched within all compartments, supporting the correlation of superior MAA-reactive TIL infiltration and improved anti-tumor efficacy. (n=5/arm; *p<0.05, **p<0.01, ****p<0.0001).

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Unengineered CytoTIL1

Figure 7. cvtoTIL15 demonstrates enrichment in genes associated with enhanced infiltration and anti-tumor effector function. Top: Representative microscopy of digital spatial profiling revealing region of interest (ROI) selection for TIL (blue) and tumor (green) regions for PDX tumors treated with unengineered TILs or cytoTIL15 therapy. Similarly, representative unsupervised clustering of unengineered TIL- and cytoTIL15 therapy-treated tumors. Middle: Spatial and single-cell transcriptomics reveal a differential gene expression profile in cytoTIL15 cells vs. unengineered TILs, underscored by an enrichment in genes associated with pro-effector function and a favorable TIL phenotype such as IL2RB, GNLY, CCL5, GZMB, and KLRC1, and a decrease in exhaustion-associated genes such as EOMES. Bottom: GeoMX and scRNAseq reveal a significant (p < 0.05) enrichment in GZMB and IL2RB occurring in infiltrating cytoTIL15 cells but not unengineered cells, which is associated with the distinct cluster profiles of each cell treatment.

> Specifically, the subpopulation of cytoTIL15 cells reactive to tumor-associated antigen displayed increased expression of TCF-1, which in melanoma patients has been associated with responses to immune checkpoint blockade, as well as progression free survival (PFS) and overall survival (OS)¹

cytoTIL15 cells showed a distinct profile of RNA expression consistent with their increased persistence and anti-tumor efficacy (e.g. IL2RB, GNLY, CCL5, GZMB, and KLRC1)

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