P141 Emergence of a Unique T Cell Population Associated with Cladribine Tablet Treatment in Multiple Sclerosis

Figure 2. Spatial

architecture and

of

proportion



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PBMC

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Background: Cladribine tablets (CladT) are efficacious for relapsing multiple sclerosis (RMS). However, the mechanisms by which cladribine exert favorable outcomes in MS have not been exhaustively identified and its effects on compartmentalized inflammation within the central nervous system remain unknown.

Objectives: To determine the extent, diversity, and phenotype of leukocyte infiltration within the cerebrospinal fluid (CSF) of RMS patients before and after treatment with CladT.

Methods: Blood and CSF samples from two individuals with RMS before and one year after treatment, plus another participant 10 weeks after start of CladT, were used to examine immune cell changes by transcriptomics. Transcriptional profiles of immune cells were obtained by single cell RNA sequencing, which served as the basis for uniform manifold approximation and projection (UMAP) visualization.



patients treated with CladT. (A) Composite UMAP of 26,102 peripheral blood (PBMC) and CSF immune cells from all participants at all timepoints. (B) Heatmap representation of the top 5 genes expressed by each cluster.



Figure 3. Transcriptional features of a unique CD4 cell population associated with CladT. (A) Sub-cluster analysis of Clad Emergent Т cells identifies 3 sub-clusters (0, 1, 2). (B) UMAP of Clad_Emergent T cell subclusters in PBMC (left) and CSF (right). (C) UMAP of Clad Emergent T cell subclusters in the blood and CSF at baseline (left) and 10 weeks (middle) or 1 year (right) post-treatment with cladribine. (D&E) Expression of selective upregulated genes expressed by subclusters of Clad Emergent T cells by heatmap (D) and displayed by UMAP (E).

CSF

15 375

CD4

CD4 T

CD4 T_2 CD4 T_3

CD4 Tree CD8 T 2

Clad-E

11 Platele

10 cDC

14 γδ T

Year 1

10,506

15 Plasmablas 16 pDC





Figure 4. Antigen receptor clonality before and after CladT. Donut charts of paired single cell RNA-seq T cell receptor (TCR) VDJ analysis from PBMCs and CSF T cells in participants 005 (A), and 006 (B). Total number of CD4 (top) or CD8 (bottom) T cells sequenced is reported for each individual below each donut chart. Clones shared between baseline and year 1 (YR1) are denoted with blue dots, while clones shared between PBMCs and CSF TCRs at each time point are indicated by red dots. The grey portion of each chart indicates clones seen in one to four cells from a sample. Colors used for expanded CD4 and CD8 T cell clones from participants 005 and 006 are the same although no clonal sequences were shared between participants.

Conclusion: These results suggest an immune cell dynamic that is associated with CladT therapy for RMS, including the emergence of a unique subset of T cells one year after treatment. This study exemplifies the utility of CSF examination for identifying mechanisms of disease-modifying therapy for, as well as pathogenesis of, MS.

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