

Interactions between B cells and CD8⁺ T cells in multiple sclerosis

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Abstract

Previous studies have identified functionally distinct human B cell sub-populations based on distinct cytokine expression profiles and characterized the functional capacities of such B cell subsets to modulate T cell and myeloid cell effector functions. Such antibody-independent B cell functions have emerged as highly relevant to disease activity in multiple sclerosis (MS), as evidenced by the ability of B-cell depleting therapy (anti-CD20 monoclonal antibody) to robustly reduce new relapsing disease activity while having minimal to no impact on the abnormal antibody profile within the central nervous system (CNS) of patients. While these results have been interpreted to reflect B cell:CD4⁺ T cell interactions, we noted that B-cell depleting therapy results in reduced proliferation and pro-inflammatory cytokine responses of both CD4⁺ and CD8⁺ T cells, suggesting that B cells and CD8⁺ T cells may also interact in disease-relevant ways. It is noteworthy that in MS, CD8⁺ T cells are actually more abundant in the inflamed MS CNS than are CD4⁺ T cells. Furthermore, among the CNS-infiltrating T cells in MS, pathologists have identified presence of clonally expanded mucosal-associated invariant T cell receptor (MAIT) cells expressing pro-inflammatory effector molecules. The overall aim of my thesis is to characterize antibody-independent interactions between human B cells and CD8⁺ T (both MAIT and non-MAIT) cells, and their possible implication in MS pathophysiology.

Chapter 1 introduces multiple sclerosis by summarizing the genetic and environmental factors associated with disease development, highlighting the roles of CD4⁺ T cells and B cells (both antibody dependent and independent functions) in disease pathogenesis and the implication of CD8⁺ T cells, including MAIT cells, in MS neuroinflammation.

Advancing our understanding of the functional response profiles of distinct cytokine-defined B cell subsets requires isolating them in a viable state. However, a major impediment to date is that the permeabilization and fixation process required for intracellular cytokine staining, and thus identification of cytokine-producing B cells, results in loss of cell viability. Other challenges include the low frequency of cytokine-expressing B cells in the circulation and the often-limiting volumes of samples available for study. In Chapter 2, I set out to optimize an approach for the simultaneous isolation of multiple rare cytokine-secreting viable human B cells. I demonstrate that

the cytokine-secretion assay can be developed and applied for the detection and isolation of multiple highly-purified, viable, low-frequency cytokine-defined B cells (i.e. cells secreting GM-CSF or IL-10), and that isolated cell fractions are amenable for downstream applications including gene expression profiling and *in vitro* culture. The assay can be multiplexed, wherein up to three cytokines can be simultaneously detected on B cells, without any impact on cell purity, though a variable loss in yields requires assay optimization. Overall, this approach is a stepping-stone in enabling future investigations into the biology of these cytokine-defined B cell subsets including their impact on responses of other cells.

In chapter 3, I examine the interactions between B cells and both CD8⁺ MAIT and non-MAIT cells using a series of *in vitro* experiments complemented by deep immunophenotyping of CD8⁺ T cells within peripheral blood mononuclear cells obtained prior to and after B cell depletion therapy in patients with MS. I found that B cells have opposing effects on different CD8⁺T cell subsets, namely induction of proliferation, pro-inflammatory cytokine responses, and cytotoxicity of MAIT cells, yet suppression of non-MAIT cell proliferation and pro-inflammatory cytokine production. *In vivo*, B cell depletion in MS patients results in reduced counts and pro-inflammatory responses of MAIT cells.

Overall, these observations provide novel insights into fundamental functions of human B cells in the modulation of CD8⁺ T cell effector responses, in both health and disease. They also add to our understanding of the complex cellular networks involving the balance between pro- and anti-inflammatory functions of different cell types and their interactions in the pathogenesis of multiple sclerosis by invoking a B cell:CD8⁺ T cell axis (and particularly the role of B cell: MAIT cell interactions), which may be therapeutically targeted by B cell depletion. Further characterization of cytokine-defined B cell responses and their interactions with CD8⁺ MAIT and non-MAIT cells could enable the development of more focused therapies that selectively impact these interactions for the treatment of autoimmune diseases.

Resumé

Les lymphocytes B acquièrent la capacité à produire des cytokines, et celle-ci est nécessaire pour contrôler les fonctions des lymphocytes T and cellules myéloïdes. Les fonctions des lymphocytes B indépendante de leur capacité à produire des anticorps s'est révélées importante dans le contexte de la sclérose en plaque, compte tenu des bienfaits cliniques des thérapies visant les lymphocytes B à base d'anticorps monoclonal dirigé contre CD20. En fait, ces thérapies ont eu un effet minimal sur les niveaux des anticorps présent au sein du système nerveux central. Nos études ont démontré que l'appauvrissement du nombre total des cellules B démunirait les fonctions effectrices des lymphocytes T CD4 et CD8, ce qui indique qu'au-delà des interactions bien décrites des lymphocytes B and T CD4, il y a peut-être lieu pour une interaction entre les lymphocytes B and T CD8. Il s'avère que les lymphocytes T CD8 sont plus nombreux que les lymphocytes T CD4 dans le cerveau des patients atteints de la sclérose en plaque, et que parmi les lymphocytes T CD8, des cellules dénotées MAIT produisant des cytokines pro-inflammatoires subsistent par une expansion clonale. Le but de mon projet de thèse est de décrire l'interaction entre les lymphocytes B et T CD8, et son implication dans la pathologie de la sclérose en plaque.

La production des cytokines par les cellules B est utile pour démarquer certains sous-types dotés de fonctions uniques. Malgré ceci, les caractéristiques de ces sous-types de cellules B restent inconnues due à l'inconvénient majeure de l'approche couramment utilisée pour mesurer l'expression des cytokines par la cytométrie en flux qui nécessite la fixation and perméabilisation des cellules. Par conséquent, cette approche s'est soldée par la perte de la viabilité des cellules. Autres défis consistent en un taux bas des sous-types des cellules B définies par la production des cytokines dans le sang et un volume du sang restreint et disponible pour la recherche. Dans le chapitre 2, j'ai développé une approche alternative pour l'isolation des cellules B produisant des cytokines. L'approche, connue comme « cytokine secretion assay », est utilisée dans le but d'isoler des cellules B capable de sécréter plusieurs cytokines rares telles qu'IL-10 et GM-CSF. Cette méthode a l'avantage de permettre l'isolation des cellules vivantes, ce qui est important pour le séquençage de prochaine génération et la culture des cellules *in vitro*. La détection de trois cytokines en parallèle est faisable, mais l'optimisation de cette manipulation est nécessaire afin de

réduire la perte de signal. En tout, cette méthode permettra des avancées considérables dans notre compréhension de la biologie des cellules B produisant des cytokines.

Dans le chapitre 3, j'examine les interactions parmi les cellules B et les sous types de lymphocytes T CD8, notamment cellules non-MAIT et MAIT. A cette fin, j'ai établi un système de co-culture de cellules B et T, et examiné le phénotype et la fonction des lymphocytes T CD8 dans le sang chez les patients traités avec l'anticorps monoclonal dirigé contre CD20. Mes observations démontrent que les cellules B interagissent différemment avec les sous types de lymphocytes T CD8. En fait, elles induisent la prolifération, la production des cytokines pro-inflammatoires et potentiel cytotoxique de cellules MAIT, mais elles suppriment la prolifération et la production des cytokines pro-inflammatoire de cellules non-MAIT. D'autant plus, l'appauvrissement des cellules B chez les patients traités réduit le nombre de cellules MAIT dans la circulation and leur production de cytokines pro-inflammatoires.

L'ensemble des mes travaux présentés dans cette thèse a approfondi notre compréhension du rôle de lymphocytes B, notamment leur capacité de contrôler les fonctions effectrices de lymphocytes T CD8 dans le contexte pathologique et physiologique sain. Cela sert a démontré que l'axe cellulaire lymphocytes B : T CD8 est pertinent dans la pathologie de la sclérose en plaque, et peut être visé par les thérapies ciblant les cellules B. Les futures recherches sur cette interaction cellulaire peuvent s'achever au développent des nouvelles thérapies dans le contexte des maladies auto-immunitaire y compris la sclérose en plaque.

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The thesis presented here reflects what for me has been an amazing scientific journey that started several years ago and still continues to this day. It is humbling to look back, and realize how far I have come. I hope it is the launchpad for a fulfilling and rewarding scientific career. Many wonderful individuals have made this journey fun and exciting to whom I wish to say – THANK YOU!

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Contribution to original knowledge

The key findings of this thesis are:

1. Newly developed cytokine secretion assay can overcome the limitation of the intracellular cytokine staining and be used for the detection and isolation of viable low as well as high frequency cytokine-secreting human B cells. Isolated fractions are highly purified and enriched for the corresponding cytokines, and can be integrated in downstream assays including next generation sequencing or cell culture.
2. The cytokine secretion assay can be multiplexed, allowing for the simultaneous detection and isolation of up to three cytokines, a particular advantage when dealing with limiting sample volume.
3. Human B cells can function as helper cells to activate MAIT cells. B cells enhance MAIT cell proliferation, cytotoxic potential, and cytokine production *in vitro*.
4. B cells can function as suppressors of CD8⁺ non-MAIT cells that down-regulate their proliferation and cytokine production.
5. B cell depletion therapy results in a shift in the distribution of circulating CD8⁺ T cell subsets, with a particular reduction in MAIT cells.
6. CD8⁺ non-MAIT and MAIT cell pro-inflammatory cytokine production is diminished following B cell depletion in multiple sclerosis patients.

Contributions of authors

Chapter 1: Introduction and literature review

A.R wrote the literature review

Chapter 2: Simultaneous detection and isolation of multiple, viable, distinct cytokine-secreting B cells

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Chapter 3: B cells regulate CD8⁺ MAIT cell effector functions: implications for multiple sclerosis

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A.B.O. provided the overall supervision, generated hypotheses, guided the experimental plan, analyzed the data and wrote/revised the manuscript.

Chapter 4

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List of abbreviations:

5-A-RU: 5-amino-6-D-ribitylaminouracil
5-OE-RU: 5-(2-oxoethylideneamino)-6-D-ribitylaminouracil
5-OP-RU: 5-(2-oxypropylideneamino)-6-D-ribitylaminouracil
ADP: Adenosine diphosphate
APC: Antigen presenting cells
APRIL: A proliferation inducing ligand
ATP: Adenosine triphosphate
BAFF: B cell activation factor
BALT: Bronchus-associated lymphoid tissues
BBB: Blood brain barrier
BCR: B cell receptor
CCL: CC chemokine ligand
CCR: CC chemokine receptor
CD: Cluster of differentiation
CIS: Clinically isolated syndrome
CNS: Central nervous system
CSF: Cerebrospinal fluid
CTLA-4: Cytotoxic T-lymphocyte-associated protein 4
EAE: Experimental autoimmune encephalomyelitis
EBNA-1: Epstein-Barr nuclear antigen 1
EBV: Epstein-Barr virus
ELISA: Enzyme linked immunosorbent assay
FOXP3: Forkhead box 3
GATA3: GATA binding protein 3
GF: Germ-free
GM-CSF: Granulocyte macrophage colony stimulating factor
GWAS: Genome-wide association studies
HLA: Human leukocyte antigen
IFN: Interferon

Ig: Immunoglobulin
IL: Interleukin
IRA: Innate response activator
iTreg: Inducible regulatory T cells
MAIT: Mucosal-associated invariant T cells
MBP: Myelin basic protein
MCAM: Melanoma cell adhesion molecule
MHC: Major histocompatibility complex
MOG: Myelin oligodendrocyte glycoprotein
MR1: Major histocompatibility complex, class I related
MRI: Magnetic resonance imaging
MS: Multiple sclerosis
NaCl: Sodium chloride
OCB: Oligoclonal bands
OR: Odd risk
PLP: Myelin proteolipid protein
PMA: Phorbol 12-myristate 13-acetate
PPMS: Primary progressive multiple sclerosis
RAR-related orphan receptor gamma
RIS: Radiologically isolated syndrome
RRMS: Relapse-remitting multiple sclerosis
RTE: Recent thymic emigrant
SNP: Single nucleotide polymorphism
SPF: Specific-pathogen free
SPMS: Secondary progressive multiple sclerosis
STAT: Signal transducer and activator of transcription
STIM: Stromal interaction molecule
T-bet: T-box transcriptional factor
Tconv: Conventional T cells
TCR: T cell receptor
Tfh: Follicular helper T cells

TGF: Transforming growth factor

Th: Helper T cells

TLR: Toll-like receptor

TNF: Tumor necrosis factor

Tr1: Type 1 regulatory T cells

TRAJ: T cell receptor alpha joining

Treg: Regulatory T cells

Chapter 1: Introduction and literature review

1.1 Introduction to Multiple Sclerosis

Multiple sclerosis is an immune-mediated and neurodegenerative disease of the central nervous system¹⁻⁴. Over two million individuals worldwide are diagnosed with the disease, which is associated with a major social and economic burden^{5,6}. The disease is most often diagnosed in individuals aged 20 to 40 years old, though pediatric-onset disease has been observed^{6,7}. Disease prevalence and incidence has steadily increased in the last five decades. In particular, female incidence has more than doubled in the last 50 years, which can explain the increasing female to male ratio estimated at 2:1 to 3:1⁸⁻¹¹. Latitudinal gradient of prevalence is still present in Europe and North America; however, recent epidemiological studies denote a disappearing gradient across the United States and elsewhere¹⁰. These relatively rapid changes in geographical and gender prevalence are likely driven by environmental rather than by genetic factors¹².

1.1.1 Clinical presentation of multiple sclerosis

Several clinical phenotypes have been described, including radiologically isolated syndrome (RIS), clinically isolated syndrome (CIS), relapsing-remitting multiple sclerosis (RRMS), secondary progressive multiple sclerosis (SPMS), and primary progressive multiple sclerosis (PPMS)^{3,13,14}. RIS patients are asymptomatic yet have magnetic resonance imaging (MRI) lesions suggestive of MS^{3,13,14}. CIS is diagnosed in patients who experience a single clinical event suggesting CNS demyelinating disease, but do not yet meet the full criterion for dissemination in time for formal MS diagnosis^{3,13,14}. Both RIS and CIS are now essentially thought of as ‘early MS’ when patients present with typical MRI appearance and spinal fluid features (such as the presence of ‘clonally-restricted’ immunoglobulin in the cerebrospinal fluid known as oligoclonal bands) seen in MS. Overall, RRMS is the most common clinical presentation found in 85% of patients, and is typically characterized by periods of clinical exacerbation (relapses) with complete or partial recovery and interim stability (remission)^{3,13,14}. The majority of RRMS patients then develop progressive clinical worsening, a disease course defined as SPMS, with a median time to progression estimated at 19 years^{3,13,14}. Finally, approximately 15% of patients experience gradual disease worsening from clinical onset with no frank relapses and remissions, which is referred to as PPMS^{3,13,14}.

1.1.2 Genetic factors in multiple sclerosis

Multiple sclerosis is a complex disease, in which an interplay between genetic and environmental factors underlies disease risk¹⁵⁻¹⁷. Indeed, monozygotic twins have a higher rate of concordance (20-30%) than dizygotic twins (2-5%) or second- and third-degree relatives¹⁸⁻²¹. Sibling recurrence risk was estimated at 7-fold in the population of Sweden²²⁻²⁴. Human leukocyte antigen (HLA) variants within the major histocompatibility complex (MHC) gene were first described in MS in the 1970's¹⁵. In fact, HLA haplotypes are a major determinant of disease risk, as individuals carrying the MHC class II variant HLA-DRB1*15.01 have three-fold increased risk, whereas individuals carrying the MHC class I variant HLA-A*02 are relatively protected (odd risk=0.6)²⁵⁻²⁸. Further, the DRB1*15 allele is more prevalent in children of European ancestry diagnosed with MS compared to normal controls or children presenting with acquired demyelinating syndromes that are not MS^{29,30}.

The genetics of MS have been extensively examined in genome wide association studies (GWAS), which have identified over 200 single nucleotide polymorphisms (SNPs) conferring increased risk of MS. These SNPs generally map to noncoding regions of the genome and are notably shared with other autoimmune conditions^{25,26,31-33}. The majority of candidate genes linked to these SNPs encode proteins that function in the immune system, such as *IL2R*, *IL7R*, *CD86*, etc., and have an influence on T cells, B cells and monocytes^{15,25,26,31,34,35}. Individual variants have rather small effects on disease risk, and such variants are present in non-diseased individuals where they have probably evolved to provide the host with a fitter immune system to fight pathogens³⁶. With few exceptions, the effects of these SNPs on gene function are not well understood³⁷⁻⁴³. One prominent example is rs1800693, which influenced the splicing *TNFRSF1A*, resulting in the production of a novel soluble form of the TNF receptor³⁹. This receptor inhibited TNF signaling in a similar fashion to TNF blocking drugs, which has been shown to dramatically increase disease activity in MS patients^{39,44-46}. Another example is an insertion-deletion variant in *TNFSF13B* encoding for BAFF, termed BAFF-var, that was associated with increased MS risk in the Sardinian population but no other European populations⁴⁷. BAFF-var was associated with increased circulating B cell numbers, decreased circulating monocyte numbers, and increased levels of soluble BAFF, IgG, IgA and IgM in the Sardinian population⁴⁷. These studies showcase the consequence of individual SNP variant on the immune system, however, their collective impact

on the immune dysregulation observed in MS is unknown as well as the putative interactions between genetic and environmental factors in dictating disease risk.

1.1.3 Environmental factors and multiple sclerosis

Classical epidemiological studies have revealed key roles for environmental factors in disease risk. These factors include low levels of vitamin D, lack of sun exposure, obesity in adolescence, tobacco smoking or second-hand tobacco exposure, and early Epstein-Barr virus (EBV) infection or development of clinical infectious mononucleosis^{12,16,48}. The environmental contributions to disease risk have also been ascertained in migrant studies. In fact, the overall disease risk in migrants is intermediate between the risk in countries of origin and residence and depends on age at migration⁴⁹⁻⁵⁴. Many of the implicated environmental factors can regulate immune responses and can interact with the HLA alleles to modulate disease risk¹².

1.1.3.1 Vitamin D and sun exposure

Vitamin D conversion into active metabolites depends on ultraviolet B radiation from sun exposure, and in countries at high latitude, sun exposure is rather limited^{12,17}. In fact, individuals exposed to higher sunlight have a reduced MS risk⁵⁵⁻⁵⁷ and disease risk declines with increasing levels of 25(OH)D^{30,58-60}. In addition, polymorphisms in genes involved in vitamin D metabolism are associated with disease risk⁶¹. Vitamin D metabolites may act as immunomodulatory agents to regulate pro-inflammatory functions of both T cells and B cells^{62,63}.

1.1.3.2 Obesity

Obesity in early life is associated with greater than two-fold increase in risk of pediatric and adult-onset multiple sclerosis, and there is a notable interaction between obesity with HLA alleles resulting in further increased disease risk (OR=14)^{12,64-68}. Obesity is associated with low grade inflammation, increased levels of leptin, and reduced levels of vitamin D, all of which can instigate detrimental pro-inflammatory immune responses^{12,16}.

1.1.3.3 Tobacco smoking

Active or passive tobacco smoking is linked to increased disease risk, with heavy smokers at higher risk (OR=1.3 to 1.6)⁶⁹⁻⁷³. Like obesity, smoking interacts with HLA alleles, resulting in increased disease risk (OR=14)¹². In one proposed model, smoking causes lung irritation and inflammation

and induces the formation of bronchus-associated lymphoid tissue, where self-reactive immune cells are activated and traffic to the CNS^{12,16}. This is based on the observation that encephalitogenic T cells were licensed in the lungs before migrating to the CNS in experimental autoimmune encephalomyelitis (EAE), the commonly used animal model of MS neuroinflammation⁷⁴.

1.1.3.4 EBV infection

EBV, a double stranded DNA γ -herpesvirus, eventually infects more than 90% of the general population, and more than 99% of the MS population^{12,16,75}. EBV seropositivity was also more prevalent in children with MS than in age- and sex-matched controls, and viral reactivation was more often observed in pediatric MS patients^{30,76-79}. Individuals who experience clinical infectious mononucleosis due to EBV have greater than two-fold increased disease risk, as demonstrated in a meta-analysis of case-control studies and in the Danish population^{75,80,81}. In a nested case control study, EBV seronegative individuals seroconverted before MS disease onset⁸². Another body of work showed that MS patients had higher levels of antibodies against EBV proteins (such as EBNA-1), as well as a higher frequency of T cells specific for EBV antigens in the blood and CSF⁸³⁻⁸⁷. In that regard, it has been hypothesized that molecular mimicry between EBV and CNS antigens can drive pathogenic T cell and B cell responses in the CNS⁷⁵. Others observed that the frequency of EBV-specific CD8⁺ T cells was reduced in MS patients, resulting in impaired control of EBV infection⁸⁸⁻⁹². Other hypotheses regarding a link between EBV infection and immune pathogenesis in MS include bystander damage in the CNS, EBV-induced aberrant B cell cytokine response and $\alpha\beta$ Crystallin ‘mistaken self’⁹³. In the mouse model experimental autoimmune encephalomyelitis (EAE), latent γ -herpesvirus 68 infection resulted in a more severe disease course that was associated with increased CD4⁺ as well as CD8⁺ T cell infiltration into the CNS and a skewed Th1 response, though the implication for MS remains uncertain⁹⁴.

1.2 From CD4⁺ T cell-mediated disease to disease of B cell:CD4⁺ T cell interactions

1.2.1 Imbalance between CD4⁺ effector and regulatory T cells in MS

The prevailing concept of MS pathophysiology has highlighted a central role for T cells, and in particular CD4⁺ T cells, in the cellular immune cascades leading to tissue injury in the MS CNS⁴. Much of this thinking has been shaped over the years by findings in the commonly used mouse model of MS, EAE⁹⁵. Described over 80 years ago, in this model, animals can be actively immunized with myelin proteins or peptides along with complete Freund’s adjuvant,

Mycobacterium tuberculosis and pertussis toxin^{96,97}. The animals develop a disease characterized by demyelination in the spinal cord and brain, with appearance of perivascular lesions and inflammatory infiltrates, gliosis, partial remyelination, and in some instances, presence of immunoglobulin in the lesions and CSF⁹⁵. Further emphasizing the role of T cells in the animal model were observations that thymectomized rats failed to develop the disease, as well as the ability to passively transfer disease into naïve animals by injecting activated lymph node cells (or activated CNS-reactive T cells) from immunized (diseased) animals⁹⁸⁻¹⁰³. Seminal observations made in EAE have been extended with the notion that CD4⁺ helper cells are instrumental in MS pathophysiology. While EAE is not actually MS in animals, there is ample evidence for over-activated CD4⁺ T cells in peripheral blood as well as the brain in MS patients⁴.

It is now well appreciated that, in general, CD4⁺ T cells can acquire distinct functional phenotypes upon encountering antigen-presenting cells (APC) in lymphoid tissues, which can be relevant in both health and disease states^{104,105}. Indeed, three signals are necessary for optimal naïve T cell differentiation upon APC encounter, including TCR engagement with peptide loaded MHC molecules (signal 1), co-stimulatory signals such as CD80 and CD86 (signal 2), and polarizing cytokines (signal 3)^{104,105}. These polarizing cytokines serve to reflect the nature of the perceived insult, thus providing a mean to mount the appropriate immune response to differing host infections. IL-12, a heterodimer of IL-12p40 and IL-12p35, binds its receptor on T cells and induces their differentiation into type 1 T helper (Th1) cells that express the master transcriptional factor T-bet and produce IFN- γ , TNF, and GM-CSF^{104,106}. IL-4 induces T cell differentiation into Th2 cells that express the transcriptional factor GATA3 and produce IL-4, IL-5, and IL-13^{104,106}. Th17 cells have emerged as distinct from the original dichotomy (Th1 versus Th2), and can be induced by a combination of IL-1 β , IL-6, IL-23 and TGF- β and maintained by autocrine IL-21 production¹⁰⁷⁻¹¹⁶. Th17 cells express the transcriptional factor ROR γ t, and produce IL-17, IL-21, and GM-CSF. These are not hard-wired phenotypes, as a degree of plasticity has been characterized reflecting the impact of the inflammatory microenvironment in which T cells operate^{104,117}.

Th17 cells are characterized by higher expression of brain-homing receptors (CCR6, CCR2 and CCR5) and adhesion molecules (CD49d, CD146 (MCAM), CD6)¹¹⁸⁻¹²⁶. IL-17 expression was

elevated in lesions obtained from post-mortem MS cases compared to controls, and higher numbers of IL-17⁺ T cells were found in active compared to inactive areas of MS lesions¹²⁷⁻¹²⁹. Th17 cells can engage in cross-talk with brain resident cells including astrocytes and blood brain barrier (BBB) endothelial cells. Human blood brain barrier endothelial cells express the cell surface receptors for IL-17 and IL-22, and exposure to IL-17 and IL-22 leads to disruption of the tight junctions and secretion of CCL2^{130,131}. This allows Th17 cells and other CNS-recruited cells to migrate more efficiently across the barrier^{121,130}. This interaction with the BBB also enhances IL-17 and IL-22 expression in T cells^{121,130}. Fetal human astrocytes stimulated *in vitro* with IL-17 and TNF express increased levels of inflammatory molecules such as IL-6 and CCL20, which can sustain local inflammation by recruiting CCR6-expressing cells (such as Th17 cells among others)¹³². CCR6 deficiency abrogated EAE disease induction, and this was associated with reduced T cell infiltration into the CNS through the choroid plexus¹²¹. It follows that the frequency of Th17 cells was increased in the cerebrospinal fluid (CSF) compared to peripheral blood, and that it was higher in MS patients compared to controls^{119,131,133-136}. IFN- γ producing Th17 cells, known as Th17.1 cells, were found in MS brain, showed preferential accumulation in the CSF, and possessed enhanced migratory capacities across endothelial cells^{129,137}. Not surprisingly, MS-derived Th17 and Th17.1 cells showed a distinct functional phenotype from normal controls cells, including lower expression of granzyme B and IL-10¹³⁶.

A pathogenic role for GM-CSF in neuroinflammatory disease was suggested by *McQualter et al.* wherein GM-CSF deficient mice were resistant to EAE induction¹³⁸. Immune cell infiltration into the brain was reduced, as was the proliferation and effector functions of splenic immune cells. Similarly, adoptive transfer of CSF2^{-/-} Th1 or Th17 cells into naïve mice failed to induce EAE^{139,140}. Therapeutic intervention with anti-GM-CSF antibody at disease initiation or at disease peak resulted in clinical benefits^{138,140}. In this model, GM-CSF induced the expression of a pro-inflammatory gene signature in monocyte-derived dendritic cells that perpetuated the inflammatory response in CNS¹⁴¹⁻¹⁴³. Indeed, GM-CSF-stimulated monocyte-derived dendritic cells up-regulated the expression of CCL6, CCL24, and CCL17 to enhance further myeloid cell recruitment into CNS and expressed IL-1 β and IL-23, which supported pathogenic T cell generation in peripheral lymph nodes and compromised the blood brain barrier integrity¹⁴¹⁻¹⁴³. In humans, the frequency of GM-CSF-producing CD4⁺ T cells was elevated in both MS peripheral

blood and CSF, with a preferential accumulation of these cells in the CSF and lesions¹⁴⁴⁻¹⁴⁹. In contrast to murine T cells, human naïve T cells express GM-CSF under Th1 and not Th17 polarizing conditions, and are dependent on IL-2-STAT5 axis and IL-12 for optimal differentiation^{144,147}. Further, a polymorphism in *IL2RA* (rs2104286) was associated with an increased propensity for CD4⁺ T cells to produce GM-CSF *ex vivo* and *in vitro* cultures¹⁴⁷.

The aforementioned changes in T cell responses were observed in adult-onset MS patients, wherein the biological onset likely preceded the clinical onset by many years and aberrant immune functions can be secondary to ongoing injury or chronic inflammation³. In contrast, pediatric-onset multiple sclerosis offers a unique window into disease relevant immune functions given the likely closer time proximity between biological and clinical onset⁷. In this setting, the frequency of blood CD4⁺ T cell population co-expressing the brain homing receptors CCR2 and CCR5 was found to be increased and produced elevated levels of IFN- γ and IL-17 in children with MS at the first clinical presentation but not in normal controls and in children with monophasic acquired demyelinating syndrome (serving as ‘other CNS inflammatory disease’ controls)¹⁵⁰.

The antigen(s) recognized by T cells in the context of multiple sclerosis remain elusive. Myelin proteins are attractive candidates, and indeed, earlier studies have found that T cell clones derived from MS patients were reactive to myelin basic protein (MBP) and myelin oligodendrocytes glycoprotein (MOG)¹⁵¹⁻¹⁶⁰. However, similar CD4⁺ T cell reactivity was also observed in normal controls¹⁵¹⁻¹⁶⁰. Furthermore, *Banwell et al.* demonstrated that T cells of children with multiple sclerosis and remote CNS injury exhibited similarly increased reactivities to CNS-derived antigens including MBP and MOG, making the point that abnormally increased T cell proliferative responses to CNS antigens may be seen as a consequence of and not necessarily the cause of CNS injury¹⁶¹. It remains possible that myelin-reactive T cells in MS are functionally distinct from the control cohort counterparts in that these T cells did not require co-stimulation for *in vitro* expansion and produced elevated levels of pro-inflammatory cytokines, including IFN- γ , IL-17, and GM-CSF, along with decreased IL-10 levels¹⁶²⁻¹⁶⁵. Other candidate antigens may be relevant, including axoglial apparatus molecules, as such proteins were enriched in the CSF of children with MS compared to controls at the first clinical presentation¹⁶⁶.

Planas et al. recently identified IFN γ producing CD4⁺ T cell clones present in the CSF of multiple sclerosis patients that recognized a ubiquitous self-antigen known as guanosine diphosphate (GDP)-L-fucose synthase¹⁶⁷. This antigen was expressed in white and gray matter of post-mortem brain tissue samples¹⁶⁷. The human protein had 40% sequence similarity with the bacterial homologue, and T cell clones were reactive to bacterial peptides, though T cell cross-reactivity was not examined in this study¹⁶⁷. Similarly, CD8⁺ T cell clones isolated from a MS patient recognizing PLP₄₅₋₅₃ in the context of HLA-A3 were (cross) reactive to another ubiquitous antigen known as glycerolphosphatidylcholine phosphodiesterase 1¹⁶⁸. This theme extends to rheumatoid arthritis where T cells and antibodies isolated from patients recognized 60S ribosomal protein L23a (RPL23A)¹⁶⁹. Altogether, this data supports a model wherein a secondary immune response is directed to ubiquitous antigens released from tissues following primary injury instigated in part by a defective immune cell repertoire.

In the normal state, effector T cells do not function in isolation but rather are controlled by cellular regulatory mechanisms to prevent immune pathologies. In this regard, regulatory T cells provide a key cellular mechanism aimed at preventing excessive effector T cell functions¹⁷⁰⁻¹⁷². This is exemplified by the systemic autoimmunity observed in humans and mice carrying mutations in the gene encoding the transcriptional factor forkhead box P3 (FOXP3)¹⁷³⁻¹⁷⁵. FOXP3 is highly expressed in CD4⁺CD25⁺ regulatory T cells and is required for their suppressive functions¹⁷⁶⁻¹⁷⁸. Scurfy mice carrying a *Foxp3* mutation have a deficiency in CD4⁺CD25⁺ regulatory T cells, accompanied by excessive T cell proliferation, multi-organ immune cell infiltration, and elevated serum cytokine levels that result in neonatal and adult death¹⁷⁶⁻¹⁷⁹. Similar outcomes were observed in athymic nude mice receiving CD25-depleted T cells or in mice with acute depletion of regulatory T cells¹⁸⁰⁻¹⁸². In the absence of regulatory T cells, T cell reactivity was directed toward self-antigens and not microbial or food antigens¹⁸³⁻¹⁸⁵.

Regulatory T (Treg) cells develop from T cells recognizing self-antigens but are not eliminated by negative selection in the thymus, and as such, their TCR repertoire is biased to self-antigens^{170,172,186,187}. Inducible Treg (iTreg) cells can be induced *in vitro* or can develop from naïve T cells in peripheral tissues such as the gut lamina propria^{184,188,189}. Regulatory T cells display an anergic phenotype to T-cell receptor stimulation, which can be overcome by co-stimulatory signals

such as CD28 and high IL-2 dose¹⁹⁰⁻¹⁹⁴. Regulatory T cells maintain peripheral tolerance through multiple suppressive mechanisms that act on antigen-presenting and/or effector T cells. These mechanisms include competition for co-stimulatory signals on antigen presenting cells via CTLA-4, consumption of locally-produced IL-2, degradation of ATP and generation of adenosine, production of immunosuppressive molecules such as IL-10 or IL-35, and cytotoxicity^{170,171}. Further, certain mechanisms are more relevant for the maintenance of tolerance in tissues, such as IL-10 production. Indeed, IL-10-deficient mice exhibited inflammation in the colon and the central nervous system, and specific IL-10 depletion in regulatory T cells resulted in spontaneous colitis and exacerbated EAE¹⁹⁵⁻²⁰². In this context, IL-10 signaling in T cells was required for the suppression of pathogenic Th17 cell responses as well as the generation of type 1 regulatory T cells (Tr1 cells)^{198,199,203-205}.

Human regulatory T cells include FOXP3⁺CD25^{hi}CD127^{lo}CD4⁺ T cells, and more recent mass cytometry and single-cell RNA-seq analysis have emphasized the presence of discrete regulatory T cell populations in human blood^{190-193,206-210}. Regulatory T cells are functionally heterogeneous, with certain subsets exerting greater suppressive effects on effector T cells, such as CD45RA⁺CD25^{hi}FOXP3^{lo} cells and CD45RA⁻CD25^{hi}FOXP3^{hi} cells, whilst others acquire a capacity to produce cytokines, such as CD45RA⁻CD25^{hi}FOXP3^{lo} cells²¹¹⁻²¹⁴. Indeed, cytokine-producing regulatory T cells have been characterized in the circulation of normal individuals and patients and are enriched within the memory T cell pool²¹⁵⁻²¹⁸. Th1-like, Th2-like, and Th17-like regulatory T cells co-express FOXP3 and T-bet, GATA-3, and ROR γ T, respectively; produce prototypical cytokines such as IFN- γ , IL-4, and IL-17; and express characteristic Th cell chemokine receptors²¹⁵⁻²¹⁸. Th-like regulatory T cells retain suppressive functions; however, they cannot be suppressive and produce cytokines simultaneously^{216,217}. Regulatory T cell sensitivity to CD3, CD28, and cytokine receptor signaling is comparatively low, which may repress cytokine expression in these cells²¹⁹. Also, Th-like regulatory T cells in humans differ from T-bet⁺, GATA3⁺, and ROR γ T⁺ regulatory T cells in mice, which fail to produce the corresponding cytokines IFN- γ , IL-4, and IL-17 under acute inflammation²²⁰⁻²²⁴. The acquisition of T-bet, GATA3, and ROR γ T appears necessary for optimal maintenance and recruitment of murine regulatory T cells to the site of inflammation, where these cells serve to regulate Th1 and Th17

cells²²⁰⁻²²⁴. Nonetheless, regulatory T cells can produce inflammatory cytokines in the context of chronic inflammation, such as cancer or CNS neuroinflammation^{225,226}.

In autoimmune diseases, defects in regulatory T cells have been observed, including a reduction in the frequency of circulating cells, aberrant and/or loss suppressive mechanisms, and resistance of effector T cells to suppression²²⁷. In multiple sclerosis, thymic output is reportedly diminished such that the number of recent thymic emigrant (RTE) T cells is reduced²²⁸⁻²³⁴. This includes reduced frequency of circulating RTE regulatory T cells and a relative increase in the frequency of memory regulatory T cells^{228,231} while the frequency of total circulating regulatory T cells is unchanged²³⁴⁻²³⁸. Further, it is now well documented that regulatory T cells from MS patients fail to suppress the expansion of autologous or allogenic effector T cells in antigen-specific or polyclonal culture systems^{234,235,237,239}. This deficient suppressive function has been linked to reduced FOXP3 expression²⁴⁰. FOXP3 serves to maintain regulatory T cell hypo-responsiveness, to amplify and stabilize the expression of suppressive soluble mediators (such as *IL10*, *Ebi3*, *GzmB*), as well as the ectonucleotidases (*Entpd1*, *Nt5e*), and to repress the expression of pro-inflammatory cytokines (such as *Il2*, *Il4*, *Il17a*, and *Ifng*)^{241,242}. In line with a reduction in FOXP3 expression, CD39 expression on regulatory T cells isolated from MS patients was reduced, and the function of CD39-expressing regulatory T cells was altered²⁴³. CD39 is an ectonucleoside triphosphate diphosphohydrolase required for the conversion of extracellular ATP into adenosine²⁴⁴⁻²⁴⁶. Paracrine or autocrine adenosine signals through A2AR and has multiple effects on T cells that include negative regulation of TCR signaling in effector T cells as well as amplification of CD39, CD73, and FOXP3 expression in regulatory T cells²⁴⁶. *In vitro*, CD39-expressing regulatory T cells can inhibit the secretion of IL-17 and IFN- γ in effector T cells, a regulatory mechanism defective in MS patients^{243,247}. The differentiation of T cells into type 1 regulatory T cells, characterized by IL-10 production upon CD2 or CD46 engagement, was less efficient in MS patients compared to normal controls^{37,248,249}.

The frequency of Th1-like, but not Th17-like, regulatory T cells was increased in the blood of MS patients compared to normal controls, whilst the frequency of IL-10⁺ regulatory T cells was reduced^{250,251}. This resulted in an increased ratio of IFN- γ ⁺/IL-10⁺ regulatory T cells in patients compared to controls. Th1-like Treg cells displayed a similar methylation pattern in Treg-cell

specific demethylated region (TSDR) than non-IFN- γ producers, demonstrating that these cells represent bone-fide Treg cells²⁵⁰. Their differentiation was dependent on IL-12 and on PI3K-AKT-FOXO1-FOXO3 pathways and could be antagonized by TIGIT signaling²⁵⁰⁻²⁵³. In MS, the suppressive capacity of Th1-like Treg cells was deficient, and this could be normalized by utilizing an IFN γ neutralizing antibody or by a TIGIT agonistic antibody^{250,253}.

Recent observations in pediatric-onset MS mirrored the abnormalities in regulatory T cells seen in adult-onset MS. Regulatory T cells from children with MS expressed lower FOXP3 levels than controls (including children with acquired-demyelinating syndrome) and possessed an impaired suppressive capacity¹⁵⁰. In addition, effector T cells from children with MS were resistant to suppression by control regulatory T cells, suggesting that aberrant effector CD4⁺ T cell functional responses can contribute to the cascade of events leading to tissue injury early in the disease¹⁵⁰.

Environmental factors can modulate the balance between effector and regulatory T cells. Salt, melatonin, and gut microbiota are emerging as putative regulators. Sodium chloride enhanced IL-17 production in effector CD4⁺ T cells *in vitro* and *in vivo* and, in parallel, impaired Treg cell suppressive capacity by promoting Th1-like Treg phenotype and reducing IL-10 production^{251,254-256}. However, the pathophysiologic relevance remains uncertain, as there was no association between the average 24-hour urine sodium levels with clinical or MRI outcomes over follow-up, nor with conversion to clinically definite MS²⁵⁷. In addition, the total dietary sodium intake at baseline was not associated with the risk of developing MS in the Nurses' Health Study I and II²⁵⁸. *Farez et al.* found that melatonin suppressed human Th1 and Th17 cells and enhanced Tr1 cells *in vitro* and in EAE mouse model²⁵⁹. In MS patients, urine melatonin levels were highest in autumn and winter, during which time patients typically see reduced rates of relapse²⁵⁹. In regards to the gut microbiota, several studies have observed that the diversity in fecal microbiota was similar between MS patients and controls²⁶⁰⁻²⁶³. However, there were subtle changes in the relative abundance of certain phyla and genera, such as an increased abundance of *Euryarchaeota*, *Verrucomicrobia*, *Methanobrevibacter*, *Akkermansia*, and *Acinetobacter* with a reduced abundance of *Parabacteroides*, *Butyrivomax*, *Prevotella*, and *Sutterella*²⁶⁰⁻²⁶³. In mouse models, the EAE disease course was attenuated in germ-free mice compared to conventionally colonized mice or specific pathogen free mice^{264,265}. In germ-free mice, pro-inflammatory Th1 and Th17 cell

responses were reduced in the gut and spinal cord concomitant with increased T cell regulatory functions and reduced dendritic cell effector functions in secondary lymphoid tissues^{264,265}. Disease susceptibility was restored in germ-free mice colonized with segmented filamentous bacteria²⁶⁵. Similarly, transfer of MS patients' microbiota into germ-free mice exacerbated EAE disease course compared to normal controls' microbiota, and this was associated with reduced FOXP3 and IL-10 expression in T cells in mesenteric lymph nodes²⁶³. Transfer of MS-affected twins' microbiota into EAE spontaneous mouse model resulted in a more severe disease course compared to the transfer of microbiota from healthy twins²⁶¹. In parallel *in vitro* studies, *Acinetobacter calcoaceticus* and *Akkermansia muciniphila* enhanced IFN- γ production in human T cells, whilst *Parabacteroides distasonis* induced IL-10 production in T cells²⁶³. Further, there was an inverse correlation between the frequency of intestinal IL-17 producing T cells and the relative abundance of *Prevotella* strains in MS patients and controls²⁶⁶. Disease modifying therapies may in part act by modifying the gut microbiota, as patients receiving interferon-beta-1a or glatiramer acetate had an increased relative abundance of *Prevotella* and *Sutterella* compared to untreated patients²⁶⁰. *In vivo*, therapeutic intervention with *Prevotella histicola* in an EAE mouse model resulted in decreased CNS infiltration by Th1 and Th17 cells and increased frequencies of tolerogenic dendritic cells and regulatory T cells in peripheral lymphoid tissues²⁶⁷. Finally, in a case-control study, Tremlett *et al.* found that the overall diversity of the gut microbiota was similar between pediatric-onset MS patients and controls²⁶⁸⁻²⁷⁰. However, the relative abundance of *Actinobacteria*, *Desulfovibrio*, *Bifidobacterium*, and *Christensenellaceae* was increased in patients' fecal microbiota, with a decreased abundance of *Lachnospiraceae* and *Ruminococcaceae*^{269,270}. In pediatric MS patients, the frequency of blood Th17 cells was negatively correlated with the relative abundance of Bacteroides but was positively correlated with Firmicutes' abundance²⁶⁸. Altogether, the dysregulated T cell functions observed in patients with multiple sclerosis may in part be controlled by a distinct gut microbial community.

1.2.2 Targeting B cells in multiple sclerosis

Initial observations on the deposition of immunoglobulin (Ig) in brain lesions and the abnormal presence of CSF oligoclonal Ig bands in MS patients were suggestive of a pathological antibody-dependent role for B cells in the disease course and provided the initial rationale for targeting B cells in patients²⁷¹. Two of the main strategies used to target B cells in clinical trials of MS, anti-

CD20 antibody (rituximab, ocrelizumab, ofatumumab) and transmembrane activator and CAML interactor (TACI)-Ig fusion protein (atacicept), had contrasting outcomes²⁷²⁻²⁷⁷. A growing understanding over the recent years of the relevant modes-of-action of these two therapies has contributed important novel insights into antibody-independent B cell functions that are now thought to play a role in MS pathophysiology, including their ability to present antigens to T cells, secrete pro- and anti-inflammatory cytokines that modulate both T cell and myeloid cell responses, and contribute to the formation of ectopic lymphoid structures²⁷¹.

CD20 is a cell surface receptor expressed at high levels on pre-B cells, transitional, naïve, and memory B cells but absent on progenitor B cells and antibody secreting/plasma cells²⁷¹. Anti-CD20 antibody binds to CD20, and can deplete B cells via complement-dependent cytotoxicity, antibody-dependent cell-mediated cytotoxicity, antibody-dependent cell-mediated phagocytosis, and induction of apoptosis²⁷¹ (with the latter likely the least relevant *in vivo*). In two phase 3 clinical trials enrolling relapsing-remitting MS patients, intravenous anti-CD20 antibody (ocrelizumab) showed substantial (over 95%) decrease in new MRI disease activity compared to patients receiving β -interferon²⁷⁴. Clinical benefits observed in MS patients treated with B cell depletion therapy (BCDT) occurred whilst CSF IgG index, IgG concentration, and oligoclonal band numbers were unaffected^{272,278-280}. This was highly suggestive that some pro-inflammatory antibody-independent function/s of B cells is/are involved in the pathological cellular cascades leading to new waves of focal inflammation and disease relapses in MS. Indeed, mechanistic studies have since demonstrated exaggerated pro-inflammatory B cell responses in untreated MS patients with the capacity to induce pro-inflammatory T cell and myeloid cell functions²⁷¹. In keeping with this, depletion of B cells using anti-CD20 resulted in diminished T cell and myeloid cell effector responses^{271,281,282}. Further, the functional profile of reconstituting B cells in patients was distinct from pre-treatment in that pro-inflammatory cytokine production by the reconstituting B cells was reduced concomitant with increased anti-inflammatory cytokine production^{271,281,283}.

In contrast to the benefit of anti-CD20, atacicept, a fusion protein of TACI and Ig, increased annualized relapse rates compared to placebo in a phase II safety and efficacy trial in MS patients²⁷⁷. TACI is a cell surface receptor that binds B cell activating factor (BAFF) and a proliferation-inducing ligand (APRIL), two B cell pro-survival factors^{284,285}. BAFF also binds to

BAFF-R, whilst APRIL binds to BCMA^{284,285}. Subsequent analysis showed that whilst transitional and naïve B cells as well as plasmablasts/plasma cells were strongly affected by this treatment, memory B cells were spared^{271,286,287}. The striking contrast in clinical outcomes of atacicept and ocrelizumab serves to highlight the diverse and functionally distinct features of B cell subsets in either activating or regulating immune responses. The subsequent sections provide further detail of both antibody-dependent as well as antibody-independent functions of B cells that are thought to be relevant in MS pathophysiology. In the context of antibody-independent B cell functions, both pro-inflammatory (and pathogenic) functions of memory B cells and potential regulatory (and beneficial) functions of naïve B cells and plasma cells will be reviewed.

1.2.3 B cell antibody-dependent functions in multiple sclerosis

A question common to MS and other autoimmune diseases in which autoantibodies are considered as potential contributors to pathophysiology is whether such abnormal antibodies are generated in a very focused way to particular target-organ antigens (e.g. CNS in MS) or whether a broader abnormality of B cell tolerance exists. In the normal state, two mechanisms of B cell tolerance (central and peripheral) exist to limit the development of potentially harmful autoreactive antibodies²⁸⁸. Central tolerance occurs during early B cell development and results in purging of up to 75% of potentially auto-reactive B cells in the bone marrow²⁸⁸. Intact B-cell receptor and toll-like receptor mediated signaling are required for this process, as individuals with mutations in BTK, PTPN22, IRAK-4, MYD88, and UNC-93B show defects in central as well as peripheral tolerance²⁸⁸. Peripheral tolerance serves as a second checkpoint to control auto-reactive clones that have escaped selection in the bone marrow²⁸⁸. This process appears to depend on regulatory T cells and BAFF concentrations. IPEX patients, patients with mutation in CD40L or MHC-II, and CD3- or AIRE-deficient patients have defects in peripheral B cell tolerance reflected in polyreactive mature naïve B cells²⁸⁹⁻²⁹¹. *Kinnumen et al.* reported a loss of peripheral (but not central) tolerance, associated with defective regulatory T cell function in MS patients^{292,293}. Mature naïve B cells of patients were polyreactive and tended to recognize antigens present in white matter extracts²⁹².

In MS, pathology studies have identified abnormal antibody deposition suggestive of binding to particular CNS target-antigens^{271,294}. Surface and cytoplasmic immunoglobulins have been reported in myeloid cells close to myelin sheaths at demyelinating plaque margins in MS, hinting

to a pathogenic role for antibodies^{295,296}. In a classical study by *Lucchinetti et al.*, four demyelinating lesion patterns emerged in post-mortem brain tissues from MS patients, with pattern II most commonly found among patients examined^{297,298}. Pattern I and II associated with inflammatory infiltrates, whereas loss of oligodendrocytes was prominent in pattern III and IV^{297,298}. Immune infiltrates in pattern II lesions were composed of T cells and macrophages around blood vessels as well as the deposition of IgG and complement C9neo antigen at sites of active myelin destruction^{297,298}. Ig bound to myelin fragments could be observed within macrophages and at the active plaque edge^{297,298}. C9neo antigen was associated with degenerating myelin and myelin degradation products^{297,298}. Ig-containing plasma cells could also be found in active MS lesions^{297,298}.

In addition, >95% of MS patients have oligoclonal immunoglobulin bands restricted to the CSF (i.e. not overlapping with serum) with a predominance of IgG bands, though IgM bands are also observed in a subset of patients^{3,299-305}. Increased intrathecal IgG synthesis rates are found in 96.2% of MS patients, with lower rates in controls, and there is overlap between CSF immunoglobulin proteomes and immunoglobulin transcriptomes of CSF B cells, which is further indicative of local immunoglobulin synthesis^{300,306}. This is also supported by the capacity for CSF clonally-expanded plasma cells to produce IgG that comprise the oligoclonal bands in the CSF^{307,308}.

Recombinant antibodies produced from plasma cells isolated from CSF of MS patients were found to cause myelin loss and astrocyte activation in spinal cord explant cultures when added in the presence of complement³⁰⁹. Continued efforts have been made to determine the target antigen(s) recognized by CSF Igs, though it has been difficult to demonstrate antibodies recognizing myelin antigens. Recent work suggested that CSF Igs of MS patients recognized ubiquitous intracellular proteins (e.g. MKNK1/2, FAM84A, and AKP17A) that were not brain specific, but were more likely generated secondary to tissue injury³¹⁰. Indeed, serum antibodies against FAM84A antigens were more prevalent in inflammatory bowel disease patients than in controls³¹¹. *Von Budingen et al.* demonstrated that monoclonal antibodies derived from clonally expanded CSF plasma cells showed reactivity to myelin and intracellular filaments but failed to react to classical myelin antigens including MOG, MBP, PLP, or common viral antigens³⁰⁷. *Ho et al.* identified CSF antibodies with higher reactivity to 17 lipids in MS patients, targeting a phosphate group in

phosphatidylserine and oxidized phosphatidylcholine derivatives³¹². Myelin phospholipids were reduced in MS lesions compared to non-MS lesions³¹². *In vivo* experiments revealed that phospholipid injection into mice immunized with PLP₁₃₉₋₁₅₁ attenuated disease course³¹². None of the observations above have been firmly replicated and, overall, the exact antigen(s) recognized by auto-antibodies present in the CNS of MS patients remain rather elusive.

There has also been interest in measuring anti-CNS (including anti-myelin) antibodies in the periphery of MS patients for potential use as biomarkers of diagnosis and/or prognosis. Numerous studies however have failed to consistently find abnormal prevalence or titers of anti-myelin (e.g. anti-MBP and anti-MOG) antibodies in MS patients³¹³⁻³¹⁵. In other cases, initial and promising findings could not be replicated by independent groups in subsequent studies, such as the case for anti-KIR4.1 antibody. Work by Hemmer's group showed that serum levels of antibodies to KIR4.1 were elevated in MS patients compared with controls and were more prevalent in MS patients compared with those with other neurological diseases (46.9% versus 0.9% of patients, respectively)³¹⁶. KIR4.1 is an ATP-sensitive inward rectifier potassium channel expressed on oligodendrocyte cell bodies and astrocyte processes³¹⁶. Injection of KIR4.1 into mice led to rapid loss of KIR4.1 expression on glial cells, altered GFAP expression on astrocytes, and activation of the complement cascade, which can lead to demyelination and/or lack of remyelination³¹⁶. However, two multi-center studies subsequently failed to detect anti-KIR4.1 antibody in the serum (or CSF) of over 500 MS patients in ELISA or cell-based assays, calling into question the initial observations^{317,318}.

Another important question in MS pertains to the relationship between B cells within the CNS and circulating B cells in the periphery. It has long-since been recognized that intrathecal B cells in MS patients are clonally expanded, show signs of somatic hypermutation indicative of antigen-driven B cell maturation in the CNS, and can persist over many years in the same patient³¹⁹⁻³²⁶. A bi-directional flow of B cells between the periphery and the brain is now recognized in MS patients^{327,328}. Initial findings demonstrated that there was a degree of sharing in VDJ sequence between CSF and peripheral blood B cell clones^{324,325,329,330}. In addition, specific peripheral blood immunoglobulin-class switched memory B cells were clonally-related to CSF B cells, and the progression of somatic mutations suggested the initial antigen encounter occurred in the periphery, with further maturation taking place within the CNS^{327,328}. This was supported by paired brain and

cervical draining lymph nodes tissue analysis, which identified that identical B cell clones were present in both tissues, with founding members of clones more frequently present in the draining lymph nodes^{327,328}. Finally, identical B cell clones populating the CNS could be found in distinct regions within the CNS, including the meninges, inflammatory plaques, normal appearing white matter, and CSF³²³.

1.2.4 B cell antibody-independent functions in multiple sclerosis

1.2.4.1 Antigen presentation to T cells

B cells recognize conformational epitopes via the B cell receptor, which is subsequently internalized^{331,332}. Antigenic epitopes are then processed and presented on MHC class I or class II molecules to T cells along with co-stimulatory signals^{331,332}. Cognate interactions occur between B cells and T cells when the interacting cells recognize the same antigen^{331,332}. These cognate interactions are thought to be critical in EAE pathogenesis. Mice with TCR and BCR restricted to MOG spontaneously developed EAE-like symptoms, with demyelination and inflammatory infiltrates observed in the spinal cord and optic nerve^{333,334}. Meanwhile, selective MHC-II ablation in B cells rendered mice immunized with MOG protein resistant to EAE, as Th1 and Th17 cell functions were diminished. Partial susceptibility was then restored upon injection of anti-MOG antibody³³⁵.

In MS patients, expression of CD40, CD80, and HLA-DR was increased on B cells^{336,337}. In both controls and MS patients, polymorphism in CD40 (rs4810845*T) resulted in reduced CD40 and IL-10 expression in B cells, whilst polymorphism in CD86 (r9282641) enhanced its expression on B cells⁴³. Recent work has highlighted the potential role of B cell:T cell interactions in MS including the observation that patients with MS harbored both B cells and T cells that were more prone to auto-proliferation, akin to the autologous-mixed lymphocyte reaction (MLR). Auto-MLR was first described over 40 years ago in a study by *Opelz et al.*, wherein human T cell-enriched fractions proliferated in co-culture with B-cell enriched fractions from the same persons in the absence of exogenous antigens³³⁸. Similar outcomes can be observed in co-culture of T cells and dendritic cells^{185,339-341}.

With this background, *Jelicic et al.* re-demonstrated that co-cultured autologous B cells and T cells undergo proliferation in the absence of exogenous antigen or stimulus, but noted higher responses in MS patients carrying HLA-DR15³⁴². This process has been termed autologous proliferation or

auto-proliferation. The proliferating MS T cells had a classical and non-classical Th1 phenotype, whereas proliferating B cells from the same patients were class-switched memory B cells³⁴². In contrast to naïve B cells, memory B cells were more potent inducers of T cell auto-proliferation³⁴². Pharmacological inhibition of TCR and BCR as well as HLA-DR neutralization abrogated cell proliferation, indicating that this response was antigen-specific³⁴². Auto-proliferating T cell clones were found to be clonally expanded in the blood and brain of MS patients³⁴². These clones recognized an antigen derived from RASGRP2, a protein expressed in B cells and in cortical grey matter³⁴². Therapeutic intervention with rituximab resulted in reduced T cell auto-proliferation, whilst natalizumab (anti-VLA-4 antibody) increased the response³⁴². This study highlights a pathogenic role for memory B cells in multiple sclerosis by provision and presentation of self-antigens to self-reactive CD4⁺ T cells in the periphery and subsequent T cell trafficking to the CNS where they can mediate local inflammation.

1.2.4.2 B cell pro-inflammatory cytokine responses

B cells can further regulate pro-inflammatory T cell functions by producing pro-inflammatory (e.g. GM-CSF, IL-6, TNF, LT, IL-15) or anti-inflammatory (e.g. IL-10, IL-35) cytokines that serve to directly modulate T cells and/or indirectly affect T cells through modulation of myeloid cell responses²⁷¹. While both murine and human B cells can produce T cell prototypical cytokines *in vitro* and *in vivo*^{271,343}, results have not always been consistent across species. In mice, B cells can produce IFN- γ , IL-4 and IL-17, which regulates T cell and myeloid cell functions³⁴³. B cells engaged in a cognate interaction with polarized Th1 cells produced IFN γ *in vitro*^{344,345}. Additional cytokines such as IL-12, IL-18, and IFN- γ were required for optimal generation and maintenance of these B cells^{344,345}. *In vivo*, IFN- γ producing B cells promoted pro-inflammatory T cell and myeloid cell functions. For instance, IFN- γ producing B cells induced TNF and iNOS activity in myeloid cells in mice infected *Listeria monocytogenes*³⁴⁶. In addition, selective IFN- γ ablation in B cells conferred resistance to arthritis in an experimental model³⁴⁷. This protective effect was associated with increased regulatory T cell frequency and decreased frequencies of Th1 and Th17 cells in the spleen³⁴⁷. IL-4 producing B cell generation was dependent on IL-4 derived from Th2 cells and IL-4R signaling, and in turn, Be-2 cells enhanced Th2 cell functions in mice infected with *Heligmosomoides polygyrus*^{345,348,349}.

Splenic B cells isolated from mice infected with *Trypanosoma cruzi* produced IL-17 at early time points post-infection, thus providing a rapid and supplemental source of this cytokine³⁵⁰. IL-17-producing B cells were positioned outside the splenic B cell follicles in proximity to the T cell zone and had a plasmablast/plasma cell phenotype (CD138⁺GL7-B220^{int})³⁵⁰. IL-17 production in B cells was dependent on CD45 and BTK signaling but was independent from AHR and ROR γ T³⁵⁰. Human tonsillar B cells secreted IL-17 in culture with *Trypanosoma cruzi* supplemented with IL-10 and BAFF³⁵⁰. IL-17 expression could also be induced in human tonsillar B cells by stimulation with IL-6, IL-23, and TGF β ³⁵¹. Potential roles for those cytokine-producing B cells in CNS neuroinflammation remain unknown.

Regarding human B cell cytokine responses, *Duddy et al.* provided early evidence that human B cells stimulated with dual signals (BCR cross-linking antibody together with CD40 engagement) produced more LT α , TNF and less IL-10^{283,352}. This double signal is meant to model B cell stimulation with its antigen and T-cell co-stimulation, respectively^{331,332}. Meanwhile, stimulation through CD40 alone (as a proxy to bystander activation via co-stimulation in the absence of B cell antigen) enhanced B cell expression of IL-10 with little or no expression of LT α and TNF^{283,352}. This paradigm subsequently served to reveal that compared to normal control B cells, untreated MS B cells secreted increased LT α , TNF, and IL-6 levels and reduced IL-10 levels, resulting in higher LT/IL-10, TNF/IL-10, and IL-6/IL-10 ratios^{282,283,353}. Studies into the mechanism underlying B-cell cytokine regulation revealed that CD40L and BCR cross-linking antibody induced expression of miR-132, a negative regulator of the NAD-dependent deacetylase sirtuin 1 (SIRT1)³⁵⁴. This miR-132-SIRT1 axis was found to be dysregulated in MS B cells, such that miR-132 knock-down or pharmacological activation of SIRT1 normalized the abnormal levels of secreted TNF and LT α in MS B cells³⁵⁴. B cell-derived TNF, LT α , and IL-6 enhanced T cell proliferation *in vitro* and *in vivo*^{282,355}. As an *in vivo* proof-of-principle that B-cell derived cytokine can influence T cell responses and CNS inflammation, in mice immunized with MOG₃₅₋₅₅ or protein, selective ablation of IL-6 in B cells resulted in reduced EAE disease severity, which was associated with diminished Th17 but not Th1 CNS-reactive T cell responses³⁵⁵. Thus, the therapeutic benefit of B cell depletion therapy can in part be due to normalizing the levels of secreted pro-inflammatory cytokines such as TNF, IL-6, and LT by MS B cells^{355,283}.

B cells can also modulate myeloid cell functions by producing granulocyte-macrophage colony-stimulating factor (GM-CSF), with prominent roles identified in mice in contexts of sepsis and neuroinflammation^{281,356-359}. Splenic GM-CSF producing B cells, termed innate response activator (IRA), were located in the red pulp of mice challenged with LPS³⁵⁶. Gene expression analysis positioned this population as distinct from other B cell subsets, including plasma cells and marginal zone or follicular B cells³⁵⁶. IRA cells differentiated from a B1a B cell precursor and required TLR-4, MyD88, and autocrine GM-CSF for full maturation³⁵⁶. Mature IRA B cells expressed IL-3 but lacked the expression of IL-1 β , IL-6, TNF, and IL-10³⁵⁶. Mouse IRA B cells were phenotyped as IgM^{hi} CD23^{lo} CD43⁺ CD93⁺ IgD^{lo} CD21^{lo} CD138⁺³⁵⁶. Selective ablation of GM-CSF from B cells rendered mice more susceptible to cecal ligation and puncture (CLP) sepsis model, with high levels of pro-inflammatory cytokine levels in the serum and peritoneum associated with inefficient bacterial clearing by neutrophils³⁵⁶. In contrast, IL-3 producing IRA cells instigated a cytokine storm by inducing myelopoiesis of Ly-6^{hi} monocytes and neutrophils, enhancing host susceptibility to sepsis³⁵⁹. Finally, IRA B cells migrated from the pleural space to the lung parenchyma and provided the host with protection against pneumonia by producing IgM in a GM-CSF dependent mechanism³⁵⁷. In humans, splenic GM-CSF producing B cells had a memory phenotype (CD27⁺CD43⁻)³⁵⁶.

In humans, *Li et al.* described a circulating GM-CSF producing B cell population that differs from murine IRA cells and was characterized by high production of pro-inflammatory cytokines TNF and IL-6 and lacked IL-10 production²⁸¹. *Ex vivo* GM-CSF⁺ human B cells were phenotyped as memory rather than naïve B cells (CD24⁺ CD25^{hi} CD27⁺ CD38^{lo} CD43⁻ CD49^{hi} CD86^{hi})²⁸¹. Their optimal differentiation from naïve B cells was dependent on three signals, namely BCR, CD40L, and IL-4 or TGF- β ²⁸¹. Surprisingly, STAT5 and STAT6 signaling cooperated to induce GM-CSF expression in B cells whilst antagonizing IL-10 expression²⁸¹. Secreted products from GM-CSF-producing human B cell culture enhanced IL-12 and IL-6 secretion from monocyte-derived macrophages and reduced secreted IL-10 levels²⁸¹. IL-12 and IL-6 are important modulators for Th1 and Th17 cell differentiation, respectively, suggesting that B cells can indirectly modulate T cell effector functions via their impact on myeloid cells. Also, naïve human B cells primed with CD40L, BCR cross-linking antibody, and IL-4 upregulated co-stimulatory molecules such as CD80 and CD86 and were more efficient at presenting antigens to T cells *in vitro* and driving their

polarization to Th1 and Th17 phenotypes in an IL-6-dependent manner³⁶⁰. Importantly, in untreated MS patients, the frequency of blood GM-CSF⁺ B cells was increased compared to controls concurrent with reduced IL-10 frequency, resulting in an increased GM-CSF/IL-10 ratio²⁸¹. In addition, GM-CSF-producing B cell culture supernatants from MS patients induced higher secretion of IL-12 and IL-6 from monocyte-derived macrophages compared to normal controls, and this was correlated with higher B cell GM-CSF levels²⁸¹. Thus, another mechanism by which BCDT may so effectively limit new MS relapses is by diminishing the ability of B cells to stimulate myeloid cells via GM-CSF secretion and in turn further contribute to diminished responses of pro-inflammatory T cells. *Knier et al.* recently showed that CNS-infiltrating, GM-CSF-producing B cells enhanced microglia activation and contributed to EAE disease severity within the CNS³⁵⁸. In a regulatory feedback loop, GM-CSF⁺ B cells induced Ly6G⁺ cell differentiation into PMN-MDSCs in a STAT3-dependent mechanism, which served to prevent B cell accumulation in the inflamed CNS³⁵⁸.

An interesting further consideration is whether the therapeutic benefit of BCDT in MS patients may extend into the B cell reconstitution phase after discontinuation of BCDT. In fact, reconstituted B cells following BCDT in patients with MS produced less GM-CSF and concomitantly higher IL-10 levels compared to B cells prior to depletion, and this resulted in persistence of the diminished pro-inflammatory myeloid cell responses (i.e. the myeloid cell production of IL-6 and IL-12 remained reduced even as B cells reconstituted)²⁸¹. These observations may reflect a restored balance between pro- and anti-inflammatory cytokine production by the reconstituted MS B cells, raising the specter of immune-regulation by B cells.

1.2.4.3 B cell anti-inflammatory cytokine production

Seminal work by *Katz et al.* and *Neta et al.* demonstrated that B cells could exert a suppressive effect on T cells in a delayed hypersensitivity model through an antibody-independent mechanism^{361,362}. *Wolf et al.* showed that mice that were deficient in B cells suffered from an exacerbated EAE disease course that was associated with enhanced Th1 cell responses³⁶³, suggesting an anti-inflammatory role for B cells in CNS inflammation. In subsequent work, selective deletion of IL-10 from B cells worsened EAE disease course, which was improved by transfer of wild-type B cells³⁶⁴⁻³⁷². The absence of IL-10 expression by B cells resulted in increased disease severity in experimental models of arthritis, lupus, colitis, and neuroinflammation, but not

in systemic autoimmunity in a similar fashion to IL-10 deficiency in regulatory T cells³⁷³⁻³⁷⁸. Thus, IL-10 is necessary in inflammatory contexts as an important mechanism for maintaining tissue homeostasis and preventing immune pathologies. As a corollary, regulatory B cells or plasma cells could hamper the host immune response to infections and tumors^{372,379-384}. Regulatory B cells suppressed the effector functions of CD4⁺ and CD8⁺ T cells as well as enhanced the generation of regulatory T cells^{271,343,385}. These effects can be mediated by direct interactions between B cells and T cells as well as B cells and myeloid cells^{271,343,384,385}. The suppressive mechanisms include secretion of anti-inflammatory cytokines, such as IL-10, IL-35, and TGF- β , as well as expression of cell surface negative-regulators, such as PD-L1, GITR-L, CD39, and CD73^{271,343,384,385}.

Most of the work to date considering regulatory B cells has focused on IL-10-producing B cells. IL-10 is a heterodimer cytokine produced by T cells, myeloid cells, NK cells, and B cells³⁸⁶. It signals through IL-10RA and IL-10RB receptors and induces STAT3 and to a lesser extent STAT1 and STAT5 phosphorylation^{386,387}. IL-10 is generally viewed as an immunosuppressive cytokine given its inhibitory effect on T cells and myeloid cells³⁸⁶. However, it should be remembered that IL-10 can also stimulate other immune cells, such as B cells and mast cells³⁸⁶. IL-10 expression is inducible in several B cell populations during inflammation. In mice, these include gut IgM^{int} CD1d^{hi} CD21^{int} CD23^{hi} CD62^{lo} B cells, spleen and peritoneal B1a cells characterized as IgM^{hi}CD23^{lo}CD43⁺CD93⁻, transitional 2 marginal zone precursor cells characterized as IgM^{hi} CD21⁺ CD23^{hi}, splenic B10 cells characterized as IgM^{hi} IgD^{lo} CD1d^{hi} CD5⁺ CD21^{hi} CD23^{lo} CD24^{hi} CD43⁺ CD11b^{hi}, plasma cells characterized as LAG3⁺ CD138^{hi} CD1d^{hi} CD22⁻ CD43^{lo} CD71^{lo} CD200^{hi} Fas^{lo} MHC-II^{lo} B220^{lo}, IgA⁺ plasma cells/plasmablasts, as well as plasmablasts characterized as CD138⁺ CD44^{hi} CD38^{lo} CD43⁺ CXCR4^{hi} CXCR5^{lo} B220^{lo} ^{372,374,383,388-392}. In humans, *ex vivo* IL-10-producing B cells are enriched in transitional (phenotyped as IgM^{hi} IgD^{hi} CD19⁺ CD5^{hi} CD1d^{hi} CD10⁺ CD24^{hi} CD27⁻ CD38^{hi}) and in memory (phenotyped as CD19^{hi}CD24^{hi}CD25^{hi}CD27^{hi}) B cells^{377,393-395}. Furthermore, *in vitro* CD40L-stimulated naïve as well as transitional B cells produced higher levels of IL-10 than memory B cells^{283,377}. In the context of human autoimmunity, regulatory B cell functions are reportedly impaired in MS, rheumatoid arthritis, diabetes, and SLE patients^{271,282,283,377,385,394,396,397}. The lack of lineage-specific transcriptional factor(s) and cell surface markers may underscore the plastic and transient nature of IL-10 expression in B cells.

Given the therapeutic implications, how IL-10 expression is regulated by B cells has been a topic of growing interest. IL-10 production by B cells is positively regulated by signaling through BCR, CD40, CD1d, TIM-1, TLRs (MyD88, TLR2, TLR4 and TLR9), and cytokine receptors such as IL-21R^{282,283,364,366,371-374,382,393,398,399}. To date, only one negative regulator of IL-10 has been described, known as Toso⁴⁰⁰. Toso, an Fc receptor for IgM, was shown to regulate the BCR activation threshold, and its selective ablation in B cells resulted in enhanced IL-10 production upon exposure to BAFF, LPS, anti-CD40, or anti-IgM⁴⁰⁰. Perturbation of the gut microbiota using antibiotics also resulted in a reduction in the numbers of IL-10 producing B cells in the spleen; however, SPF and gnotobiotic mice showed no difference in splenic IL-10-producing B cells^{390,401}, suggesting that the impact of the gut microbiota on regulatory B cell functions remains to be fully elucidated. Unlike T cells and myeloid cells, the transcriptional regulation of IL-10 expression by B cells remains elusive. Sequential TLR and BCR ligation induced NFAT activation in a Ca²⁺ dependent fashion³⁶⁹. STIM-1 and STIM-2 are calcium sensors located to the endoplasmic reticulum and are necessary for productive BCR signaling³⁶⁹. Selective STIM-1 and STIM-2 deletion in B cells impaired IL-10 production³⁶⁹. BCR and TLR signaling also induced ERK and STAT3 phosphorylation, and pharmacological inhibition of these pathways reduced IL-10 expression by B cells^{402,403}. Whilst master transcriptional factor(s) for regulatory B cells are lacking, two transcriptional factors have emerged as positive regulators of IL-10. Interferon regulatory factor 4 (IRF4) was induced by sequential ligation of TLR and BCR in plasmablasts and bound an upstream region from the IL10 transcriptional start site³⁹². Selective deletion of IRF4 in B cells resulted in diminished IL-10 secretion³⁹². Hypoxia-inducible factor 1-alpha (HIF1a) was induced by BCR or TLR signaling and cooperated with phosphorylated STAT3 to induce IL-10 expression in CD1d^{hi}CD5⁺ B cells⁴⁰⁴. HIF1a also regulated the expansion of CD1d^{hi}CD5⁺ B cells in a glycolysis-dependent mechanism⁴⁰⁴.

More recent investigation identified a capacity for B cells to produce the immune-regulatory cytokine IL-35. Murine CD138⁺CD22⁻ plasma cells and CD1d^{hi}CD5⁺CD19⁺B220^{lo} cells produced IL-35 upon stimulation^{372,405,406}. *Wang et al.* showed that treatment of naïve B cells with IL-35 induced IL-35 and IL-10 expression, and acquisition of this regulatory phenotype was necessary to suppress effector Th1 and Th17 responses and induce regulatory T cells, which culminated in

reduced disease activity in experimental autoimmune uveitis⁴⁰⁵. IL-35 signaling in B cells is dependent on IL-12R β 2 and IL-27Ra as well as STAT1 and STAT3 phosphorylation^{405,406}. *Shen et al.* found constitutive IL-12p35 expression in naive B cells, whilst Ebi3 induction was dependent on BCR, CD40, and TLR4 signaling³⁷². Selective IL-12p35 or Ebi3 deletion in B cells resulted in failure to recover from EAE and a reduced susceptibility to Salmonella infection³⁷². In both instances, effector Th1 and Th17 as well as myeloid cell functions were enhanced, without any functional impact on regulatory T cells^{372,405}. Human IL-35-producing B cells remain to be identified.

Together, studies in humans and animals have established important antibody-independent functions of B cells that are highly relevant to MS pathophysiology, including B cell functions as APCs to T cells and as producers of cytokines that can either activate or regulate T cells and myeloid cells. The abnormal pro-inflammatory responses of B cells in untreated MS patients likely explains the observation that BCDT is highly effective at limiting new relapses, as B cell depletion results in diminished pro-inflammatory responses of both T cells and myeloid cells^{271,282,355,360}. While this body of work has strongly implicated interactions between B cells and CD4⁺ T cells, our own lab reported that CD8⁺ T cell responses are also diminished post-B cell depletion in MS patients, raising the possibility that B cell-CD8⁺ T cell interactions are also relevant in MS²⁸². It is noteworthy that unlike EAE, which is largely a CD4⁺ T-cell mediated disease, the pathology of MS lesions demonstrates a predominance of CD8⁺ T cells over CD4⁺ T cells, with the CD8⁺ T cells in the MS lesions also exhibiting clonal expansion^{95,294}. The following sections will expand on the roles of CD8⁺ T cells, including a subset known as mucosal-associated invariant T (MAIT) cells, in MS and EAE.

1.3 Implication of CD8⁺T cells in the MS central nervous system

Classical histopathological observations of post-mortem tissues from MS patients demonstrate that CD8⁺ T cells, and not CD4⁺ T cells, predominate among T cells in the perivascular space of veins, tissue parenchyma, and normal appearing white matter in both acute and progressive disease^{86,297,298,407-413}. The predominance of CD8⁺ T cells was not unique to the MS CNS, as they could also be observed in brain tissues from inflammatory controls^{413,414}. Nonetheless, these findings challenge the view that MS is solely a CD4⁺ T cell-mediated disease. CNS-infiltrating

CD8⁺ T cells have an effector memory phenotype, characterized by the expression of CD45RO (and lack of CCR7), PD-1, CTLA-4, and TIM-3^{86,413-416}. In addition, a subset expressed CD69 and/or CD103 and lack S1P1 expression, consistent with tissue resident memory cell phenotype^{86,413-416}. Infiltrating CD8⁺T cells appeared activated and expressed pro-inflammatory molecules such as IFN- γ , TNF, IL-17, granzyme B, and perforin^{86,413-416}. The secretion of cytokines by CD8⁺ T cells may modulate brain resident cells, including glial cells and myeloid cells, and could promote local inflammation and tissue injury. This is supported by findings indicating a positive correlation between the expression of APP on axons, a marker for axon transection and damage, with the numbers of CD8⁺ T cells and myeloid cells in lesions^{417,418}. CD8⁺ T cells could also be found in close proximity to glial cells in white matter lesions^{86,411}. In addition, MHC-I was constitutively expressed on microglia, macrophages, and endothelial cells and to a lesser degree on astrocytes, oligodendrocytes, neurons and axons. Among the CNS-infiltrating CD8⁺ T cells in the MS CNS are MAIT cells. MAIT cells can be found in multiple locations in the MS CNS, including perivascular and parenchymal lesions as well as in meningeal infiltrates⁴¹⁹⁻⁴²⁴. Additionally, MAIT-cell activating cytokines (IL-18 and IL-23) were expressed in MS lesions⁴²². A major focus of this thesis relates to the effects of B cells on MAIT cells, which are described in greater detail in subsequent sections.

Studies employing CDR3 spectratyping on single cells demonstrated that MS brain infiltrating CD8⁺ T cells were clonally expanded, with a high degree of sharing among cells present in demyelinating lesions, NAWM, and CSF, and less so with blood T cells^{410,425-434}. This suggested that CD8⁺T cells locally responded to antigenic stimulation and/or to bystander inflammation. The former is supported by the expression of TCR downstream signaling molecule NFAT in CD8⁺ T cells present in active lesions⁴¹³. Clonally expanded CD8⁺ T cells expressing the MAIT cell invariant TCR (V β 1-J α 2.3-V α 7.2) were also found in MS brain lesions and in blood samples, and the canonical V α 7.2 MAIT cell clones identified in brain lesions were found among circulating CD8⁺ T cells even 18 years later, showing signs of clonal expansion⁴²³. However, the antigenic specificity of CD8⁺ T cells (both MAIT and non-MAIT) in MS remains elusive. Some studies found that CD8⁺ T cell clones isolated from MS CSF and lesions were not reactive to CNS antigens such as MBP, MOG, and MAG^{86,435,436}, while others found that CD8⁺ T cells could lyse myelin-pulsed target cells, including oligodendrocyte cell lines, and could secrete pro-inflammatory

cytokines⁴³⁷⁻⁴⁴⁴. It is unclear if these functional responses are different in magnitude in MS patients.

A potentially MS-relevant interaction between CD8⁺ T cells and B cells is supported by observations that human B cells stimulated with CD40L expressed IL-15 *in vitro* and enhanced CD8⁺ T cell cytotoxic functions as well as cell migration across the inflamed blood brain barrier⁴⁴⁵. In MS lesions, brain-infiltrating CD8⁺ T cells were located in proximity to IL-15 expressing cells, which could enhance granzyme B expression⁴⁴⁶. Potentially relevant to the observation that TACI-Ig (atacept) treatment worsened MS disease activity is the observation that murine splenic B cells isolated from TACI-Ig treated mice upregulate IL-15 expression and, conversely, that BAFF suppresses IL-15 expression by B cells⁴⁴⁷. Taken together, these findings support a potentially MS-relevant role for B cell:CD8⁺ T cell interactions. The actual roles, however, of CD8⁺ T cells and their subsets (e.g. both MAIT and non-MAIT) in MS remains unclear, with some studies attributing pro-inflammatory and pathogenic properties to CD8⁺ T cells, while other studies suggest they may have regulatory roles in the context of CNS inflammation. The following sections will explore these different roles of CD8⁺ T cells and their potential implication in MS.

1.3.1 Opposing roles for CD8⁺ T cells in neuroinflammation

The functions of CD8⁺ T cells in the context of neuroinflammation have predominantly been examined in the EAE mouse model, with contrasting observations indicating both regulatory and pathogenic roles for CD8⁺ T cells in the course of the disease.

1.3.1.1 CD8⁺ T cell pathogenic functions in neuroinflammation

Huseby *et al.* demonstrated that adoptive transfer of MBP-specific CD8⁺ T cells into C3H mice (or C3H SCID mice) resulted in CNS inflammatory injury⁴⁴⁸. In line with MS pathology, these mice displayed perivascular cuffs around capillaries and venules, inflammatory brain lesions in the white matter of the cerebellum, and meningeal inflammation specifically in severe cases⁴⁴⁸. This disease was attenuated in mice treated with anti-IFN- γ antibody, but not with anti-TNF antibody, findings that are also consistent with results from MS clinical trials⁴⁴⁸. Notably, the same cannot be said about CD4-induced EAE, as results in murine experiments failed to predict outcomes in clinical trials of MS patients⁴⁴⁸. Similar pathogenic CD8⁺ T cell effector functions were observed in other EAE mouse models⁴⁴⁹⁻⁴⁵⁴. Class I MHC (HLA-A2 and HLA-A3) influence

CD8⁺ T cell functions in the course of CD8⁺ T-cell mediated disease. HLA-A3 / 2D2 TCR double transgenic humanized mice immunized with PLP45-53 exhibited mild disease with a fraction developing a more severe late disease course⁴⁵⁵. Demyelination, axonal transection, and degeneration were observed⁴⁵⁵. Immune cells including T cells and myeloid cells infiltrated the spinal cord, the cerebellum, and the optic nerve, with an enrichment for CD8⁺ T cells in early disease and CD4⁺ T cells in late disease⁴⁵⁵. CD4⁺ T cells and/or B cells drove the late disease, as MHC-II^{-/-} and Rag2^{-/-} mice failed to develop this phase⁴⁵⁵. In contrast, HLA-A3/HLA-A2/2D2 TCR triple transgenic mice failed to develop early and late disease, without evidence of demyelination or axonal and neuronal degeneration⁴⁵⁵. This may relate to HLA-A2 mediating negative selection of 2D2-TCR CD8⁺ T cells in these mice, resulting in reduced peripheral accumulation of these cells and protection from disease⁴⁵⁵. More recently, CD8⁺ T cells were shown to drive relapsing remitting-like disease in MOG₃₅₋₅₅ immunized mice injected with plasma extracellular vesicles isolated from donor EAE mice⁴⁵⁶. Disease was dependent on CD8⁺ T cells and on the enrichment of fibrinogen on extracellular vesicles^{456,457}. Fibrinogen injection into MOG₃₅₋₅₅ immunized mice enhanced T cell and myeloid cell recruitment into the CNS⁴⁵⁶⁻⁴⁵⁸. In addition, fibrinogen activated macrophages and microglia via CD11b/CD18 and enhanced their antigen presentation capacities to facilitate local T cell IFN γ production⁴⁵⁶⁻⁴⁵⁸. Even in CD4⁺ T-cell induced EAE, MBP-specific CD8⁺ T cells were primed by CNS infiltrating Tip⁺ dendritic cells and oligodendrocytes, upon which these cells potentiated tissue damage⁴⁵⁹. CD8⁺ T cells, and in particular Tc17, could provide help to CD4⁺ T cells and were required for initiation of typical MOG₃₇₋₅₀ or MOG₃₅₋₅₅ CD4-induced EAE^{416,460}. Together, the animal model-based studies suggest that CD8⁺ T cells can both drive various aspects of CNS inflammation (including playing a role in either early or later phases of CD8⁺ T-cell mediated EAE) as well as cooperate with CD4⁺ T cells in CD4⁺ T cell-mediated EAE. Supporting a pro-inflammatory role of CD8⁺ T cells in the human disease are reports of increased frequencies of GM-CSF⁺ and IL-17⁺ CD8⁺ T cells in blood and/or CSF of MS patients^{146,148,460,461}.

1.3.1.2 CD8⁺ T cell regulatory functions in neuroinflammation

Suppressor CD8⁺ T cells have been described in mice that have recovered from EAE or have received oral MBP tolerization. Splenic CD8⁺ T cells isolated from Lewis rats recovering from EAE induced by adoptive transfer of CD4⁺ MBP-specific T cells lysed the CNS-reactive T cells

in vitro and suppressed their encephalitogenic property *in vivo*^{462,463}. Further, the CD4⁺ T cell TCR repertoire was modulated by CD8⁺ T cells in recovering mice, such that it was more diverse in these animals compared with CD8⁺ T-cell deficient mice⁴⁶³. Similarly, MBP-immunized mice were resistant to second disease induction unless CD8⁺ T cells were removed^{464,465}. In addition, optimal *in vivo* tolerization with MBP was dependent on CD8⁺ T cells and their production of TGF- β ⁴⁶⁶⁻⁴⁶⁸. Suppressor CD8⁺ T cells downregulated the expression of co-stimulatory molecules on antigen-presenting cells to indirectly inhibit CD4⁺ T cell effector functions, while also directly targeting CD4⁺ T cells in certain contexts⁴⁶⁸⁻⁴⁷⁴. More recent studies identified a murine CD8⁺ regulatory T cell population that suppressed follicular helper T cells in a Qa-1-dependent mechanism⁴⁷⁵⁻⁴⁷⁷. Analogous human CD8⁺ T cells have been characterized that co-express KIR2DL2/3 or KIRDL1, CD44, CD122, and Helios. Their implication in neuroinflammatory disorders remains uncertain^{475,478,479}.

1.4 Mucosal associated invariant T (MAIT) cells

Mucosal associated invariant T (MAIT) cells are innate-like T cells that, as noted previously, express the semi-invariant TRAV1.2-J α 12/20/33 and a restricted TCR- β repertoire⁴⁸⁰⁻⁴⁸². *Porcelli et al.* described a CD4⁺CD8⁻ (double-negative; DN) T cell population that expressed Va7.2-J α (IGRJ α 14) paired with V β 2, 8, 11, or 13 in human blood⁴⁸³. Lantz's group found that this population was conserved in three species, including human, mice, and cattle⁴⁸⁴. These cells had an oligoclonal TCR-V β repertoire and were present in MHC-II- and TAP-deficient patients as well as in MHC-I- or CD1d-deficient mice, indicating that these cells are neither selected by nor dependent on classical MHC molecules⁴⁸⁴. Indeed, further investigation revealed that MAIT cells were absent in β 2-microglobulin and MHC related protein 1 (MR1)-deficient mice^{484,485}. An evolutionary biology analysis found that MR1 appeared 170 million years ago and was a highly conserved molecule across mammalian species but was lost in three instances (carnivores, armadillos, and lagomorphs)⁴⁸⁶⁻⁴⁸⁸. Interestingly, genes encoding TRAV1-2 and MR1 were interconnected, such that MR1 was absent in species lacking TRAV1-2⁴⁸⁶. Further, MR1 molecules isolated from different species were cross-reactive, in that human MAIT cells can be activated by antigen-loaded rat, mouse, or bovine MR1 molecules⁴⁸⁷.

Whilst MR1 ligands remain incompletely elucidated, cells infected with bacteria or fungi were shown to induce MAIT cell activation *in vitro* and *in vivo* in an MR1-dependent mechanism⁴⁸⁹⁻⁴⁹¹. *Kjer-Nielsen et al.* elegantly demonstrated that riboflavin (vitamin B2) metabolites such RL-6,7-diMe, RL-6-ME-7-OH, and rRL-6-CH₂OH could bind to the MR1 antigen-binding pocket and activate MAIT cells, whilst 6-formyl-pterin (6-FP), a folic acid metabolite, could bind to MR1 but fails to induce MAIT cell activation⁴⁹². Further, 5-amino-6-D-ribitylaminouracil (5-A-RU) reacted with glyoxal and methylglyoxal to form the pyrimidine adducts 5-(2-oxypropylideneamino)-6-D-ribitylaminouracil (5-OP-RU) and 5-(2-oxoethylideneamino)-6-D-ribitylaminouracil (5-OE-RU), two activating MAIT cell ligands^{493,494}.

The TCR- β repertoire on MAIT cells is restricted to certain chains including TRBV6 and TRBV20⁴⁹⁵⁻⁴⁹⁷. Nonetheless, recent evidence points to a role for TCR- β chains in regulating the magnitude of MAIT cell activation in response to different antigens. For instance, diclofenac metabolites could activate TRBV6-1 but not TRBV6-4 or TRBV20 expressing cells⁴⁹⁸. Likewise, TCR-V β 8, 13.1 and 13.6 expressing MAIT cells produced lower amounts of TNF and IFN β in response to stimulation with *Escherichia coli*-pulsed monocytes *in vitro*⁴⁹⁷. This denotes a clonal heterogeneity in MAIT cell population in regard to their capacity to mount a response against pathogens and to respond to therapeutics.

1.4.2 MAIT cell development

MAIT cells develop in the thymus like conventional T cells and are selected by MR1-expressing double positive cortical lymphocytes⁴⁹⁹⁻⁵⁰³. The antigen(s) required for successful selection have not been defined but appear not to be derived from gut microbiota⁵⁰¹. Analysis of murine and human thymus using MR1 tetramer loaded with 5-OP-RU revealed three developmental stages that give rise to effector, terminally differentiated MAIT cells^{501,504}. In mice, CD24⁺CD44⁻ T cells represented stage 1 and had the potential to differentiate into stage 2 (CD24⁻CD44⁻) and stage 3 (CD24⁻CD44⁺)^{501,504}. Stage 1 and stage 2 cells lacked expression of the transcriptional factors PLZF, T-bet, and ROR γ T and could not produce effector cytokines (IFN- γ and IL-17) upon *in vitro* stimulation^{501,504}. The transition from stage 1 to stage 2 was dependent on MR1^{501,504}. Gut microbiota, PLZF, and miRNAs were indispensable for the differentiation from stage 2 to stage 3, at which point MAIT cells acquired the expression of PLZF, T-bet, or ROR γ T and produced

effector cytokines such IFN- γ or IL-17^{501,504}. A recent analysis found that PLZF was highly expressed in innate T cells and was associated with the expression of all cytokine and chemokine receptor genes⁵⁰⁵. The frequencies of NKT and MAIT cells were correlated in blood; however, these two innate-like T cell subsets competed for resources, as CD1d deficient mice had increased MAIT cell numbers in the periphery^{501,505-507}.

In adult humans, CD27⁻CD161⁻, CD27⁺CD161⁻, and CD27^{+/-} CD161⁺ T cells represented stage 1 to 3 MAIT cells, respectively^{501,508}. Stage 3 was represented by effector MAIT cells that express high levels of PLZF, T-bet, and ROR γ T and produce effector cytokines (IFN- γ and TNF)^{501,508}. Circulating stage 3 MAIT cells in adult blood are found within CD4⁻CD8⁺ and DN T cell fractions, and they are phenotypically characterized as effector memory T cells with diverse chemokine receptor expression, including CCR2, CCR6, CCR5, CXCR4, CXCR6, and CCR9^{497,508-512}. Their expression of diverse chemokine receptors is reflective of an enhanced migratory capacity to diverse tissues in inflamed conditions^{480,513}. Functional heterogeneity among MAIT cell subpopulations was associated with TCR- β usage and could be denoted by cell surface markers, such as CD56 and CD94^{497,508,514}.

There is also phenotypic and functional diversity among MAIT cells found in fetal tissues as well as cord and adult blood^{502,503,506,509}. In fetal thymus, spleen, and mesenteric lymph nodes, MAIT cells have a naïve phenotype, express CD62L and CCR7, express low levels of IL-18R and PLZF, and do not respond to *in vitro* stimulation^{502,503,506,509}. In contrast, MAIT cells found in fetal small intestine, liver, and lung are mature, lack expression of lymphoid tissue homing receptors, express high levels of IL-18R and PLZF, and respond to *in vitro* stimulation by expanding and producing cytokines^{502,503,506,509}. MAIT cells present in cord blood have a naïve phenotype, whilst in adult blood, they display a memory phenotype^{502,503,506,509,515}. MAIT cell frequency is higher in adults than neonates, reaching a peak in the third decade of life and thereafter decreasing^{506,516-518}. In human adults, MAIT cell frequency varies between 0.1 to 15% in blood, and up to 45% in liver^{495,502,503,505,506,509,519,520}.

The signals necessary for MAIT cell peripheral expansion remain largely unknown, but recent studies in individuals with monogenic primary immunodeficiencies provided some clues. In fact,

MAIT cell numbers were diminished in individuals with heterozygous loss of function mutation in STAT3 that resulted in autosomal-dominant hyper IgE syndrome⁵²¹⁻⁵²³. Residual circulating MAIT cells secreted diminished levels of IL-17, but not IFN- γ , TNF, and granzyme B, in spite of normal ROR γ T and PLZF expression⁵²¹. Peripheral MAIT cells were absent in patients with bi-allelic RORC mutation, which contributed to increased susceptibility to *Candida* and *Mycobacterium* infections⁵²⁴. MAIT cell deficiency was also observed in patients with loss of function mutations in IL-12RB1, IL-21R, IL-12RB2, and IL-23R that resulted in Mendelian susceptibility to mycobacterial disease^{523,525}. X-linked inhibitor of apoptosis (XIAP) deficiency resulted in reduced MAIT and iNKT cell numbers in patients with X-linked lymphoproliferative syndrome⁵²⁶. Normal MAIT and iNKT cells have a pro-apoptotic functional phenotype characterized by high expression of active caspase-3 and caspase-7⁵²⁶. The XIAP protein negatively regulates caspase-3 and caspase-7 activity, thereby promoting iNKT and MAIT cell survival⁵²⁶.

Environmental factors influence the frequency of circulating MAIT cells. Indeed, MAIT cell number was correlated between monozygotic and dizygotic twins at birth, was higher in females than males across the age span, and was lower in CMV seropositive individuals and active smokers^{505,506,516-518,527,528}. Additionally, MAIT cell frequency in neonates was not influenced by month of birth or birth delivery method and was not correlated with mother's MAIT cell frequency⁵⁰⁶. Given that the gut microbiota is indispensable for MAIT cell development, it is plausible that its composition regulates the magnitude of MAIT cell peripheral expansion as well as their effector functions^{485,501,502}.

1.4.3 MAIT cell anti-microbial and anti-viral functions

Similar to conventional CD8⁺ T cells, MAIT cells require three signals to acquire full effector functions necessary for eliminating pathogen-infected cells, namely TCR signaling, co-stimulatory signals and innate cytokines^{480,529-531}. Innate cytokines produced upon pathogen receptor stimulation by invading pathogens serve as checkpoint to regulate MAIT cell responses against commensal bacteria⁵³². MAIT cells can produce IFN γ and granzyme B in response to innate cytokines and thus contributing to anti-viral immune responses in a bystander fashion^{491,533-536}.

MAIT cells contribute to tissue immunity by ongoing migration from the periphery and/or acquisition of tissue-residence signature. In fact, MAIT cells are present and can rapidly expand in the liver, gut, lung, and genital mucosa upon pathogen exposure^{485,490,495,519,534,536-544}. MAIT cells can contribute to mucosal immunity, as they can produce elevated levels of IL-17 and IL-22, two cytokines critical for the maintenance of barrier integrity, in the colon and female genital mucosa^{540,541,545}. Further, recent evidence indicated that MAIT cells can acquire tissue-residency program in the liver and the skin, and thus they are strategically positioned in tissues and are poised to produce effector molecules critical for host defense against invading pathogens, similar to tissue-resident conventional T cells^{480,546-548}.

The rapid-fire nature of MAIT cell responses is integral to an effective anti-pathogen immune response. Recently, *Gutierrez-Arcelus et al.* showed that MAIT cell innate characteristics were ingrained in their gene expression⁵⁰⁵. The authors sequenced conventional CD4⁺ and CD8⁺ T cells, MAIT cells, iNKT, V- δ 1, V- δ 2, and NK cells and found a continuous ‘innateness’ gradient that separated the different immune cell subsets, with conventional T cells on one end and innate T cells on the other⁵⁰⁵. Over 1500 genes were associated with this innateness gradient, such as perforin, granzyme B, granulysin, CCL3, CCL4, CCL5, XCL1, XCL2, and IFN γ ⁵⁰⁵. In fact, the sum expression of 37 cytokines and chemokines followed the innateness gradient, with higher expression in MAIT cells compared with conventional T cells⁵⁰⁵. In contrast, ‘adaptiveness’ was associated with proliferation and ribosome biogenesis⁵⁰⁵. POLR1D, an RNA I polymerase component involved in ribosomal RNA transcription, was associated with adaptiveness, whilst POLR2G and POLR2K, RNA polymerase II components involved in transcribing mRNA, were associated with innateness⁵⁰⁵. Altogether, this data suggests that T cell adaptiveness is associated with cell growth, while their innateness is associated with rapid effector functions.

1.4.4 MAIT cells in autoimmune diseases

The observation that MAIT cells express diverse chemokine receptors that effectively license them to migrate into multiple different tissues in inflammatory conditions suggests that they may respond in both the normal context and in an autoimmune disease context in a relatively antigen-agnostic fashion (as far as the organ is concerned) and mediate their effects mainly through bystander mechanisms^{480,513}. However, it cannot be ruled out that certain TCRs on MAIT cells

recognize endogenous (self) antigens that can trigger a response to self. This is supported by recent evidence for a broader MR1 ligand library that extended beyond riboflavin and folate metabolites to include organic compounds as well as the finding that MR1-restricted T cells were reactive towards hydrophilic molecules in THP-1 lysate and the MR1 molecule itself^{498,549,550}.

The roles of MAIT cells in autoimmune disease may include both pro-inflammatory and anti-inflammatory/regulatory effects^{513,551}. MAIT cells exhibit fast effector functions initiated by TCR-dependent and/or independent signaling that include release of pro-inflammatory cytokines and cytotoxic granules. While these effector functions may be protective as part of normal anti-pathogen immunity, these effects could be detrimental in the autoimmune disease context. It is conceivable that the dysregulated immune cellular networks described in MS can set in motion aberrant MAIT cell functions that contribute to local CNS inflammation and tissue injury. However, as detailed below, MAIT cells may also play acquiescing roles in the autoimmune disease context.

In type 1 diabetes, the frequency of blood MAIT cells were lower in children with recent onset disease compared to controls⁵⁵². MAIT cells produced elevated levels of TNF, IL-4, and granzyme B, and the frequency of granzyme B-producing MAIT cells correlated with age at diagnosis and HbA1c%⁵⁵². In NOD mice, MAIT cells seemed to have two opposing roles—maintaining gut barrier permeability by producing IL-17 and IL-22 and promoting inflammatory infiltrates into pancreatic islets. MR1^{-/-} mice had a more severe diabetic disease course, suggesting that the protective role prevailed in this model⁵⁵². This was further supported by a histopathology study, which found no evidence for MAIT cell infiltration into pancreatic islets in biopsy tissues from recent onset T1D subjects (3-9 weeks from diagnosis)⁵⁵³. In contrast, reduced peripheral blood frequencies of MAIT cells were associated with accumulation of these cells in target organs of other immune-mediated conditions, including celiac disease, inflammatory bowel disease, systemic lupus erythematosus, rheumatoid arthritis, type 2 diabetes, and obesity⁵⁵⁴⁻⁵⁶⁰. In inflammatory bowel disease, SLE, and obesity, blood MAIT cells produced elevated levels of IL-17 compared to controls⁵⁵⁴⁻⁵⁶⁰.

In multiple sclerosis, MAIT cells can be found, as noted above, among immune-cell infiltrates in multiple sub-compartments within the MS CNS⁴¹⁹⁻⁴²⁴. There are inconsistent reports of MAIT cell frequencies in peripheral blood of MS patients, with some studies identifying increased frequencies, while others reported no differences or decreased frequencies in the circulation of patients compared to controls^{420-422,561}. The factors underlying this discrepancy in different studies are unknown.

The increased propensity of MAIT cells to produce pro-inflammatory mediators, their presence in perivascular lesions, and their sustained depletion in patients benefiting from durable disease quiescence after aggressive bone marrow transplantation in MS all suggest that CD8⁺ MAIT T cells have a disease promoting function in MS^{150,419,420}. More recently, *Mexhitaj et al.* demonstrated increased frequency and pro-inflammatory cytokine (e.g. IFN γ and IL-17 secretion) responses of blood MAIT cells in children with MS soon after their initial presentation compared to children with monophasic inflammatory demyelinating disease and normal controls¹⁵⁰. The strength of studies in children compared to adults is the time proximity between biological and clinical disease onset, which reduces the influence of chronic inflammation on circulating immune cell functional phenotype⁷. Of note, it is entirely plausible that MAIT cells play different roles (i.e. both pro- and anti-inflammatory) at different stages of the disease course.

1.5 Summary

The clinical success of B cell depletion therapies targeting CD20, in spite of no changes in CSF immunoglobulin synthesis and levels, emphasizes the contribution of B cell antibody-independent functions to the pathological cascade leading to new inflammatory disease activity in MS. While B cell engagement in bi-directional interactions with CD4⁺ T cells has been the focus of many recent studies, histopathological studies demonstrate a predominant CD8⁺ T cell infiltrate, including a population of CD8⁺ T cells termed MAIT cells, that may interact with B cells in the CNS of MS patients. Our lab's observation that BCDT results in reduced CD8⁺ T cell proliferation and pro-inflammatory cytokine production further hints at *in vivo* interactions between B cells and CD8⁺ T cells, which may be disease-relevant. However, little is known about the nature of such putative interactions which are the focus of this thesis.

Preface: Chapter 2

As part of my overarching interest in studying B cell:CD8 T cell interactions, I wished to understand whether functionally distinct B cells have differing effects on (or respond differently to) CD8⁺ T cells. To do so, I needed to develop a technique that would enable isolation and better characterization of viable, functionally distinct B cell subpopulations. One of the important functional responses of B cells relates to their capacity to produce different cytokine profiles, which has been found to be an important mechanism by which B cells regulate CD4⁺ T cell and myeloid cell effector functions in autoimmunity and infectious diseases. Human B cells can produce pro-inflammatory cytokines such as GM-CSF, TNF, and IL-6 as well as anti-inflammatory cytokines such as IL-10. Abnormalities in both the circulating numbers and cytokine responses of B cells have been demonstrated in several disease contexts; however, our understanding of the development and differentiation of such cytokine-defined B cells and how they may differentially impact other cells remains limited. This is due in part to a lack of validated and specific cell surface markers that allow their isolation in a pure and viable state. In this chapter, I show that the cytokine secretion assay represents an attractive approach for the detection and isolation of viable cytokine-secreting B cells from humans *ex-vivo*. I demonstrate the assay can be multiplexed, allowing for the isolation of B cells simultaneously expressing up to three distinct cytokines, including both low frequency and high frequency cytokine-secreting B cells. I further show that the cytokine-secreting B cells isolated using this approach are amenable to gene expression profiling and *in vitro* culture. Altogether, this work highlights the utility of a multiplexed cytokine secretion assay in simultaneously isolating B cell sub-populations defined by multiple different cytokines and, ultimately, providing an alternative avenue for characterizing these populations in depth using next-generation sequencing and other platforms.

Chapter 2: Simultaneous detection and isolation of multiple, viable, distinct cytokine-secreting B cells

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Author contributions

AR generated all hypotheses, designed and performed all the experiments, analyzed the complete data sets and wrote the manuscript

RL assisted with human cell isolation and helpful research discussions

J.G and A.P were involved in research plan and discussion and helped with manuscript revision

A.B.O. provided the overall supervision, generated hypotheses, guided the experimental plan, analyzed the data and wrote/revised the manuscript.

Abstract

Secreted cytokines by B cells have now been shown to modulate both CD4⁺ T cell and myeloid cell functions, with relevance in host immunity and disease pathogenesis. However, a current limitation to further functional characterization of these cytokine-secreting B cells (in the absence of specific subset-defining cell-surface markers that would enable sorting viable cells) is that their detection using intracellular cytokine measurements results in non-viable cells. An alternative approach to isolating viable cytokine-defined B cells could be the use of a cytokine secretion assay, based on capturing cytokine secreting cells using a bi-specific cell surface antibody for CD45 and a specific cytokine, thereby preserving cell viability and integrity. However, cytokine capture assays have not been developed for simultaneous sorting of multiple viable human cytokine-secreting immune cell subpopulations, which is especially challenging for low-frequency cell subsets. We therefore set out to optimize a multi-parametric cytokine secretion assay that would address this gap. We first show that low-frequency GM-CSF⁺, IL-10⁺ and higher frequency TNF⁺ B cells can be individually isolated using cytokine-capture assays, yielding highly purified B cell populations (confirmed by unique expression of *CSF2*, *IL-10*, and *TNF RNA*, respectively) that are viable and able to secrete high levels of their corresponding cytokines upon further activation. We demonstrate successful co-staining of a high (TNF) and low (GM-CSF or IL-10) frequency B cell subpopulations, with minimal loss of signal compared with single staining. In contrast, co-staining with two low-frequency (GM-CSF and IL-10) can result in significant competition for CD45 and loss of signal that requires careful assay optimization. Finally, we show for the first time a triple detection and isolation of TNF⁺, GM-CSF⁺, and IL-10⁺ B cells. We conclude that the cytokine secretion assay is suitable for multi-parametric fluorescent activated cell sorting of distinct, viable, cytokine-defined B cell sub-populations for further investigations including RNA-profiling and *in vitro* functional assays.

Introduction

Cytokines have an essential role in immune cell development and function, shaping the nature and the magnitude of immune responses in health and disease⁵⁶²⁻⁵⁶⁴. Deleterious consequences are observed in individuals with monogenic mutations in genes encoding for molecules involved in cytokine signaling⁵²³. Cytokine secretion is a common feature of immune cells, such as B cells. Indeed, B cells are multifunctional and capable not only of differentiation into immunoglobulin secreting cells, but they also function as antigen presenting cells and modulators of inflammatory responses through cytokine secretion^{271,332,343}. The latter function has emerged as essential for bi-directional interactions with T cells and myeloid cells and has been implicated in infectious and autoimmune diseases and their therapies^{271,343}.

Human B cells can secrete multiple cytokines in a context-dependent manner, including pro-inflammatory cytokines such as GM-CSF, TNF, and IL-6 as well as anti-inflammatory cytokines such as IL-10^{271,343}. It is notable that certain cytokines are commonly expressed in *ex vivo* human blood B cells including IL-6 and TNF, representing high frequency cells, while others such as GM-CSF and IL-10, have a limited expression and represent low frequency circulating cells²⁸¹. Expression of particular cytokines can be enriched in certain B cell subpopulations; however, unique cell surface markers are still lacking to distinguish them^{281,377,389,392,393}. The absence of unique cell surface markers for cytokine-producing B cells has hampered further investigations into their biology including gene expression profiles, regulatory networks controlling their development and maintenance, contributions to disease states, and therapeutic manipulation. While detecting the actual cytokine/s expressed by the B cells has remained the only approach for studying these cytokine-defined B cell subpopulations^{281,372,377,383,389,392,393}, use of intracellular cytokine staining involves cell fixation and permeabilization which results in loss of cell viability and integrity, seriously limiting cell usage in downstream applications⁵⁶⁵.

The cytokine-secretion assay (herein referred to as CSA) was designed to overcome this limitation and to allow for the isolation of viable cytokine-defined immune cells^{566,567}. CSA relies on bispecific antibodies (bsAbs) bound to the cell surface that capture secreted cytokines on viable cells, thereby preserving cell viability and integrity, in contrast to intracellular cytokine staining⁵⁶⁵⁻⁵⁶⁷. In essence, CSA can be divided into four major steps: (1) polyclonal or antigen-specific

activation of cells; (2) labelling of cells with bsAbs that binds to cell surface antigen (CD45) and a particular cytokine; (3) secretion and capture of cytokines; and (4) detection of cytokine-secreting cells with fluorochrome-conjugated anti-cytokine antibodies for flow cytometry analysis^{566,567}. However, cytokine capture assays have more typically applied to high frequency cells and, in particular, have not been used for simultaneous isolation of multiple low frequency cytokine secreting cells. The latter would be particularly beneficial when sample volumes and cell numbers are limiting, such as in many human cellular immunology contexts. In this study, we adapted CSA for the simultaneous detection and isolation of viable human cytokine-secreting immune cells, and particularly low frequency B cell subpopulations. We found that this approach allows for the simultaneous isolation of both low and high frequency cytokine secreting B cells, which have high purity and viability and are amenable to subsequent *in vitro* culture or to gene expression profiling. We also show that while simultaneous detection and isolation of up to three viable cytokine-secreting B cell subpopulations is feasible using CSA, assay optimization is required to minimize cell losses and optimize the ability to detect each subset when assessed in combination. Overall, our study provides a newly adapted multiplexing CSA approach for isolating multiple viable human cytokine-secreting immune cells that can be used for multiple applications.

Materials and Methods

Cell Isolation and culture

Fresh blood was obtained from healthy individuals recruited from the Montreal Neurological Institute and Hospital (MNI/H), McGill University, and the University of Pennsylvania. All subjects provided informed consent as approved by the corresponding institutional ethics review boards. Peripheral blood mononuclear cells (PBMC) were isolated from whole blood using Ficoll-Paque density gradient centrifugation (GE Healthcare) and a strict standardized protocol¹⁵⁰. B cells were selected from PBMC using CD19 microbeads (Miltenyi Biotec) according to manufacturer's recommendations. Typical purities routinely assessed by flow cytometry were >98%. B cells were cultured in serum-free X-Vivo medium (Lonza) and plated in flat-bottom 24-well plates at a concentration of 2×10^6 cells/well in a total volume of 1000 μ l of medium. Cells were activated with phorbol 12-myristate 13-acetate (PMA; 20ng/ml, Sigma-Aldrich) and Ionomycin (500ng/ml, Sigma-Aldrich) for 4 hours. Golgi stop (Monensin, BD Biosciences) was added at the start of stimulation for intracellular cytokine staining (ICS).

Flow cytometry

Intracellular cytokine staining of human B cells was performed as previously described²⁸¹. Briefly, cells were stained with LIVE/DEAD fixable Aqua dead cell stain (Thermo Fisher Scientific) for 20 minutes on ice, following which cell-surface marker staining was performed using mouse anti-human CD20 (BD Biosciences; clone: 2H7) and mouse anti-human CD3 (BD Biosciences; clone: UCHT1). Cells were then fixed and permeabilized using fixation/permeabilization buffer (BD Biosciences). Rat anti-human GM-CSF (clone: BVD2-21C11), rat anti-human IL-10 (clone: JES3-19F1), and mouse anti-human TNF (clone: MAb11) antibodies (BD Biosciences) or matching isotype controls were added, and cells were incubated for 30 minutes on ice. Cells were washed and resuspended in FACS buffer (PBS/1%FCS) until analysis on a FACS LSR Fortessa (BD Biosciences).

For the cytokine-secretion assay, cells were harvested and washed once in ice-cold MACS buffer (PBS/2mM EDTA/5%BSA). B cells were then resuspended in serum-free X-VIVO medium and labelled with capture antibodies for GM-CSF (final dilution 1:20), IL-10 (final dilution 1:10), or TNF-alpha (final dilution 1:10) (Miltenyi Biotec) for 10 minutes on ice. Cells were further diluted in pre-warmed medium at 1×10^5 cells/ml and incubated while rotating (using a MACS rotor) at 37°C/5% CO₂ for 45 minutes. B cells were then placed on ice for 10 minutes to terminate the secretion phase. Cells were subsequently washed twice in ice-cold MACS buffer before labelling with detection antibodies for GM-CSF (final dilution 1:20), IL-10 (final dilution 1:10), or TNF (final dilution 1:10) along with mouse anti-human CD20 (clone: 2H7) and mouse anti-human CD3 (clone: UCHT1) antibodies. We employed the anti-human TNF antibody (clone: MAb11) conjugated to BUV395TM (BD Biosciences) as a detection antibody. Of note, we also validated an alternative detection antibody for GM-CSF (clone: BVD2-21C11) that performs equally well as the reagent provided in the manufacturer's kit (data not shown). Where indicated, mouse anti-human CD45 antibody (ThermoFisher Scientific; clone: HI30) was added to measure the expression of unbound CD45 following capture phase. In other experiments we used anti-human TNF antibody (MAb11; 1:50) and anti-human GM-CSF antibody (BVD2-21C11; 1:100) as alternative detective reagents. B cells were washed once in ice-cold MACS buffer and analyzed on BD LSRFortessaTM (BD Biosciences). Data analysis was performed with FlowJo Software (TreeStar).

Enzyme-linked immunosorbent assay (ELISA)

Cytokine levels in cultured supernatants were measured by OptEIA ELISA kit (GM-CSF, IL-10, and TNF; BD Biosciences) following the manufacturer's protocols.

Quantification of mRNA expression by quantitative, real-time polymerase chain reaction

Total RNA extraction was performed using RNeasy Plus Micro kit (Qiagen, Valencia, CA), following manufacturer's protocols. The RNA was stored -80C and used to generate single-stranded cDNA in a standard reverse transcription (RT) reaction using high-capacity cDNA reverse transcription kit with RNase inhibitor (Thermo Fisher Scientific). Analysis of gene expression was performed using the following TaqMan® probes: *CSF2* (*Hs00929873_m1*), *IL10* (*Hs00961622_m1*), and *TNF* (*Hs01113624_g1*). *18s* (*Hs03003631_g1*) was used as a housekeeping gene. Fold-change calculations were performed using the $-\Delta\Delta CT$ method.

Statistics

All values are expressed as mean $\pm$ SEM for individual measurements made across multiple experiments. Student's paired t-test or one-way ANOVA with a Tukey post-hoc test was used for statistical comparisons between two groups. GraphPad Prism 6 was used to perform all the statistical analyses. P values of 0.05 or less were considered statistically significant.

Results

Detection of single low frequency cytokine-secreting human B cells *in vitro*

We first employed the cytokine secretion assay (CSA) in parallel with the intracellular cytokine staining (ICS) to determine its suitability for the detection of low-frequency cytokine-producing B cells. B cells isolated from PBMC were stimulated with PMA and ionomycin for 4 hours with or without monensin A for ICS and CSA, respectively. Upon stimulation, B cells produce IL-10 and GM-CSF, which can be detected by either approach (Fig.1A and B). Additionally, we found that CSA performed equally as well as ICS for the detection of IL-10⁺ (CSA: 2.22 ± 0.59 % vs. ICS: 0.81 ± 0.28 %, $p=0.1620$ Fig.1C) and GM-CSF⁺ (CSA: 5.49 ± 1.18 % vs. ICS: 2.65 ± 0.60 %, $p=0.2514$ Fig.1C) B cells.

Isolation of low frequency cytokine-secreting human B cells using CSA

We next assessed the ability to sort the low-frequency cytokine-defined B cell subpopulations and their degree of enrichment following isolation. In line with published work, we found that co-

staining of IL-10 and GM-CSF in B cells by ICS revealed that IL-10⁺ and GM-CSF⁺ B cells were two mutually exclusive subpopulations (Fig.2a)²⁸¹. B cells stimulated with PMA and ionomycin for 4 hours were used to sort IL-10⁺ or GM-CSF⁺ cells using fluorescence-activated cell sorting (FACS). We determined the purity of sorted fractions by flow cytometry, with typical enrichment confirmed as >95% (Fig.2b). As part of the purity confirmation, we found that *Il10* and *CSF2* expression were strikingly enriched in the sorted IL-10⁺ and GM-CSF⁺ B cells, respectively (Fig.2c). We next demonstrated that the sorted cells were able to respond to subsequent restimulation, with induction of secreted IL-10 or GM-CSF (measured by ELISA) confirmed in culture supernatants of the respectively sorted sub-populations (Fig.2d). The concordance between the *ex vivo* detection and ICS demonstration of mutually exclusive expression of IL-10 and GM-CSF, coupled with the qPCR and ELISA readouts obtained post-CSA isolation and subsequent activation of the sorted sub-populations, is reassuring and indicates that the activation used for the CSA did not modify the cytokine profile of the cells to now express cytokines that were not expressed by these cells when assessed immediately *ex vivo*. These initial experiments demonstrate that sorted low-frequency cytokine-producing B cells are of high purity and quality and can be integrated into downstream applications such as gene expression arrays, proteomic arrays, or *in vitro* cell cultures.

Simultaneous isolation of two low-frequency cytokine-secreting human B cells

We next sought to adapt the CSA for the concurrent detection and isolation of two low-frequency cytokine-secreting B cell sub-populations. Multiplexed CSA can in principle allow for efficient use of limited cell numbers obtained from rare and/or limited clinical samples. Therefore, we tested the impact of combining two capture reagents on the detection and purity of IL-10⁺ and GM-CSF⁺ B cells. Compared with single captured B cells, the presence of a second capture reagent resulted in slight reductions in the frequencies of IL-10 (single: 3.83 ± 0.84 % vs. double: 2.88 ± 0.65 %, p<0.0001) and GM-CSF⁺ (single: 5.25 ± 1.26 % vs. double 4.28 ± 1.08%, p=0.0139) B cells (Fig.3a, b). In addition, the mean fluorescence intensity of either population was consistently reduced in the presence of a second capture reagent, suggesting that dual staining resulted in a reduction of the binding of cytokine-specific capture antibody on a cell basis. Multiplexing did not appear to adversely impact cell purities of the cytokine-captured sub-populations obtained post-FACS isolation (Fig.3c).

Concurrent detection of three cytokine-secreting B cell subpopulations

We next wished to assess the feasibility of simultaneous sorting of both low-frequency as well as higher frequency cytokine-defined B cell subpopulations. IL-6 and TNF are both expressed by relatively higher frequencies of circulating human B cells compared to IL-10 and GM-CSF expressing populations²⁸¹. After first validating the detection and isolation of TNF⁺ B cells using CSA (Fig.S1), we then integrated TNF capture into our multiparametric CSA to test the feasibility of simultaneous detection of three cytokine-secreting B cell subsets of differing frequencies. IL-10⁺, GM-CSF⁺, and TNF⁺ B cells could all be detected simultaneously, as shown on t-SNE plot (Fig.4a). Next, we evaluated the impact of co-staining two or three cytokines on the detection of cytokine-positive B cells. In these experiments, we diluted cells in a final volume suitable for single TNF detection to minimize detection of non-specific cytokine-secreting cells. For IL-10, co-staining with GM-CSF ($-24.02 \pm 2.34 \%$, $p < 0.0001$) or with GM-CSF and TNF ($-27.89 \pm 2.42 \%$, $p < 0.0001$) resulted in greater loss of signal than with TNF ($-11.29 \pm 2.56\%$, $p = 0.0046$; Fig.4b). There was a variable degree of reduction in the frequency of GM-CSF⁺ B cells when combined with IL-10 ($-22.72 \pm 7.18\%$, $p = 0.0528$), TNF ($-14.31 \pm 6.88\%$, $p = 0.2381$) or IL-10 and TNF ($-34.00 \pm 6.31\%$, $p = 0.0029$; Fig.4b). For TNF, co-staining with IL-10 ($-14.27 \pm 2.08\%$, $p = 0.0006$) and/or GM-CSF ($-20.54 \pm 2.46\%$, $p = 0.0001$) caused a modest decrease in yield, with greater loss with IL-10 and GM-CSF ($-26.15 \pm 3.24\%$, $p = 0.0002$; Fig.4c). Nonetheless, IL-10⁺, GM-CSF⁺ and TNF⁺ cell fractions isolated in a four-way FACS isolation along with triple negative cells showed excellent purity (Fig.4c) and viability (data not shown). Also, sorted and re-stimulated IL-10⁺ and GM-CSF⁺ cells secreted IL-10 and GM-CSF respectively, while all sorted subsets secreted TNF (Fig.4d). Thus, simultaneous detection and isolation of low and high frequency B cell subsets is feasible using CSA, with relatively greater impact on the yield of the low-frequency vs. the high-frequency subpopulations.

Discussion

Cytokine-secreting B cells, including low frequency subsets, orchestrate immune responses in infectious and inflammatory diseases and, consequently, there is a growing interest in their detection and isolation in order to better define the molecular mechanisms driving their development and functions^{271,343}. Such efforts have been constrained by the lack of validated and unique cell surface markers to detect cytokine-secreting subpopulations, which has limited their isolation in a viable state suitable for downstream applications^{281,377,389,392,393}.

In this study, we have adapted and validated the use of cytokine-secretion assay (CSA) for the detection and isolation of viable low- and high-frequency cytokine-secreting human B cells. We have shown that CSA performed equally as ICS in the detection of cytokine-producing B cells *ex-vivo*, and could be used for the isolation of single low- and high-frequency cytokine-secreting cells. We further extended the utility of this approach by demonstrating that dual and triple simultaneous detection and isolation of distinct cytokine-secreting cells could be achieved without loss of purity, though with variable reductions in cytokine detection. Sorted cytokine-secreting cells were viable, and can be integrated in other assays including gene expression analysis and *in vitro* cell culture.

We have insofar demonstrated the utility of the cytokine secretion assay by utilizing PMA and ionomycin for the induction of cytokine secretion by B cells *ex-vivo*. These compounds activate protein kinase C (PKC) and Ca^{2+} /calmodulin dependent signaling pathways which mobilize NFAT and its partners AP1/Fos/Jun⁵⁶⁸. Treatment with PMA and ionomycin can imprint a gene signature on immune cells, characterized by up-regulation of genes encoding for cytokines and chemokines as well as it can induce chromatin changes⁵⁶⁹⁻⁵⁷¹, and as such we recognize that this mode of activation may not always be optimal for certain downstream applications. Alternatively, the cytokine-secretion assay could be validated for the detection of antigen-specific B cells *ex-vivo* or upon *in vitro* expansion. In fact, *Pinder et al.* adapted the principle of this assay and developed a flow cytometry-based Ig capture assay for the detection of live antibody-secreting cells *ex-vivo* in recently immunized individuals⁵⁷². Whether antigen-specific human B cells also produce cytokines *ex-vivo* requires further investigation.

It is arguable that the diminished signals observed upon CSA multiplexing was caused by the saturation of surface CD45. The capture reagents are bi-specific antibodies that bind to CD45 for cell anchoring, and upon saturation of CD45 by a mixture of multiple distinct (two or more) bispecific antibodies, the level of individual cytokine-capture reagent can be diminished. This can result in diminished yields but preserved purities. Titration of the capture reagents is warranted and could help optimize CSA assays developed for different combinations of cytokines, though may not entirely resolve this issue.

Proper dilution of cells in the appropriate medium during the secretion phase is important to reduce false positive and background signals. The appropriate cell concentration in this assay is dependent on the expected frequency of cytokine-secreting cells, such that higher frequencies of positive cells require greater cell dilution^{566,567}. This should be kept in mind when performing dual and triple staining, as it follows that cells should be diluted according to the highest expected frequency of cytokine-secreting cells in the mixture to reduce non-specific binding during the capture phase.

In summary, we present a method for the simultaneous isolation of viable low- and high-frequency cytokine secreting human B cells and we highlight its strengths and limitations. This newly adapted and validated CSA provides an opportunity to carry out in-depth analyses of low-frequency functionally-distinct cytokine-defined immune cell subpopulations, with multiple applications including reliable RNA expression-profiling and use in a range of functional assays.

Disclosures

The authors have no financial conflicts of interest

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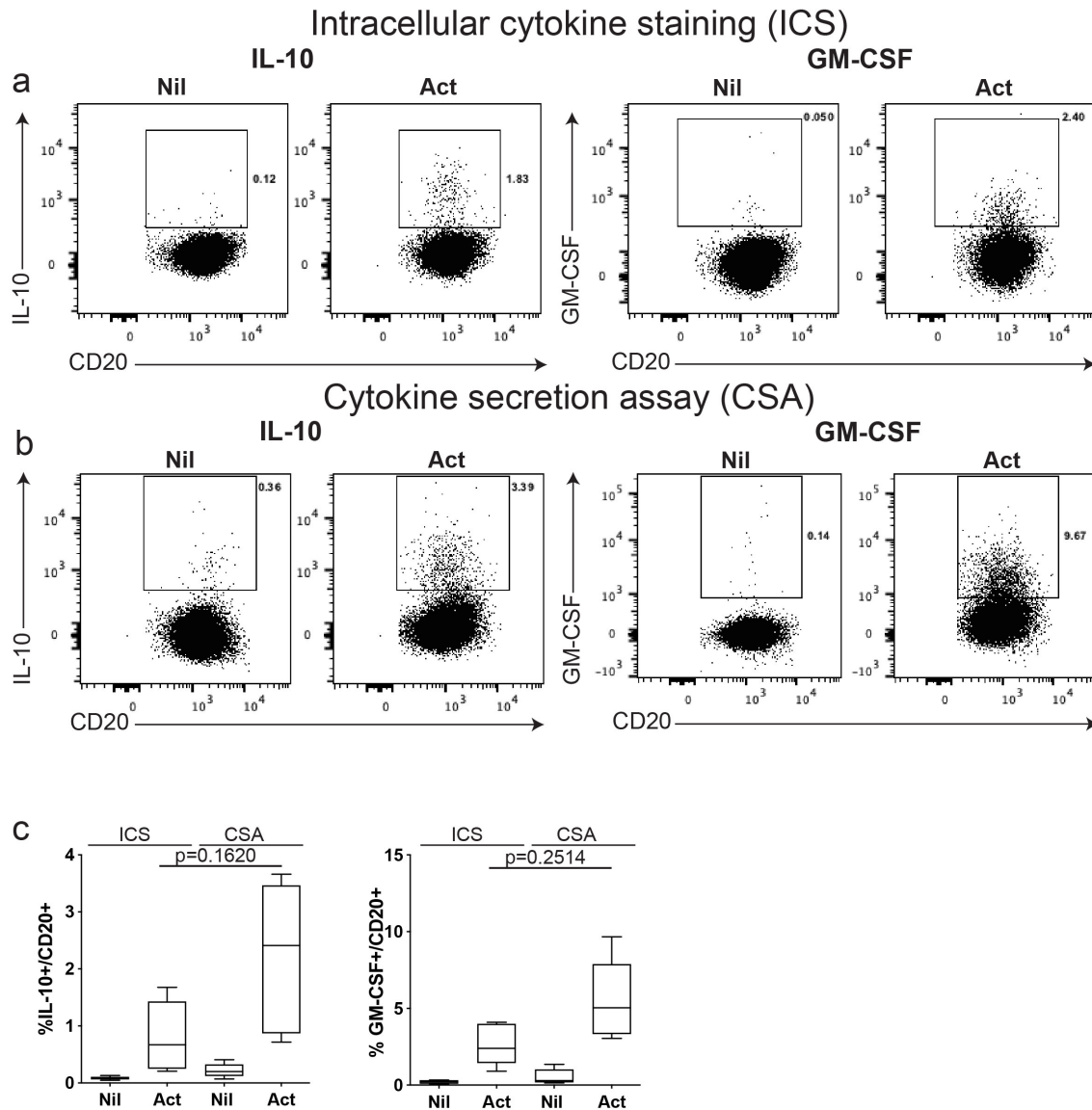


Figure 1. Cytokine expressing human B cells detected using intracellular cytokine staining versus a cytokine-secretion assay optimized for detection of low-frequency cytokine-secreting B cells. Human B cells were isolated from peripheral blood mononuclear cells (PBMC) using CD19-microbeads (purity routinely confirmed by flow cytometry as >97%). Cells were left unstimulated (Nil) or briefly activated (Act) with PMA (20ng/ml) and ionomycin (500ng/ml) for 4 hours before assessing IL-10 and GM-CSF expression by either intracellular cytokine staining (ICS) or cytokine-secretion assay (CSA). Representative FACS profiles are shown for ICS (**a**) and CSA (**b**), with results of n=5 independent experiments summarized in (**c**).

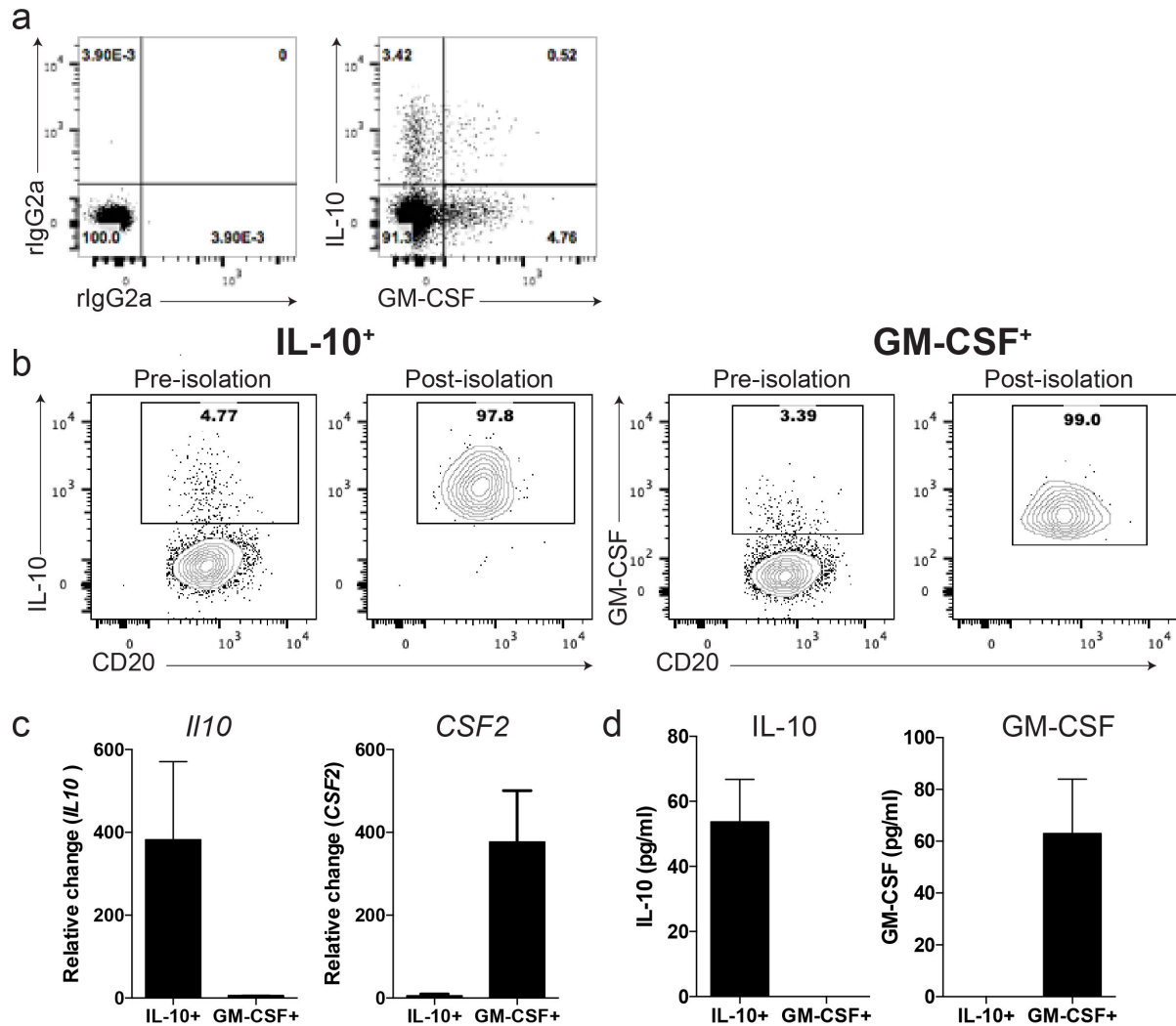


Figure 2. Validation of the cytokine secretion assay as an approach for isolating viable low-frequency cytokine-defined human B cells. Purified human B cells were activated with PMA and ionomycin for 4 hours prior to detecting the expression of either IL-10 or GM-CSF using the cytokine secretion assay. **(a)** *Ex vivo* co-concurrent intracellular cytokine staining (ICS) confirms essentially mutually exclusive expression of IL-10 and GM-CSF by distinct B cells subpopulations. **(b)** Representative cytokine-secretion assay (CSA) FACS profiles prior to and following sorting of either IL-10⁺ or GM-CSF⁺ human B cells (BD FACS Aria). **(c)** RNA expression levels for IL10 (left) and CSF2 (right) measured by qPCR in freshly sorted CSA-captured and sorted IL-10⁺ and GM-CSF⁺ B cells (n=3). **(d)** Levels of IL-10 and GM-CSF secreted by viable CSA-captured and sorted IL-10⁺ and GM-CSF⁺ B cells; 5000 cells/well were

rested overnight and re-stimulated with PMA and ionomycin for 12 hours (n=3). Data shown are the mean $\pm$ SEM (error bars). Statistical analysis carried out with paired Student's t-test. ND, non-detectable.

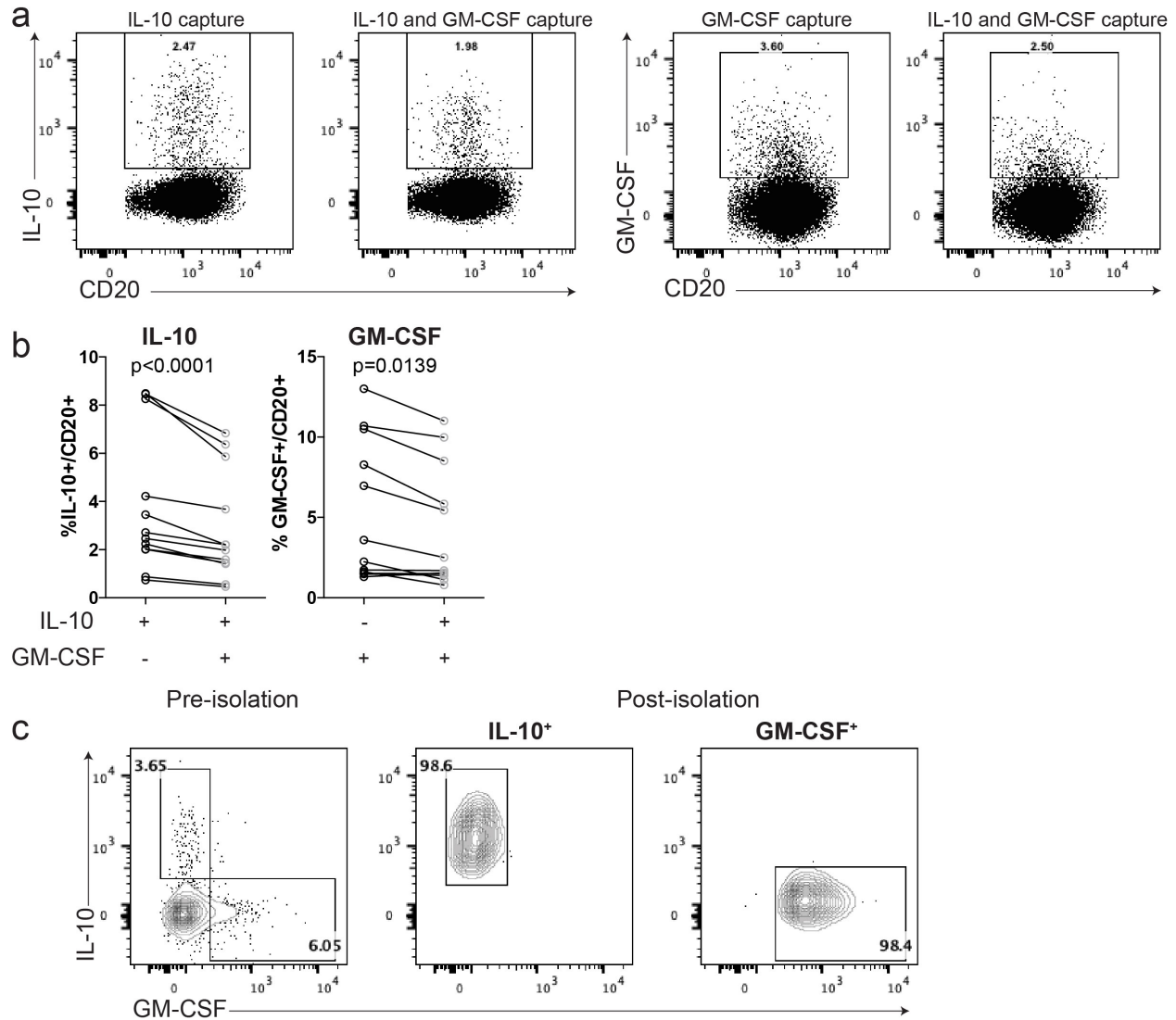


Figure 3. Concurrent isolation of two low-frequency cytokine-secreting B-cell subpopulations using the cytokine secretion assay. Human B cells were activated with PMA (20ng/ml) and Ionomycin (500ng/ml) for 4 hours before carrying out the cytokine secretion assay. The frequencies of live IL-10⁺ and GM-CSF⁺ cells were examined following ex-vivo B cell stimulation and either single cytokine capture (IL-10 or GM-CSF alone), or dual cytokine capture (both IL-10 and GM-CSF simultaneously); **(a)** staining from representative experiment; **(b)** summary of n=12 independent experiments. **(c)** A representative staining of IL-10⁺ and GM-CSF⁺ B cells, prior to and following isolation using simultaneous dual cytokine-capture. Statistical analysis carried out with paired Student's t-test.

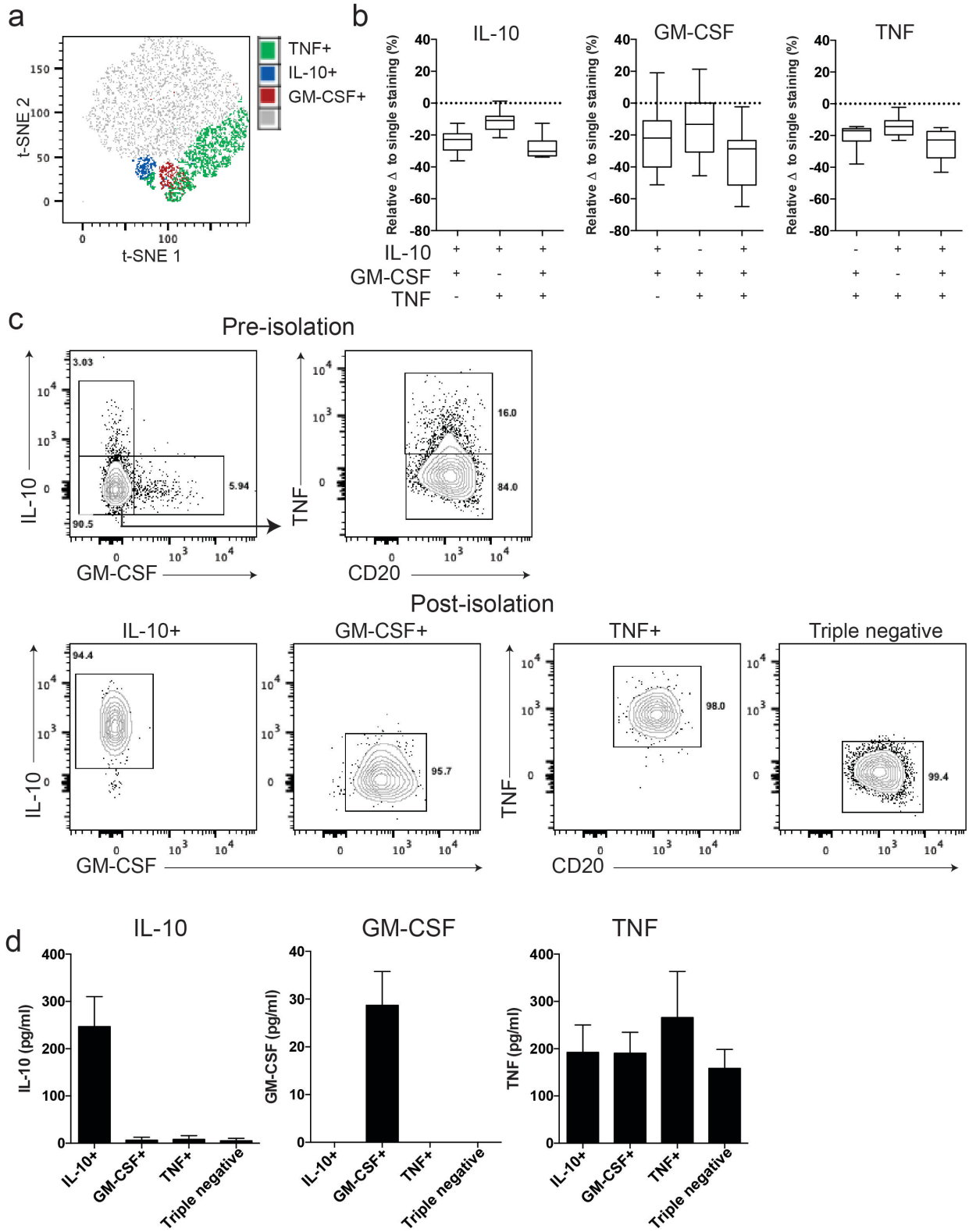
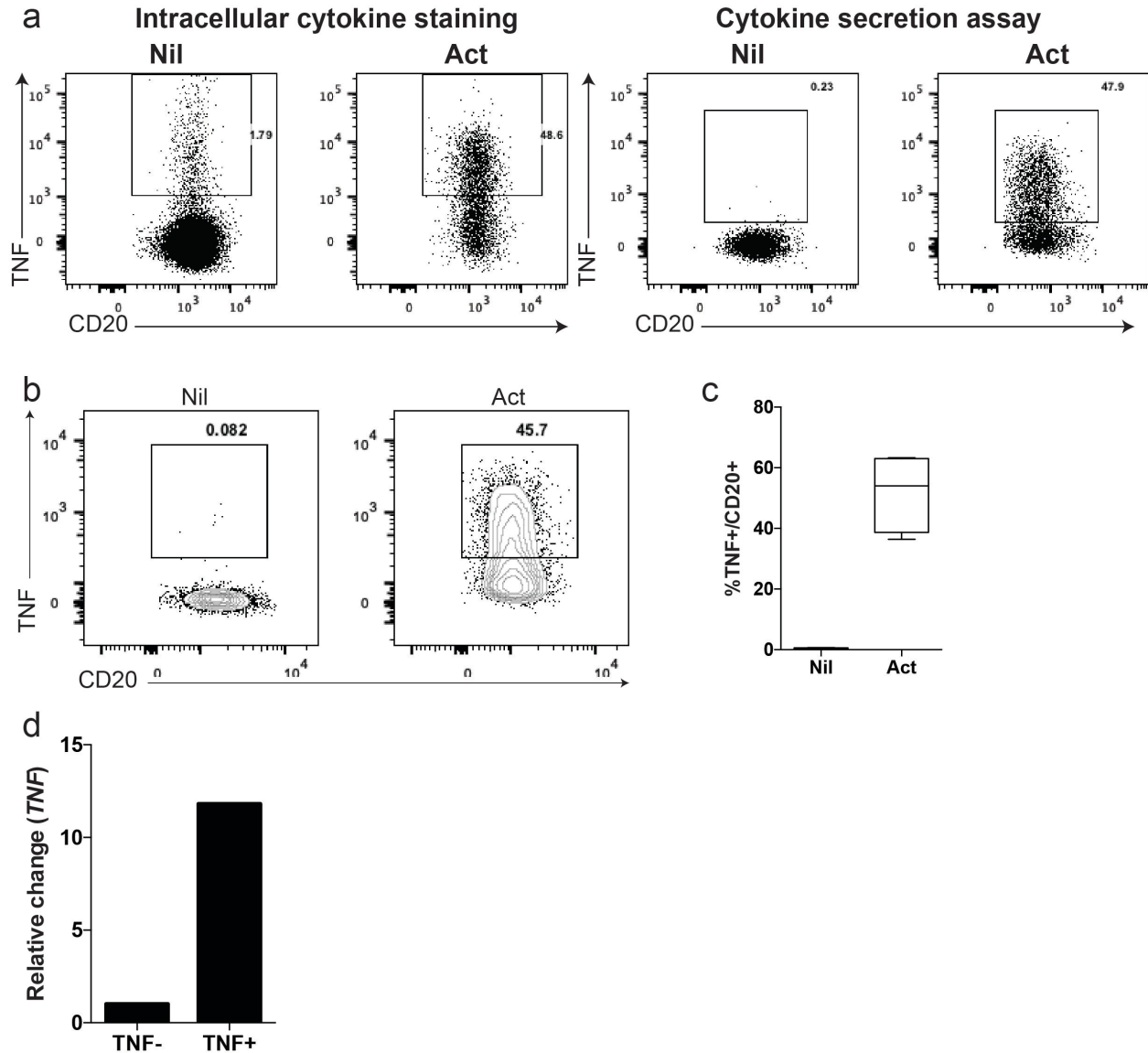


Figure 4. Simultaneous detection and isolation of three cytokine-secreting B cell subpopulations using the cytokine secretion assay. (a) Concurrent detection of three cytokine-secreting B cell populations in one sample visualized on t-SNE plot. (b) Relative change in the frequency of IL-10, GM-CSF and TNF in samples stained with different combinations of capture and detection reagents, as compared to individual staining (n=9). Data are shown as box with 5-95%whiskers. (c) A representative staining of IL-10⁺, GM-CSF⁺ and TNF⁺ B cells, prior to and following isolation using simultaneous triple cytokine-capture. (d) Sorted B cell subpopulations were rested overnight and re-stimulated with PMA and ionomycin for 12 hours. Levels of secreted cytokines were assessed by ELISA. Data shown are the mean +/- SEM (error bars). Statistical analysis carried out with paired Student's t-test.



Supplementary figure 1. Detection and isolation of viable TNF-secreting B cells using the cytokine secretion assay. (a) Representative FACS profile of TNF production by B cells upon short-stimulation detected by ICS (left) or CSA (right). (b) B cells were left unstimulated or stimulated with PMA and ionomycin for 4 hours prior to detection of TNF-secreting B cells using CSA as shown in a representative experiment and summarized in (c, n=4 independent experiments). (d) RNA expression for *TNF* measured by qPCR in freshly sorted TNF⁺ or TNF⁻ CSA-captured B cells, and represented as relative change to TNF⁻ (n=1).

Preface: Chapter 3

In the previous chapter, I described a cytokine-secretion assay developed and optimized for the purpose of detecting and isolating viable, functionally-distinct, low- and high-frequency cytokine-secreting B cells, which will enable in-depth characterization of these B cell subpopulations as well as assessment of their functional properties in culture. We have previously defined several abnormalities of B cells in untreated MS patients that we have implicated in the abnormal induction of pro-inflammatory responses of CD4⁺ T cells and myeloid cells. In keeping with these *ex-vivo* and *in vitro* observations, we have also shown that B-cell depletion with anti-CD20 monoclonal antibody, which is very effective at limiting new MS activity, diminishes CD4⁺ T cell and myeloid cell pro-inflammatory responses in patients. An intriguing observation is the parallel reduction in CD8⁺ T cell pro-inflammatory cytokine responses in the same treated patients. This suggests that B cells and CD8⁺ T cells can interact *in vivo* and raises the possibility that such interactions are relevant to MS pathophysiology and possibly also to the therapeutic effect of anti-CD20 therapy in MS. Both conventional CD8⁺ T cells as well as mucosal-associated invariant T (MAIT) cells have been identified within the MS brain where they are clonally-expanded and express pro-inflammatory/effector molecules. My overarching hypothesis is that human B cells can interact with and modulate CD8⁺T cells in ways that will explain the diminished CD8⁺T cell responses seen in patients undergoing B cell depletion. Surprisingly little is known about the potential for human B cell: CD8⁺T cell interactions, and it is essentially unknown whether and how functionally distinct B cells will have a different impact on CD8⁺T cells or on their subsets. My work on this part of the project integrates a series of observations from *in vitro* experiments demonstrating that differentially activated human B cells can have a distinct impact on human conventional versus innate-like CD8⁺ T cells. I further demonstrate the *in vivo* consequences that B cell depletion has on CD8⁺T cell subsets in patients with MS. Together, my results provide novel fundamental insights into the complexity of potential interactions between functionally distinct human B cell subsets and distinct CD8⁺T cell subsets and point to *in vivo* interactions between B cells and CD8⁺T cells that appear to be relevant to disease pathophysiology and potentially to therapeutic targeting of such interactions in patients with MS.

Chapter 3: B cells regulate CD8⁺ MAIT cell effector functions: implications for multiple sclerosis

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AR generated all hypotheses, designed and performed all the experiments, analyzed the complete data sets and wrote the manuscript

KS assisted with data generation

RL assisted with data generation and helpful research discussions

A.B.O. provided the overall supervision, generated hypotheses, guided the experimental plan, analyzed the data and wrote/revised the manuscript.

Abstract

B cells carry out antibody-independent functions that serve to orchestrate other cellular immune responses, important for both host protective immunity and in the context of inflammatory diseases. Among these, bi-directional interactions between B cells and CD4⁺ T cells have been well-described. Indeed, pro-inflammatory CD4⁺ T cell responses are diminished by depleting B cells with anti-CD20 antibody, which is highly effective at limiting new disease activity in patients with multiple sclerosis (MS). However, initial studies in patients undergoing the same *in vivo* B cell depletion indicated that CD8⁺ T cell function may also be affected, suggesting *in vivo* interactions take place between these two immune cell subsets and that such interactions may be relevant to the pathophysiology and potential therapeutic targeting in the context of autoimmune disease. Here we set out to study potential interactions between B cells and both conventional CD8⁺ T cells (non-MAIT) and innate-like CD8⁺ T cell cells known as mucosal-associated invariant (MAIT) cells. We find that, *in vitro*, human B cells can suppress the proliferation of conventional CD8⁺ T cells yet significantly promote MAIT cell expansion both polyclonally and at the antigen-specific level. This differential B cell effect on CD8⁺ T cell subsets is rather dependent on the differentiation stage and activation of the B cells. Activated B cells also differentially enhanced CD8⁺ T-cell subset cytotoxicity, an effect that did not require cell:cell contact, as it could be mediated through B-cell secreted products. B cells further modulated cytokine production in CD8⁺ T cells by selectively enhancing IFN γ production by MAIT cells, while suppressing GM-CSF and TNF production by non-MAIT cells. Finally, B cell depletion using anti-CD20 monoclonal antibody in patients with MS resulted in an *in vivo* shift in the profile of circulating CD8⁺ T cells, including a reduction in MAIT cells and diminished CD8⁺ T cell pro-inflammatory functions including cytokine production, that mirrored aspects of our *in vitro* findings. Together, these findings reveal the capacity of activated human B cells to reciprocally impact distinct CD8⁺ T cell subsets and indicate that *in vivo* cross-talk between B cells and CD8⁺ T cells may be relevant to inflammatory disease activity. The particular capacity of B cells to induce activation and effector responses of MAIT cells may be especially relevant to MS pathophysiology and possibly to the therapeutic mode of action of anti-CD20 therapy in patients.

Introduction

B lymphocytes are multifunctional cells with a capacity to secrete immunoglobulins, present antigens, and produce cytokines^{271,332,343}. The latter two functions are essential for bi-directional interactions between B cells and CD4⁺ T cells as well as with invariant natural killer T (iNKT) cells^{271,343,573,574}. B cells can produce pro- as well as anti-inflammatory cytokines depending on integration of signals downstream of B-cell receptor (BCR), co-stimulatory CD40L, toll-like receptors, and cytokine receptors^{281,372,383,391,393}. This integration allows B cells to acquire inflammatory or suppressive (regulatory) functions in a context-dependent manner^{271,343}. Accordingly, B cell depletion or the manipulation of cytokine production by B cells can modulate functions of different cells such as CD4⁺ T cell subsets, inducing them to exhibit enhanced or diminished inflammatory responses²⁷¹. B cell:CD4 T cell interactions appear to have notable *in vivo* relevance for infectious diseases, autoimmune diseases, and other inflammatory conditions^{281,282,342,360,372,382}. How responses of CD8⁺ T cells and their subsets may be modulated by B cells, and what the relevance of such modulation may be in the context of human disease and therapeutics, remain poorly-defined^{382,575-578}.

CD8⁺ T cells are phenotypically and functionally heterogeneous. Among CD8⁺ T cells, a subset known as mucosal-associated invariant T (MAIT) cells is emerging as relevant for host defense against pathogens and inflammatory diseases^{480,513,551}. MAIT cells are an innate-like T cell subset expressing TRAV1 (TCR-V α 7.2) and a restricted TCR- β repertoire that recognize conserved microbial antigens derived from vitamin B metabolites and presented on MHC-related protein 1 (MR1)^{485,492,493,497,508}. In this regard, 5-(2-oxopropylideneamino)-6-D-ribitylaminouracil (5-OP-RU) is a MAIT cell activating antigen that is commonly used as part of the MR1-tetramer to identify MAIT cells^{493,542}. Upon antigen recognition, MAIT cells release pro-inflammatory cytokines and cytotoxic granules necessary for the elimination of pathogen-infected target cells^{480,529}. Their transcriptome is distinct from conventional CD8⁺ T cells, yet similar to iNKT cells, with enhanced expression of genes encoding for cytokines, cytotoxic molecules, and chemokine receptors^{505,511}. In humans, MAIT cells circulate in the blood, representing 0.1 to 15% of CD8⁺ T cells, and traffic to the liver, lung, and gut, where they can acquire tissue-residence signature^{502,505,507,510}. MAIT cells have also been implicated in autoimmune disease, including multiple sclerosis, where they have been found to be clonally expanded and expressing pro-

inflammatory effector molecules within the inflamed central nervous system of patients^{150,419,420,422,423,561}.

Since B cells have been known to engage in productive bi-directional interactions with iNKT cells, serving to modulate iNKT effector functions^{573,579-583}, and given the similarities between iNKT and MAIT cell transcriptional profiles^{505,507}, it is tempting to speculate that B cells and MAIT cells may also be ‘interacting partners’ *in vivo*. In this study, we sought to investigate the interactions between human B cells and both conventional and innate-like CD8⁺ T cell subsets using two complementary approaches: a series of *in vitro* experiments assessing interactions between functionally distinct human B cells and CD8⁺ T cell subsets and *ex vivo* functional immunophenotyping of CD8⁺ T cells within peripheral blood mononuclear cells (PBMC) obtained from MS patients prior to and after *in vivo* B cell depletion therapy (BCDT) with anti-CD20 antibody. We hypothesized that B cells can stimulate MAIT cell pro-inflammatory functions, which would then be attenuated following B cell depletion. Our study highlights the capacity of B cells to differentially regulate MAIT and conventional non-MAIT cell pro-inflammatory responses *in vitro* and *in vivo*.

Materials and methods

Human subjects and ethics approval

All subjects provided written informed consent as approved by the Montreal Neurological institute and Hospital Ethics Review Board and the University of Pennsylvania Institutional Review Board. Normal controls were recruited at the Montreal Neurological institute and University of Pennsylvania. Ocrelizumab-treated patients were recruited at the Hospital of the University of Pennsylvania. Patient demographics are described in supplemental table 1.

Cell isolation

Peripheral blood mononuclear cells were isolated from whole blood by Ficoll-Paque density gradient centrifugation (GE Healthcare), as described previously¹⁵⁰. B cells were positively selected using CD19 microbeads (Miltenyi Biotec), and CD8⁺ T cells were negatively selected using CD8⁺ T cell isolation kit (Miltenyi Biotec) according to manufacturer’s instructions. Typical post-isolation purities assessed by flow cytometry were >95% (Figure S1).

B cell and T cell activation

Isolated CD8⁺ T cells were labelled with CellTrace Violet (ThermoFisher Scientific) to monitor cell proliferation, resuspended in X-VIVO medium (Lonza) and seeded at 1×10^5 cells per well in U-bottom 96-well plates. In parallel, isolated B cells were either left unstimulated or activated overnight (16-18 hours) with either of three activation conditions: CpG DNA (1 μ M, ODN2006; InvivoGen) alone, CD40L (1 μ g/ml; Enzo Life Sciences) alone, or a combination of CD40L with goat anti-human BCR F(ab)² fragment antibody (10 μ g/ml; Jackson ImmunoResearch Laboratories) and recombinant IL-4 (20ng/ml, R&D systems). B cells were then harvested and washed in X-VIVO medium prior to co-culture with autologous T cells, where they were added into co-culture at 2×10^5 cells per well in a total culture volume of 200 μ l. Isolated T cells were polyclonally activated with beads coated with anti-CD2, anti-CD3, and anti-CD28 antibodies (Miltenyi Biotec). Where indicated, neutralizing antibodies targeting IL-10 (JES3-19F1, 2.5 μ g/ml), TGF-R (1D11, 2.5 μ g/ml), IL-12p35 (27537, 2.5 μ g/ml), (all from R&D systems), PD-L1 (29E.2A3, 2.5 μ g/ml) (Biolegend), and matching isotype controls were added to cell culture. Recombinant IL-2 (1-100U/ml; Sigma Aldrich) was used where indicated.

Flow cytometry

Expression levels of T cell and B cell surface and intracellular proteins were quantified by flow cytometry using fluorochrome-conjugated antibodies: CD3 (SK7, 1:50), CD8 (RPA-T8, 1:50), CD20 (2H7, 1:20), CD25 (M-A251, 1:100), CD27 (M-T271, 1:50), CD38 (HIT2, 1:20), CD69 (FN50, 1:20), CD71 (M-A712, 1:20), CD107a (H4A3, 1:40), CD161 (REA631, 1:200), CD138 (clone, 1:50), IL-2 (MQ1-17H12, 1:50), IL-6 (MQ2-6A3, 1:400), IL-10 (JES3-19F1, 1:50), IFN γ (B27, 1:50), TNF (MAb11, 1:400), GM-CSF (BVD2-21C11, 1:400), granzyme B (GB11, 1:400), perforin (δ G9, 1:50), and TCR-Va7.2 (3C10, 1:50). Phorbol 12-myristate 13-acetate (PMA; 10ng/ml; Sigma Aldrich), ionomycin (1 μ g/ml; Sigma Aldrich) and Golgi Stop (monensin; BD Biosciences) were added on day 3 for the last 5 hours of culture in order to detect intracellular cytokine production. CD107a and Golgi Stop were added on day 3 for the last 5 hours of culture to quantify cell degranulation. Cells were harvested and stained with a viability dye (Live/Dead fixable aqua dead cell stain, ThermoFisher Scientific) as per manufacturer's instructions. Where indicated, MR1 tetramers loaded with 5-OP-RU or 6-Ac-FP were used to confirm the identity of MAIT cells. Cell surface staining using pre-mixed antibody cocktails was performed at room temperature for 30 minutes, with the use of Brilliant buffer (BD Biosciences) to mitigate non-

specific interactions among brilliant violet conjugated antibodies. Cells were fixed and permeabilized using Cytofix/Cytoperm (BD Biosciences). Intracellular molecules were stained using pre-mixed antibody cocktails for 30 minutes on ice. Cells were resuspended in PBS prior to flow cytometry data acquisition on LSRFortessa. Data analysis was carried out using FlowJo (Tree Star).

Enzyme-linked immunosorbent assay (ELISA)

Levels of secreted cytokines in culture supernatants were measured by OptiEIA ELISA kits for IFNG, GM-CSF, TNF, IL-10, and IL-6 (all from BD Biosciences), according to the manufacturer's instructions.

PBMC immunophenotyping prior to and following B cell depletion

PBMC were isolated from whole blood obtained from MS patients prior to and on-treatment (3 months post-treatment) with the anti-CD20 monoclonal antibody ocrelizumab. PBMCs were then cryopreserved using standardized operating procedures developed and validated for all steps of sample procurement, processing, cryopreservation, storage, and thawing¹⁵⁰. Thawed PBMC samples with cell viability of less than 70 % were excluded from analysis. Functional immunophenotyping was performed in batch by a blinded operator. Each batch included pre- and on-treatment PBMC samples and an internal control sample used consistently across batches. Multiparametric flow cytometry panels were developed and validated on fresh and cryopreserved PBMC before their application to the patient cohort (Supplemental Tables 2 and 3).

Statistical analysis

All values were expressed as the mean measurements across experiments $\pm$ standard errors of the means. Statistical testing across groups employed as appropriate either one-way ANOVA with a Dunn's post-hoc test, two-way ANOVA with Tukey's post-hoc test or two-tailed ratio paired t test, using GraphPad Prism version 6. P values less than 0.05 were considered statistically significant.

Results

Human B cells differently impact CD8⁺ T cell subset proliferation

To examine potential interactions between human B cells and CD8⁺ T cells, we set up an *in vitro* co-culture system, wherein autologous polyclonally activated CD8⁺ T cells were co-cultured with unstimulated B cells or with B cells pre-activated with either CpG (toll-like receptor 9 agonist),

CD40L, or a combination of CD40L, BCR-cross-linking antibody, and IL-4 (herein referred to as 40X4). These stimuli have been previously shown to induce distinct human B cell cytokine profiles and cell surface phenotypes²⁸¹⁻²⁸³. We defined conventional MAIT cells as CD3⁺CD8⁺ T cells that were CD161^{hi} TCR-V α 7.2⁺ and defined non-MAIT cells as CD3⁺CD8⁺ T cells that were CD161^{-int} TCRV α 7.2^{+/-}. As expected, *ex vivo* CD161^{hi} TCRV α 7.2⁺ CD8⁺ T cells recognized 5-OP-RU presented on MR1 tetramers, whilst CD161^{-int} TCRV α 7.2^{+/-} cells did not (Fig.S2). Upon activation, MAIT cells proliferated less vigorously than conventional non-MAIT cells (Fig.1a), which may reflect a higher TCR threshold and/or a requirement for additional co-stimulatory signals to enter the cell cycle^{505,584-586}. We found that pre-activated B cells efficiently suppressed conventional non-MAIT cell proliferation, while they significantly enhanced MAIT cell proliferation (Fig.1a-b). The B cells exerted suppression of non-MAIT cell proliferation across a range of strengths of T cell stimulation and across a range of B cell to T cell ratios, with stronger suppression observed at early time points in the co-culture (Fig.1c-e). Unstimulated B cells also suppressed non-MAIT cells, albeit they were less potent than pre-activated B cells. In sharp contrast, unstimulated and pre-activated B cells stimulated MAIT cell proliferation with greater strength of T cell stimulation and with higher B cell: T cell ratios, effects that were observed at later time points in the co-culture (Fig.1c-e). In contrast to earlier studies, we found that MAIT cells were not more prone to cell apoptosis than non-MAIT cells upon activation (data not shown)^{526,587} and that B cell effects on CD8⁺ T cell subset proliferation were independent of any changes in CD8⁺ T cell survival (data not shown).

While these initial experiments suggested that B cells have contrasting effects on non-MAIT versus MAIT cell proliferation, MAIT cells are known to be effector memory cells, while the non-MAIT cells included both naïve and memory CD8⁺ T cells. For a better comparison, we therefore examined the impact of B cells on sorted MAIT cells and sorted naïve (CCR7⁺CD45RO⁻), effector memory (CCR7⁻CD45RO⁺), and terminal effector (CCR7⁻CD45RO⁻) CD8⁺ T cell subsets (Fig.S3). We found that pre-activated B cells suppressed naïve T cell proliferation and enhanced MAIT cell proliferation (Fig.2a-c), while they did not consistently modulate terminal effector and effector memory proliferation (Fig.2a-c).

Human B cells are functionally heterogeneous, with naïve and transitional B cells in particular possessing regulatory functions^{271,283,377}. To determine whether the capacity of B cells to differentially modulate CD8⁺ T cell subset proliferation was similar for all B cell subsets, we isolated transitional (CD24^{hi}CD38^{hi}), naïve (CD27⁺IgD⁺), class-switched memory (CD27⁺IgD⁻), and non-class switched memory (CD27⁺IgD⁺) B cells by FACS and co-cultured them with autologous CD8⁺ T cells. We observed that while all B cell subsets enhanced MAIT cell proliferation, the naïve and transitional B cells were more effective than the memory B cell subsets at suppressing non-MAIT T cell proliferation (Fig.S4). Our data highlights functional heterogeneity among conventional and innate-like T cells that can be differentially regulated by B cells.

Human B cells enhance CD8⁺ T cell cytotoxic potential

MAIT cells, similar to conventional CD8⁺ T cells, are poised to release cytotoxic granules in a TCR dependent and/or independent manner^{491,529,533}. We sought to extend our initial findings on CD8⁺ T cell proliferation and examined the capacity of B cells to modulate non-MAIT and MAIT CD8⁺ T cell cytotoxic phenotypes *in vitro*. Activated non-MAIT and MAIT cells markedly up-regulated the expression of granzyme B, perforin, and CD107a (Fig.3a-c). B cells pre-activated with CpG induced non-MAIT cell degranulation and granzyme B expression but not perforin expression (Fig.2a-c). In contrast, all pre-activated B cells amplified MAIT cell cytotoxic potential (Fig.2a-c). Further, soluble factors present in supernatants of B cells could recapitulate the changes in non-MAIT and MAIT cell cytotoxicity observed in co-culture (data not shown). Altogether, our data reveal that B cells can regulate CD8⁺ T cell subset cytotoxicity in a context-dependent manner.

Human B cells modulate CD8⁺ T cell cytokine production

We next assessed the levels of secreted cytokines in culture supernatants and found substantially increased IFN γ and decreased GM-CSF levels in co-culture supernatants of CD8⁺ T cells and B cells pre-activated with CpG (Fig.4a-b), with minor reduction in TNF levels in co-culture supernatants of CD8⁺ T cells and B cells pre-activated with CD40L or 40X4. We next employed intracellular cytokine staining to examine the production of these cytokines in CD8⁺ T cell subsets. Whilst the frequency of IFN- γ ⁺ CD8⁺ T cell subsets did not significantly differ upon co-culture with B cells (data not shown), the mean fluorescence intensity of IFN- γ ⁺ non-MAIT and MAIT cells was significantly increased in co-culture with CpG-primed B cells (Fig.4d-e). This data

combined with the proliferative response of non-MAIT cells demonstrate a dissociation between these two effector functions, suggesting that non-overlapping mechanisms of regulation are exerted by B cells on non-MAIT cells. It is notable that MAIT cells express higher levels of IFN- γ than non-MAIT, suggesting a greater contribution to overall secreted levels. Further, the frequency of GM-CSF-producing non-MAIT cells, and to a lesser extent MAIT cells, was decreased in co-culture with pre-activated B cells (Fig.4f-g). A similar trend of change was observed for TNF (Fig.4h-i). Altogether, our data suggests that B cells can differentially regulate cytokine production by non-MAIT and MAIT cells.

B cell depletion therapy shifts the distribution of blood CD8⁺ CD161⁻ and MAIT cells

To validate our *in vitro* observations on the effects of B cells on CD8⁺ T cell functional responses, we turned to peripheral blood mononuclear cells (PBMC) obtained from patients with multiple sclerosis treated with B cell depletion therapy (BCDT, ocrelizumab). BCDT has demonstrated significant clinical efficacy in reducing new disease activity in patients with multiple sclerosis^{273,274}. Samples collected prior to and after treatment initiation were analyzed using validated multi-parametric flow cytometry panels that included relevant cell surface markers, cytokines, and cytotoxic molecules for use on cryopreserved PBMC (Table 2 and 3). The gating strategy used in this analysis is presented in Fig.S5.

Analysis of major T cell subsets revealed that B cell depletion did not impact the absolute cell counts of circulating CD8⁺ T cell subsets, including naïve, central memory, effector memory and terminal effector cells (Fig.5a-d and summarized in table 4), though we observed a minor shift in CD8⁺ T cell subset distribution with an increased frequency of naïve T cells (41.52 ± 7.51 pre- to 48.33 ± 7.80 on-treatment, $p=0.0076$, table 5) and a decreased frequency of effector memory T cells (25.68 ± 4.40 pre- to 21.65 ± 4.06 on-treatment, $p=0.0105$, table 5). Further, and in line with our *in vitro* CD8⁺T cell proliferation data, we found that B cell depletion resulted in a decreased absolute cell counts (Fig.5f) and frequency of MAIT cells (4.78 ± 0.84 pre- to 3.85 ± 0.71 on-treatment, $p=0.0472$, table 5).

CD8⁺ T cell pro-inflammatory cytokine production is diminished after B cell depletion therapy

We next examined the expression of pro-inflammatory cytokines and cytotoxic molecules expressed by non-MAIT (CD161^{-int} TCR-V α 7.2^{+/-}) and MAIT (CD161^{hi} TCR-V α 7.2⁺) CD8⁺ T cells. *Ex vivo*, MAIT cells produced higher levels of cytokines (TNF, IFN γ , and GM-CSF) compared to non-MAIT cells, but were mostly devoid of granzyme B and perforin (Fig.S5) as expected. The absolute cell counts and frequencies of granzyme- and perforin-expressing non-MAIT and MAIT cells were unchanged after B cell depletion (Fig.S6, table 4-5). Further, B cell depletion was associated with a reduction in the absolute cell counts of IFN- γ ⁺ (Fig.6a), GM-CSF⁺ (Fig.6b) and TNF⁺ (Fig.6c) MAIT cells, whilst only the numbers of GM-CSF⁺ (Fig.6b) and TNF⁺ (Fig.6c) non-MAIT were reduced. Overall, our data indicate that B cell depletion results in reduced CD8⁺ T cell subset pro-inflammatory cytokine production.

Discussion

In this study, we examined the capacity for human B cells to regulate CD8⁺ T cells functions both *in vitro* and *in vivo*. Results of prior studies addressing interactions between B cells and CD8⁺ T cells, mostly carried in animal systems, have yielded mixed reports. In fact, some studies highlighted B cell regulatory capacity that could suppress CD8⁺ T cell effector functions, and others found an activating role for B cells, such as through MHC-I-dependent antigen presentation that enhanced CD8 T-cell functions^{382,575-578,588}. Our *in vitro* studies using an autologous human system demonstrated the capacity for B cells to differentially impact distinct CD8⁺ T cell subsets. B cells could induce substantial activation of MAIT cells, resulting in their enhanced proliferation, cytotoxicity, and IFN γ expression. In contrast, B cells substantially and consistently suppressed proliferation of conventional CD8⁺ T cells, while enhancing their cytotoxicity under a limited set of conditions. By examining the effects of removing B cells *in vivo* in MS patients undergoing anti-CD20 therapy, we identified changes in circulating CD8⁺ T cell subsets that corresponded with our *in vitro* findings. In particular, the demonstration that MAIT cell numbers and frequencies decreased in patients following the removal of B cells was consistent with the capacity we discovered for B cells to selectively activate and induce MAIT cell expansion. Given the highly pro-inflammatory nature of MAIT cells, we speculate that decreased peripheral activation of MAIT cells may represent a relevant aspect of the therapeutic mode-of-action of anti-CD20 therapy which has proven highly effective at limiting new MS relapses³⁴⁸.

MAIT cells express diverse chemokine receptors that effectively license them to migrate into multiple different tissues under inflammatory conditions^{480,513}. This enhanced migratory capacity suggested that they may become activated and relatively agnostic to the target organ or its unique antigens, and possibly mediate their effects principally through bystander mechanisms^{480,513}. However, it may well be that certain TCRs on MAIT cells recognize endogenous (self) antigens that can trigger a response to self, given recent findings for a broader MR1 ligand library that extended beyond the initially identified riboflavin and folate metabolites and included other organic molecules^{498,549,550}. Of interest in this regard are our observations that B cells could enhance MR1-restricted MAIT cell expansion, while suppressing the expansion of MR1-restricted non-MAIT cells. These findings extend a recent report that B cells can present antigen to MAIT cells in an MR1-restricted fashion⁵³⁸ with the demonstration of contrasting effects of the B cells on different MR1-restricted CD8⁺T cells. These observations support a model wherein B cells have the capacity to regulate CD8⁺T cell proliferation while discerning among CD8⁺ T cells even with similar antigenic specificity, presumably based on one or more other yet to be determined functional and/or phenotypic characteristic/s of the CD8⁺ T cells.

Consistent with prior reports, we also noted a reduced capacity of MAIT cell to undergo TCR-driven proliferation compared to non-MAIT cells^{505,584}. This may be explained by results of gene expression analysis of MAIT cells that found they expressed reduced levels of signaling molecules downstream of the TCR and were transcriptionally biased towards higher expression of effector molecules and lower expression of genes encoding for ribosomal proteins necessary for cell growth^{505,584}. We also found that B cells could provide soluble growth factors to MAIT cells that acted in conjunction with high TCR strength of stimulation to further promote cell expansion. The co-stimulatory signals that promote MAIT cell expansion remain poorly understood. Innate cytokines can drive CD8⁺ T cell proliferation in the absence of TCR signaling and can also serve to reduce the TCR threshold required for MAIT cell cycle entry^{491,584-586,589,590}. Studies in patients with primary immunodeficiencies highlighted the importance of the IL-23-STAT3 axis in maintaining peripheral MAIT cell number and IFN γ production^{521-523,525,591}. In a preliminary analysis, we found that B cells, particularly those pre-activated with CpG, selectively enhanced STAT3 phosphorylation in MAIT cells (data not shown). IL-23 expression in B cells has not been

reported, but like other cytokines expressed by these cells, the context of their interaction with other immune cells may be critical for its induction.

There have been inconsistent reports of MAIT cell frequencies in peripheral blood of adult MS patients (some identifying increased frequencies, with others reporting no differences or decreased frequencies compared to controls)^{420-422,561}. While the factors underlying these discrepancies are not clear, they have raised questions about whether MAIT cells play pro-inflammatory or anti-inflammatory roles in MS. Our results, based on assessment of B cell: MAIT cell interactions using a combination of *in vitro* co-culture experiments and examination of the effects of *in vivo* B cell depletion on MAIT cell biology, support a pro-inflammatory role for MAIT cells in the pathophysiology of MS disease activity. These findings are consistent with the known propensity of MAIT cells to produce pro-inflammatory and cytotoxic mediators^{480,529}, the documented presence of clonally expanded MAIT cells within the perivascular inflammatory lesions of MS brains⁴¹⁹⁻⁴²³ (where MR1 and innate cytokines are expressed)⁴²², and their sustained depletion in patients benefiting from durable disease quiescence after aggressive bone marrow transplantation in MS⁴¹⁹. It is noteworthy that we have recently observed increased frequency and pro-inflammatory cytokine (e.g. IFN γ and IL-17) responses of circulating MAIT cells in children developing MS soon after their initial presentation compared to children with monophasic inflammatory demyelinating disease and normal controls¹⁵⁰, which, taken together, further supports a pro-inflammatory role for MAIT cells in the disease.

MAIT cells are known to accumulate in mucosal tissues (such as liver, lung, and gut, where they strategically positioned to mediate early and efficient immune response against invading pathogens)^{480,513}. Why MAIT cells would then migrate to the CNS, is not clear. It is noteworthy that MAIT cells may interact with IgA⁺ plasma cells that express MR1⁵⁹². The significance of such interaction is unknown, though in the context of neuroinflammation, *Rojas et al.* recently demonstrated that gut lamina propria IgA⁺ plasma cells/plasmblasts could migrate to the central nervous system where they exerted IL-10-dependent suppressive functions that reduced local inflammation³⁹¹. Whether MAIT cells follow similar trafficking patterns as IgA⁺ plasma cells, including a gut-CNS axis would be of interest for future study.

Overall, our study points to a capacity for human B cells to differentially regulate effector functions of distinct CD8⁺ T cell subsets *in vitro* and *in vivo*. Particular interactions between B cells and MAIT CD8⁺ T cells may contribute to the development of new MS disease activity in untreated patients. In turn, these interactions may represent a relevant therapeutic target for the highly effective B cell depleting therapies currently in use, and potentially for new therapies selectively targeting MAIT cell responses.

Disclosures

The authors have no financial conflicts of interest

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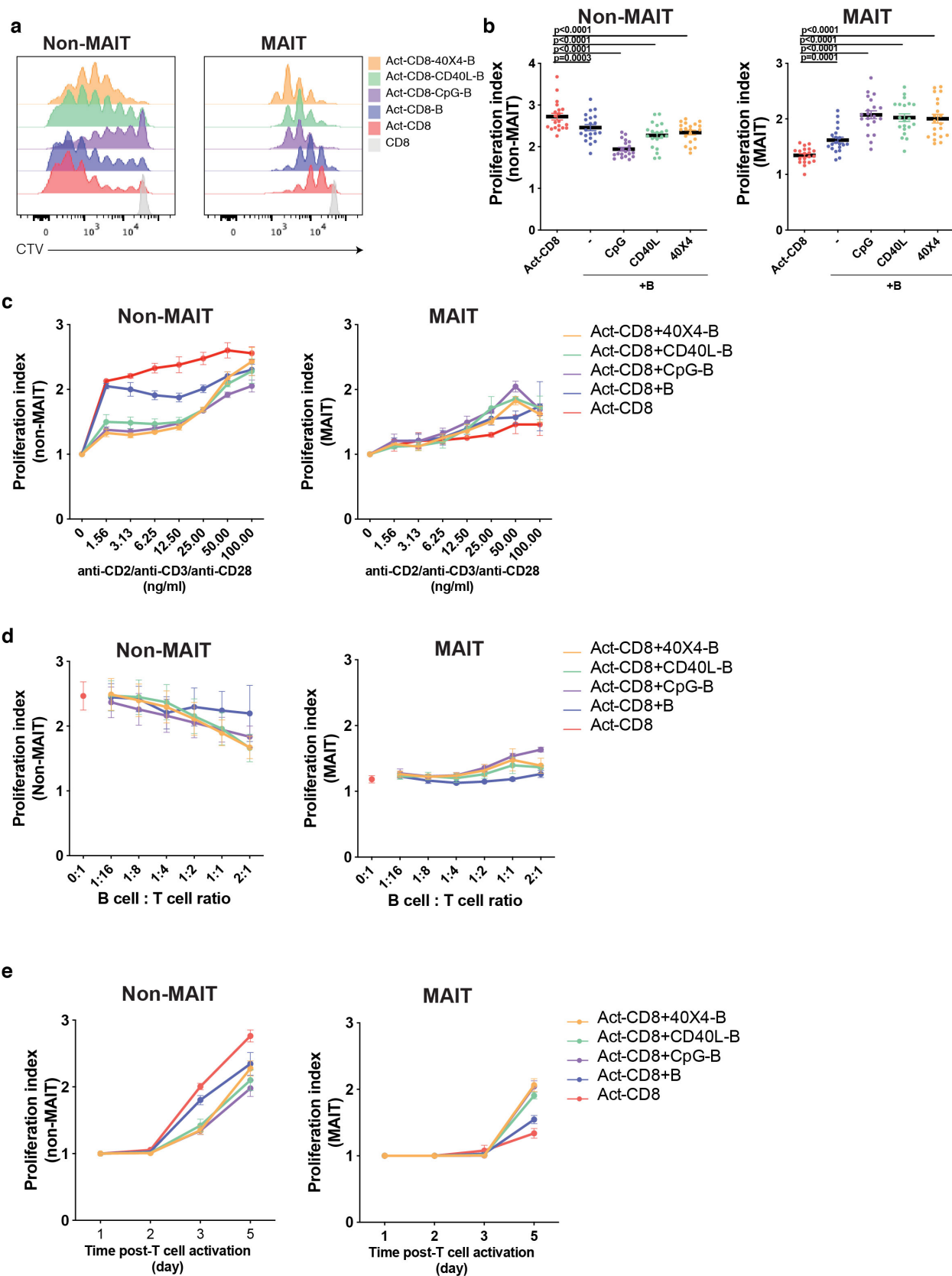


Figure 1. B cells reciprocally regulate non-MAIT and MAIT CD8⁺ T cell proliferation. MACS-sorted CD8⁺ T cells were activated with beads coated with anti-CD2, anti-CD3 and anti-CD28, and co-cultured with MACS-sorted autologous B cells (either unstimulated, or pre-activated with CpG, CD40L or CD40L + anti-IgM + IL-4) for up to 5 days before assessing T cell proliferation by flow cytometry. Non-MAIT were identified as CD161⁻ TCR-Va7.2^{+/-} and MAIT cells were identified as CD161^{hi} TCR-Va7.2⁺. (a) Representative experiment demonstrating that non-MAIT cell proliferation is diminished in the presence of B cells, while MAIT cell proliferation is enhanced. (b) Summary of n=19 independent experiments. B cell regulation of CD8⁺ T cell proliferation is dependent on (c) the strength of T cell stimulation (n=3); (d) the B cell to T cell ratio (n=4); and (e) the duration of T cell activation (n=5). All values are represented as mean $\pm$ SEM, and p-values were assessed by two-way ANOVA followed by Tukey's test.

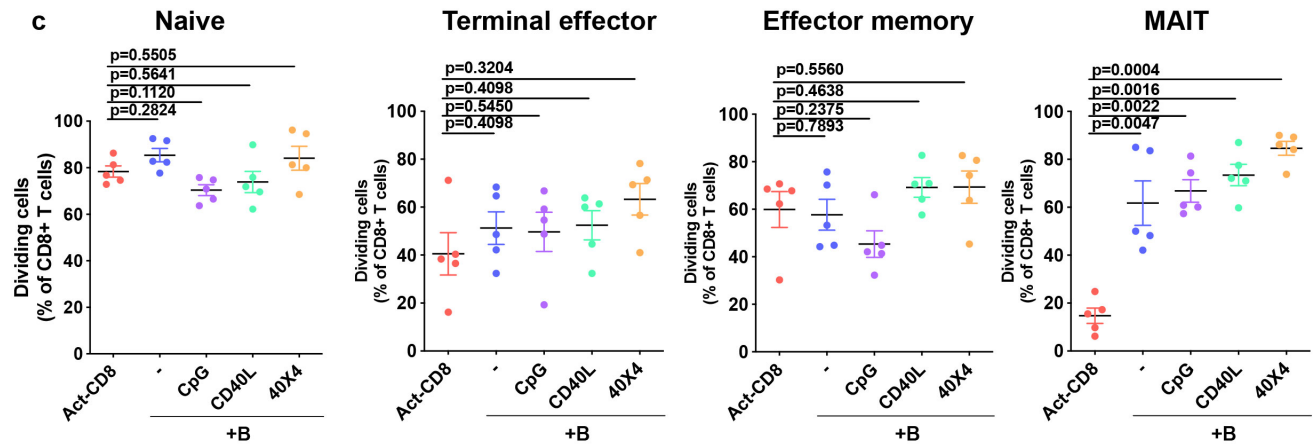
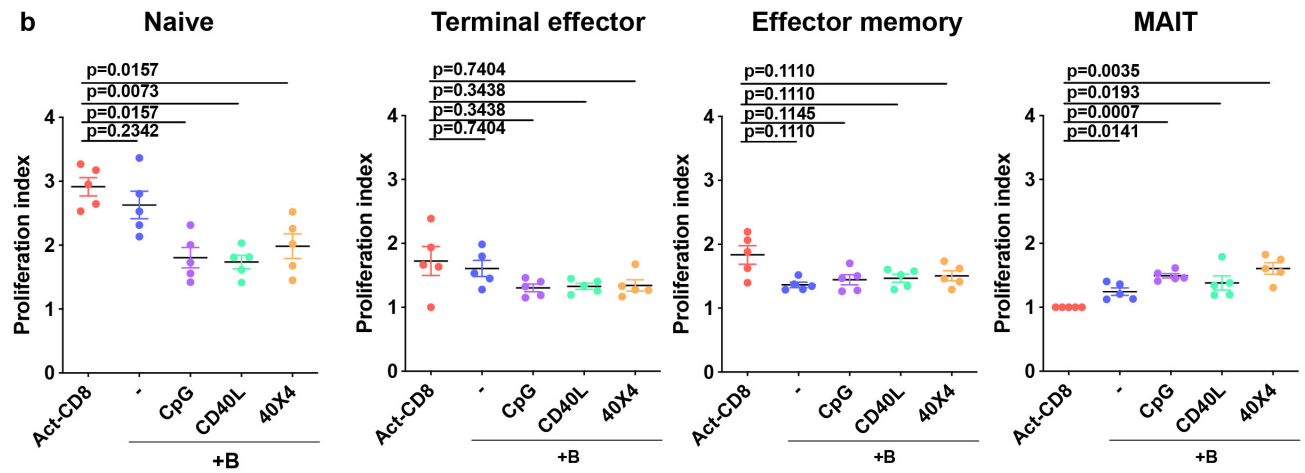
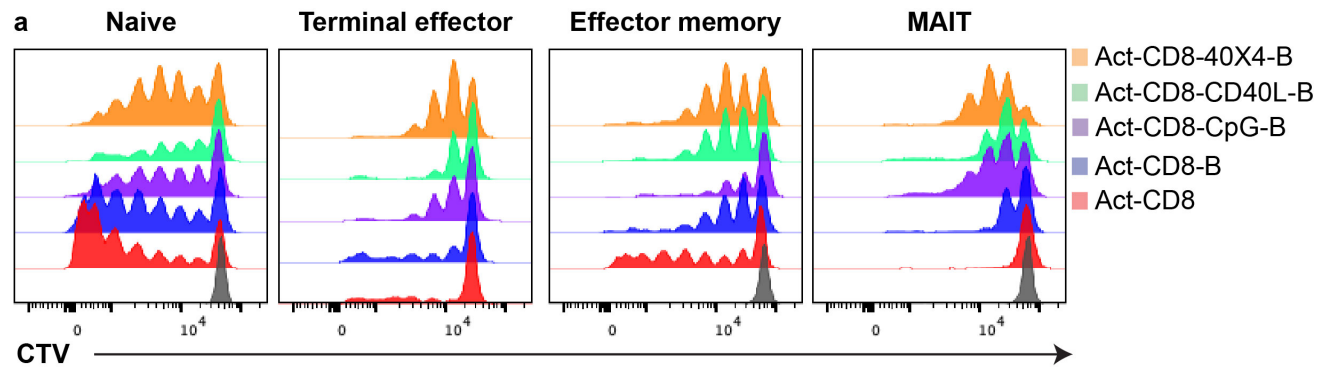


Figure 2. B cells reciprocally modulate the proliferation of FACS-sorted non-MAIT and MAIT cells. FACS-sorted CD8⁺ T cell subsets were activated with beads coated with anti-CD2, anti-CD3 and anti-CD28, and co-cultured with MACS-sorted autologous B cells (either unstimulated, or pre-activated with CpG, CD40L or CD40L + anti-IgM + IL-4) for up to 5 days before assessing T cell proliferation by flow cytometry. (a) Representative experiment demonstrating that naive cell proliferation is diminished in the presence of B cells, while MAIT cell proliferation is enhanced. (b) Summary of n=5 independent experiments. All values are represented as mean $\pm$ SEM, and p-values were assessed by one-way ANOVA followed by Dunn's test.

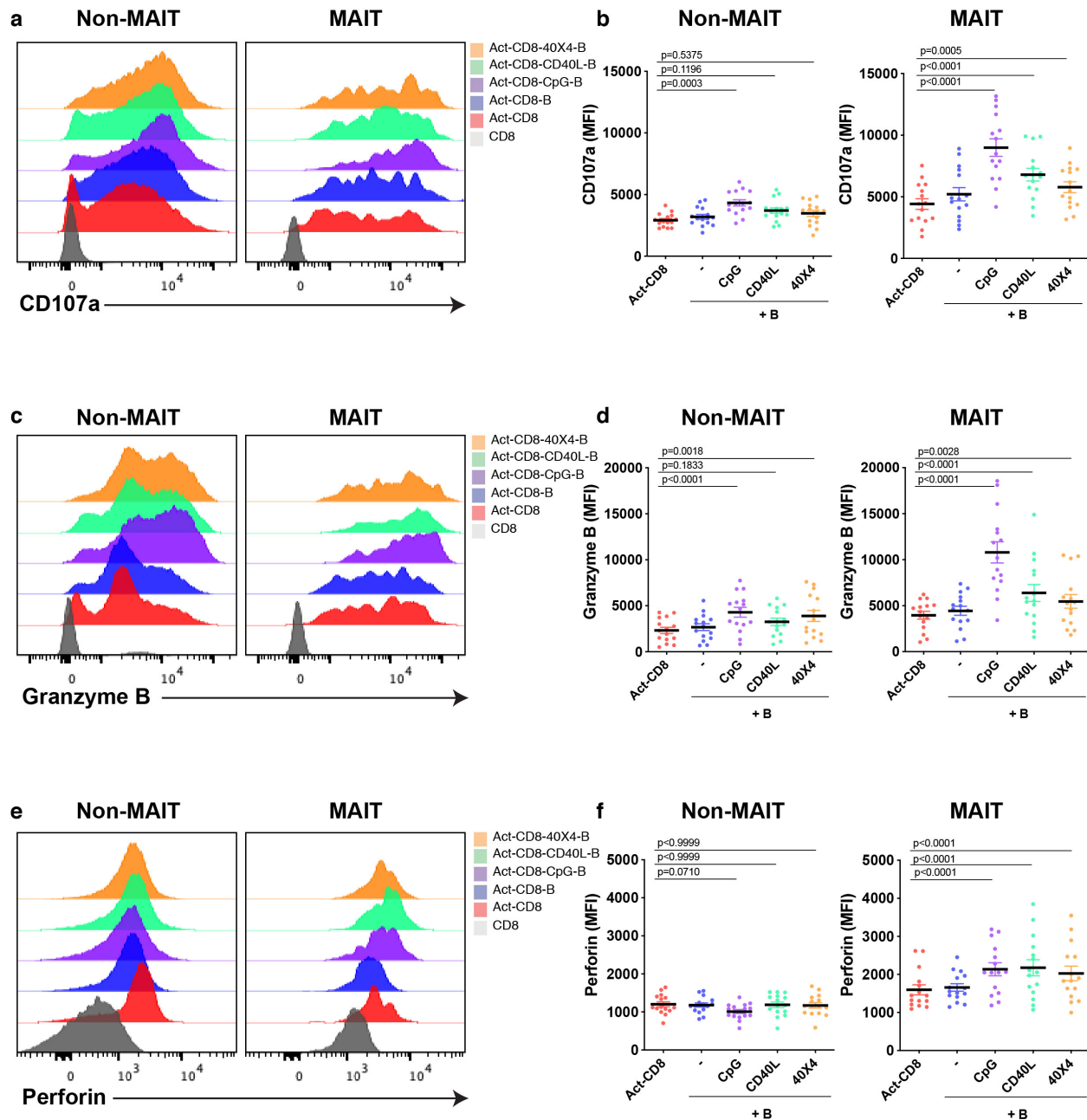


Figure 3. B cells enhance CD8⁺ T cell subset cytotoxic potential. MACS-sorted CD8⁺ T cells were activated with beads coated with anti-CD2, anti-CD3 and anti-CD28 and co-cultured with MACS-sorted autologous B cells (unstimulated or pre-activated with CpG, CD40L or CD40L + anti-IgM + IL-4) for 3 days before assessing the expression of CD107a (**a**), granzyme B (**b**) and perforin (**c**) in both non-MAIT and MAIT cell. All values are represented as mean $\pm$ SEM, and p-values were assessed by two-way ANOVA with Tukey's test.

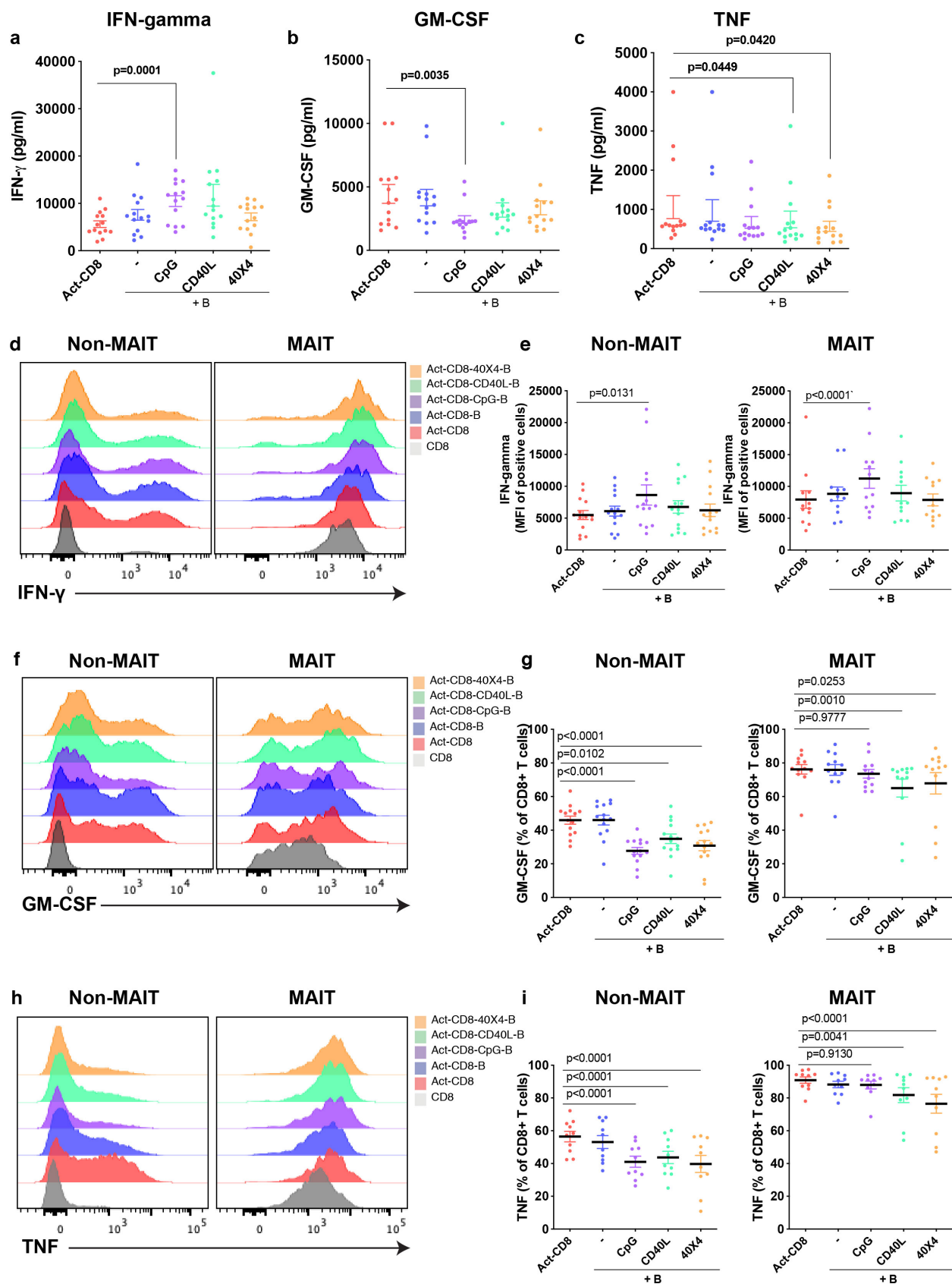


Figure 4. Pre-activated B cells shape CD8⁺ T-cell subset cytokine production.

MACS-sorted CD8⁺ T cells activated with beads coated with anti-CD2, anti-CD3 and anti-CD28 were co-cultured with MACS-sorted autologous B cells (unstimulated or pre-activated with CpG, CD40L or CD40L + anti-IgM + IL-4) for up to 5 days before assessing levels of secreted cytokines by ELISA and intracellular T-cell cytokine expression by flow cytometry. **(a-c)** Levels of secreted IFN γ were increased while levels of GM-CSF and TNF were decreased in co-culture supernatants of activated CD8⁺ T cells with pre-activated B cells (n=14). IFN γ expression was increased in both non-MAIT and MAIT cells co-cultured with CpG-B cells as shown in **(d)** and summarized in **(e, n=12)**. The frequencies of GM-CSF⁺ non-MAIT and MAIT cells were reduced in co-culture with pre-activated B cells as shown in **(f)** and summarized in **(g, n=12)**. The frequencies of TNF⁺ non-MAIT and MAIT cells were reduced in co-culture with pre-activated B cells as shown in a representative experiment **(h)** and summarized in **(i, n=11)**. All values are represented as mean $\pm$ SEM, and p-values were assessed two-way ANOVA with Tukey's test.

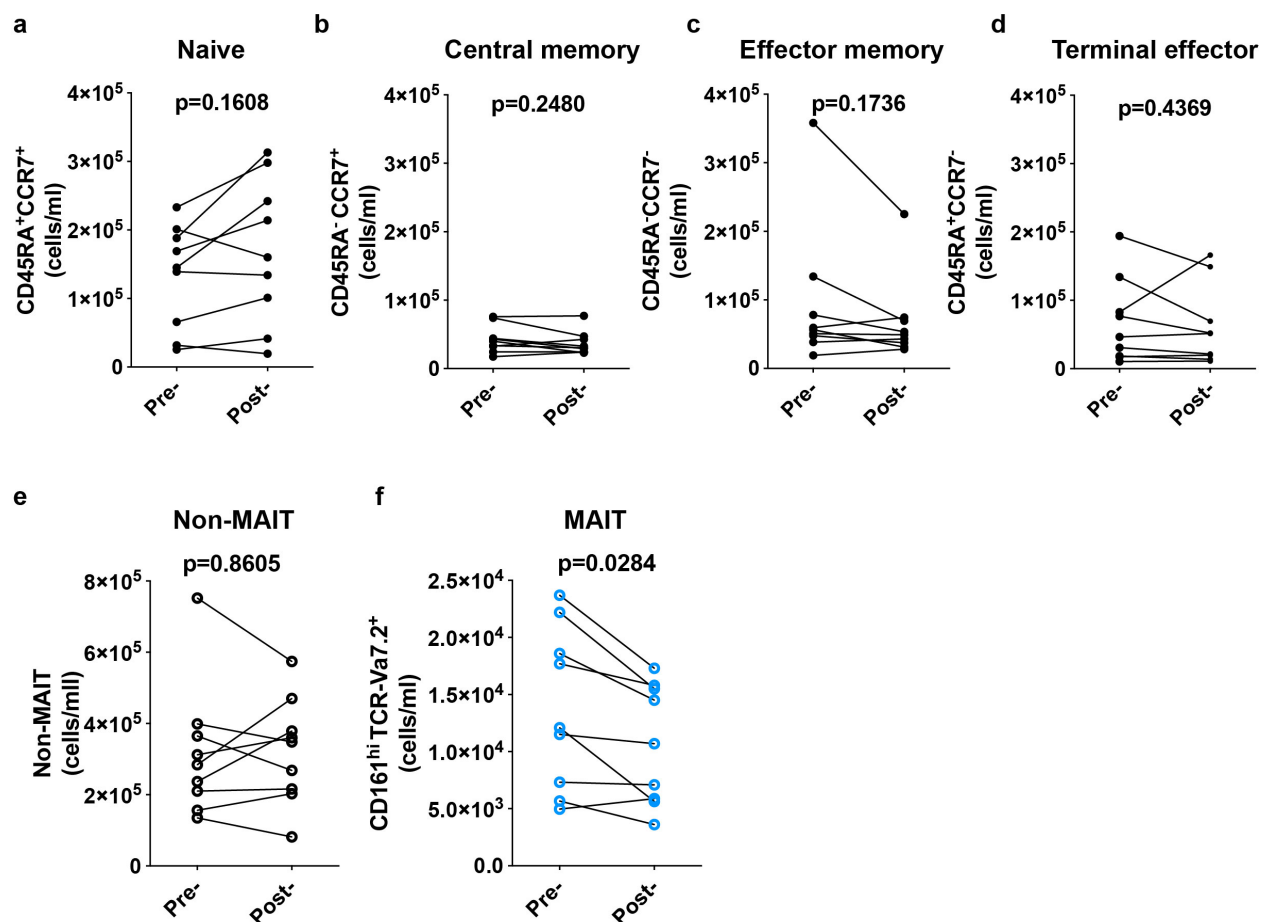


Figure 5. Circulating MAIT cells are reduced post-B cell depletion in MS patients.

CD8⁺ T cell subsets were quantified based on surface phenotype by flow cytometry within PBMC obtained prior to (Pre) and following (Post) B cell depletion. The gating strategy is shown in Figure S5. Absolute counts per volume of (a) CCR7⁺CD45RA⁺ (naïve), (b) CCR7⁺CD45RA⁻ (central memory), (c) CCR7⁻CD45RA⁻ (effector memory) and (d) CCR7⁻CD45RA⁺ (effector) CD8⁺ T cell subsets were quantified (n=9 donors). CD8⁺ Non-MAIT and MAIT cells were identified based on the expression of CD161 and TCR-Vα7.2, such that CD161^{-int} TCR-Vα7.2^{+/-} were considered non-MAIT cell and CD161^{hi} TCR-Vα7.2⁺ were considered MAIT cells. Cell counts of non-MAIT (e) and MAIT (f) were quantified (n=9 donors). P-values were assessed by two-tailed ratio paired t-test.

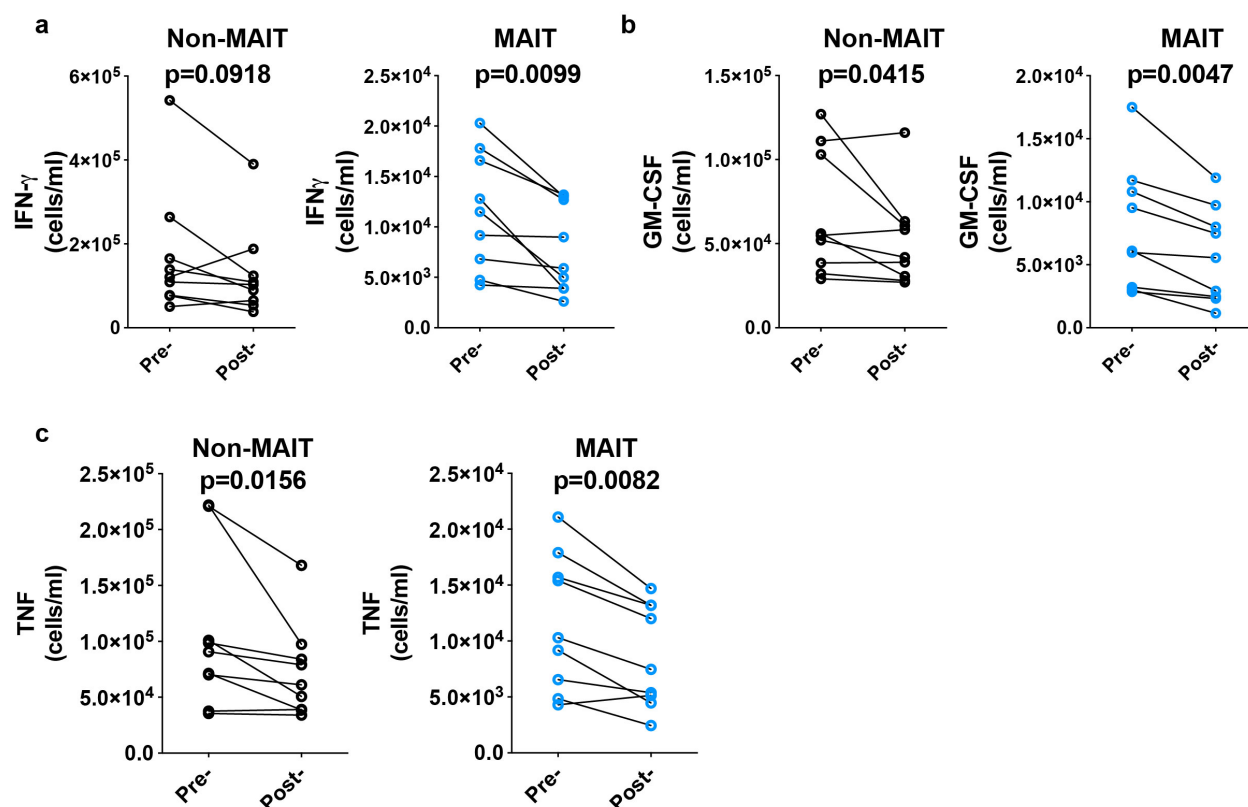


Figure 6. CD8⁺ T cell pro-inflammatory cytokine production is diminished following B cell depletion therapy. Cryopreserved PBMC obtained from MS patients prior to (pre) and following B cell depletion (post) were short-term stimulated with PMA and ionomycin (cytokine production) for 5 hours to quantify non-MAIT (CD161⁺ TCR-Va7.2^{+/-}) and MAIT (CD161^{hi} TCR-Va7.2⁺) effector functions (a). P-values were assessed two-tailed ratio paired t-test.

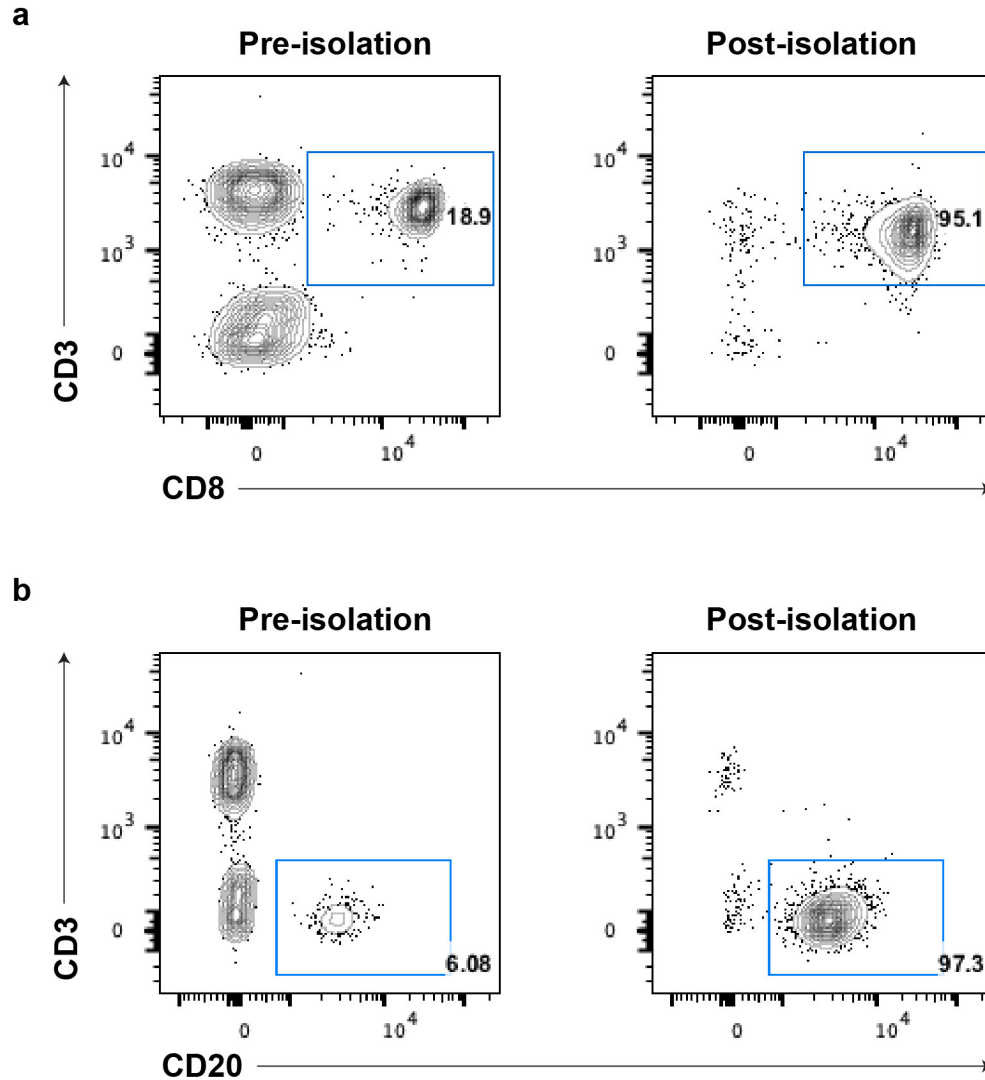


Figure S1. Purity confirmation of MACS-sorted CD8⁺ T cells and B cells.

CD8⁺ T cells and B cells were routinely isolated from PBMC using magnetic microbeads (Miltenyi Biotec), and purity assessment was carried out by flow cytometry. Representative FACS staining of **(a)** CD8⁺ T cells and **(b)** B cells pre- and post-isolation. Typical purities were >95%.

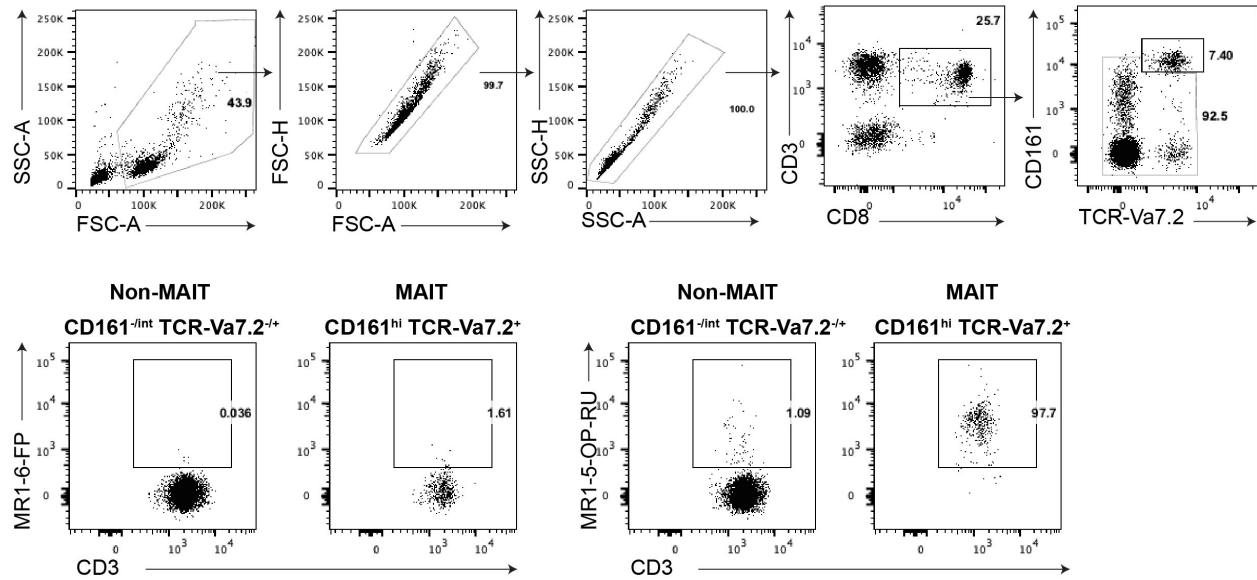


Figure S2. Human mucosal associated invariant T (MAIT) cells recognize vitamin B metabolites presented on MR1 and can be distinguished by the expression of CD161 and TCR-V α 7.2. Freshly isolated PBMC were labelled with MR1-5-OP-RU or MR1-6-Ac-FP followed by cell surface staining for CD3, CD8, CD161 and TCR-V α 7.2. Within the CD8⁺ T cell population, two major subsets were identified based on CD161 and TCR-V α 7.2 expression namely CD161^{-int} TCR-V α 7.2^{-/+} and CD161^{hi} TCR-V α 7.2⁺. While very few CD8⁺ T cells bound to MR1-6-Ac-FP, CD161^{hi} TCR-V α 7.2⁺ bound MR1-5-OP-RU with high affinity, thus distinguishing MAIT cells from other CD8⁺ T cell subsets. Shown is a representative staining from n=3 independent experiments.

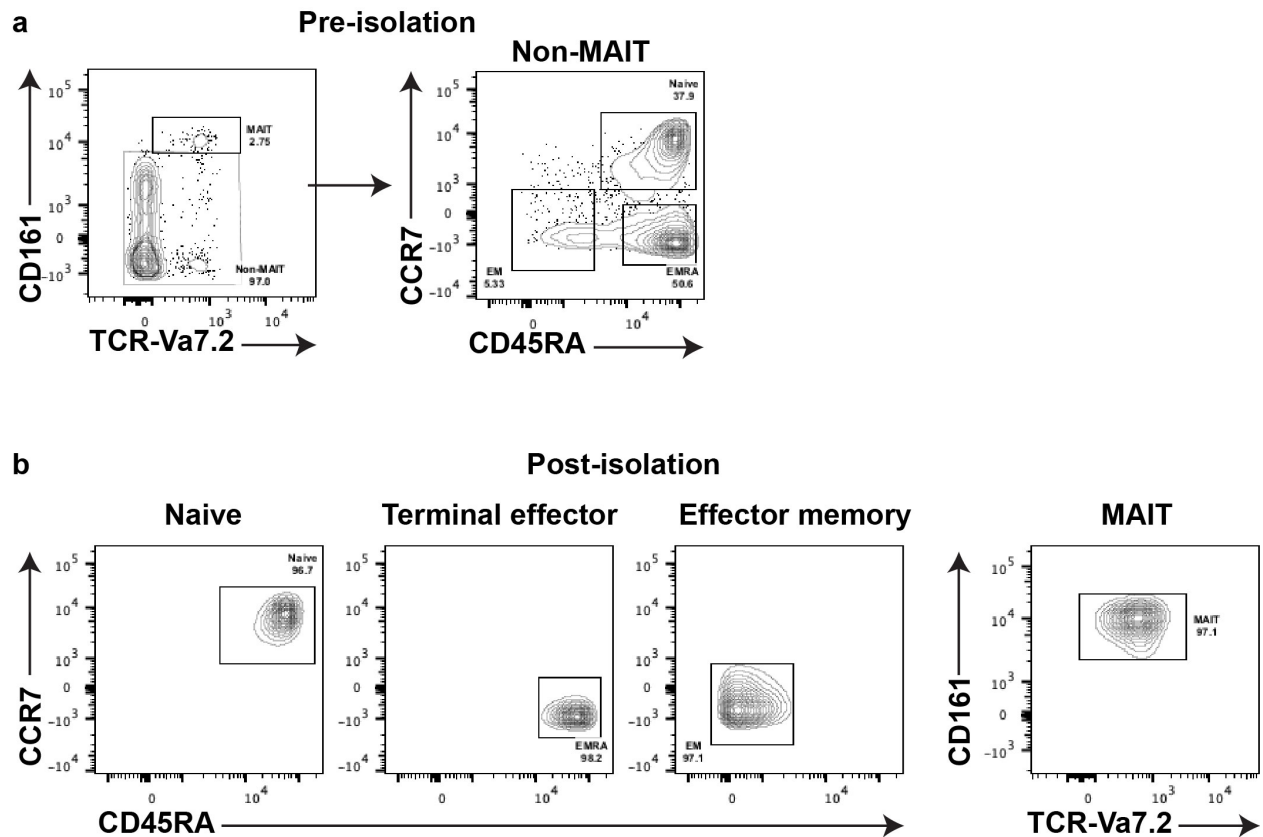


Figure S3. Purity confirmation of FACS-isolated CD8⁺ T cell subsets. MACS-sorted CD8⁺ T cells were labeled with a cocktail of antibodies that included anti-CD3, anti-CD8, anti-CCR7, anti-CD45RA, anti-CD161 and anti-TCR-V α 7.2 prior to FACS isolation. **(a)** Representative gating strategy is shown, in which CD161^{hi} TCR-V α 7.2⁺ (MAIT) and CD161^{int} TCR-V α 7.2⁺ (non-MAIT) were first distinguished, and then non-MAIT cells were separated into additional three populations, namely CCR7⁺CD45RA⁺ (naïve), CCR7⁺CD45RA⁺ (terminal effector) and CCR7⁺CD45RA⁺ (effector memory). **(b)** Representative post-isolation confirmation purity is shown for all four sorted CD8⁺ T cell populations, with typical purities >95%.

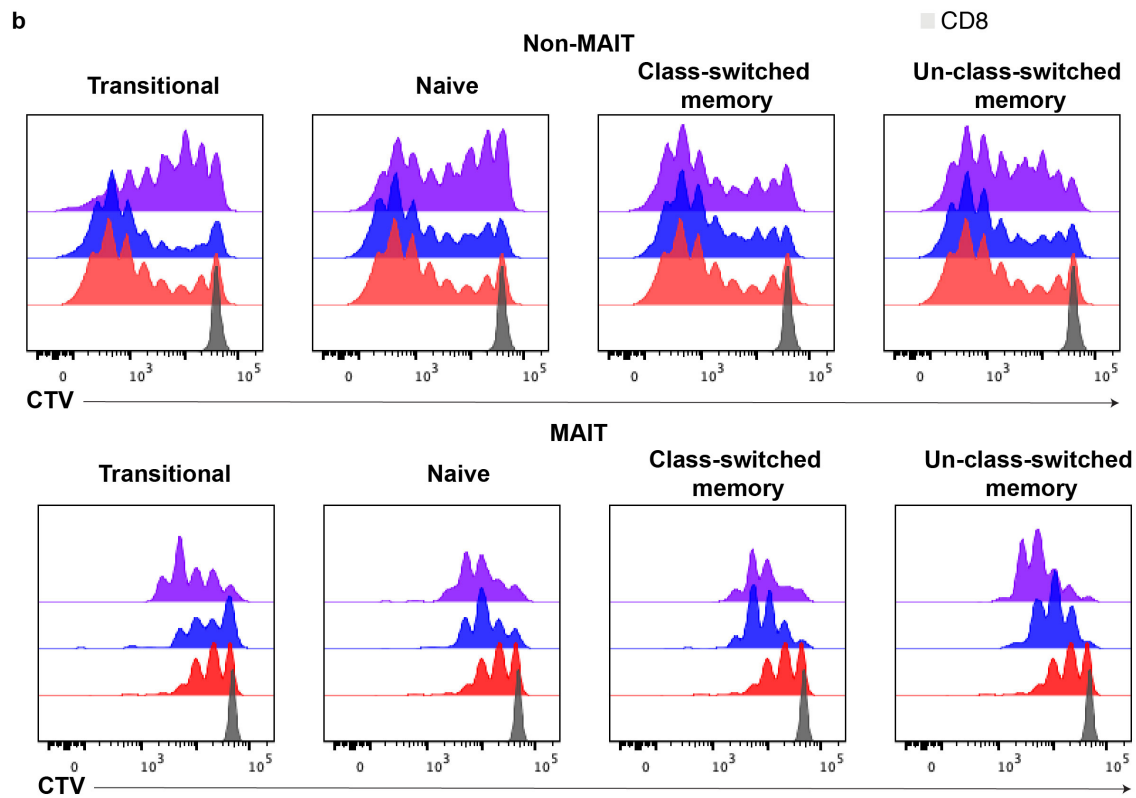
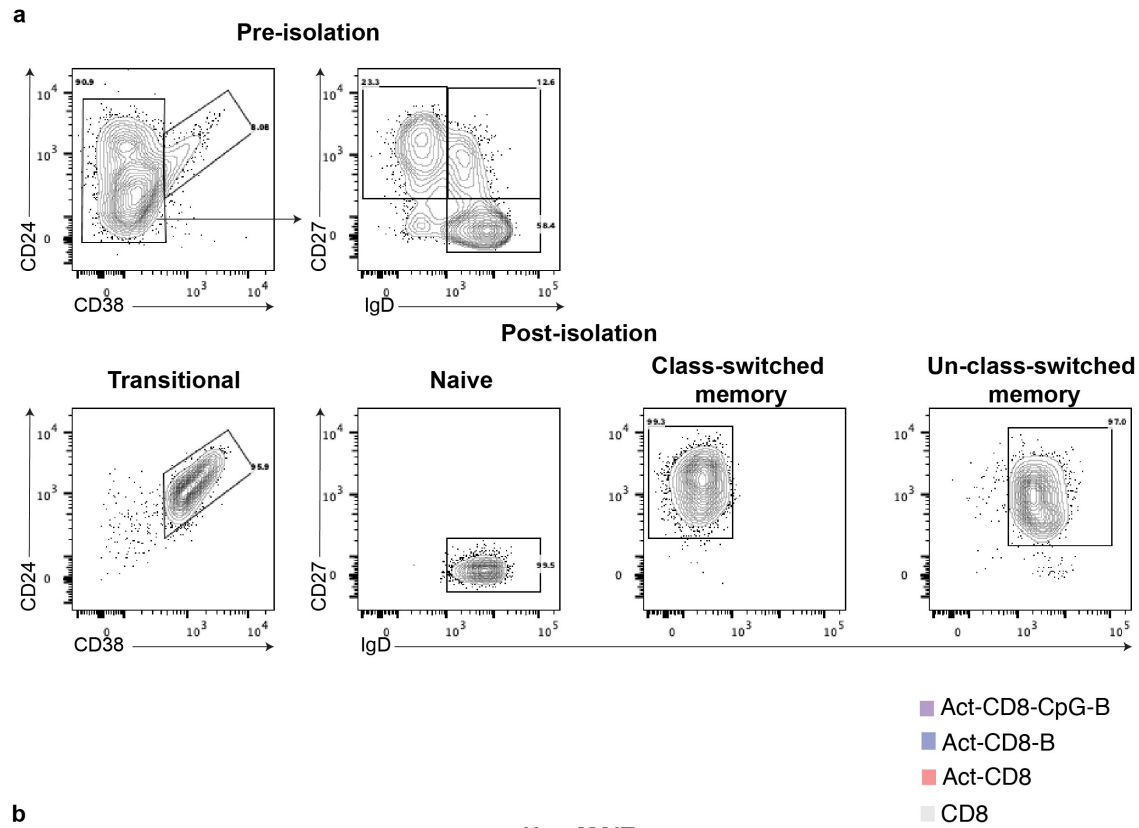
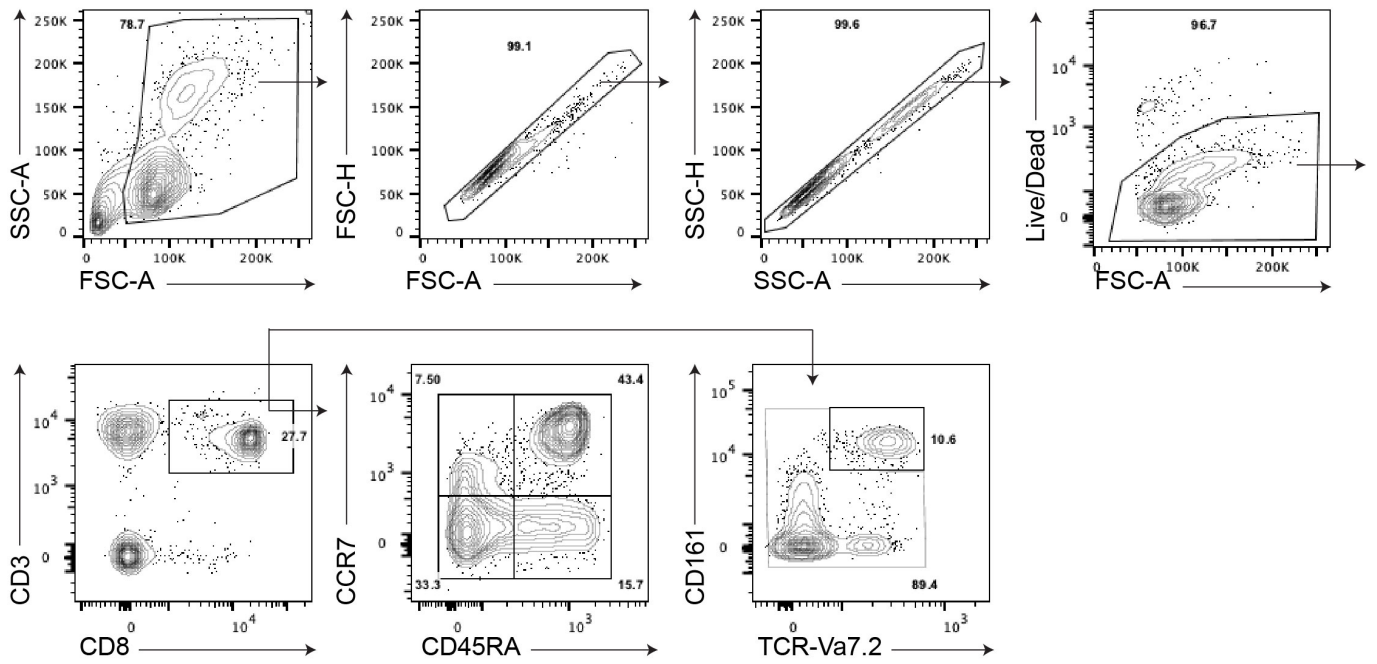
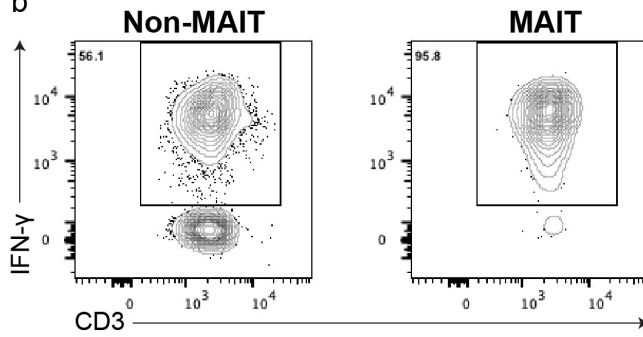


Figure S4. Distinct capacities for B cell subsets to regulate CD8⁺ T cell proliferation. MACS-sorted B cells were labeled with a cocktail of antibodies that included anti-CD20, anti-CD24, anti-CD38, anti-CD27 and anti-IgD prior to FACS isolation. **(a)** Top: Representative gating strategy is shown, in which CD24⁺CD38^{hi} (transitional) and CD24^{-/+}CD38⁻ (mature) were first distinguished, and then mature B cells were sorted into three populations that included CD27⁻IgD⁺ (naïve), CD27⁺IgD⁺ (un-class switched memory) and CD27⁺IgD⁻ (class-switched memory). Bottom: Post-isolation purity confirmation is shown, with typical purities >95%. **(b)** MACS-sorted CD8⁺ T cells activated with anti-CD2, CD3 and CD28 were co-cultured with autologous FACS-sorted B cell subsets (naïve, transitional, class-switched and un-class switched memory B cells) that were either unstimulated or pre-activated with CpG, for 5 days before measuring T cell proliferation by flow cytometry. Representative experiment demonstrates that naïve and transitional B cells acquire suppressive capacities towards non-MAIT cells, and all B cells provide helper functions to MAIT cells (representative of four independent experiments).

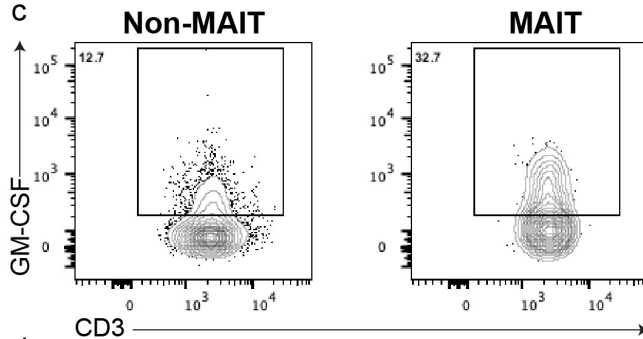
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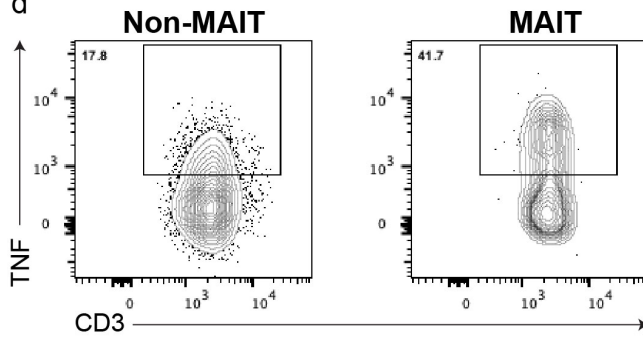
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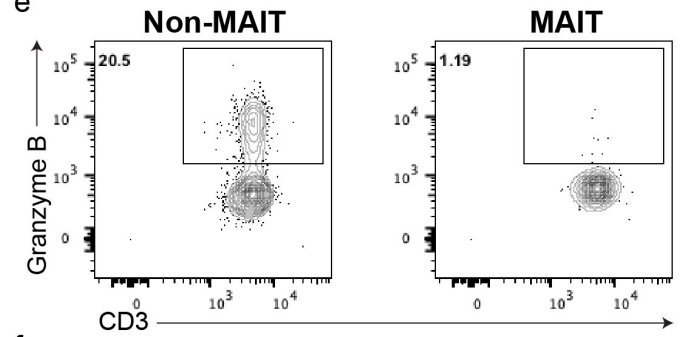
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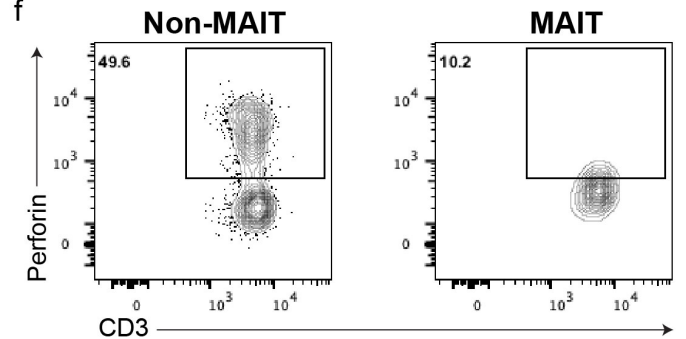


Figure S5. Flow cytometry gating strategy used to distinguish various CD8⁺ T cell subsets in PBMC. (a) PBMC were first gated based on FSC and SSC followed by exclusion of doublets and dead cells. CD8⁺ T cells were gated as CD3⁺CD8⁺. Within CD8⁺ T cells, CCR7⁺CD45RA⁺ (naïve), CCR7⁺CD45RA⁻ (central memory), CCR7⁻CD45RA⁻ (effector memory) and CCR7⁻CD45RA⁺ (terminal effector) were identified. Alternatively, CD161^{-int} TCR-Va7.2^{-/+} (non-MAIT) and CD161^{hi} TCR-Va7.2⁺ (MAIT) were identified. PBMC were stimulated for five hours with PMA, ionomycin in the presence of monensin A to examine intracellular expression of IFN- γ (b), GM-CSF (c) and TNF (d) in non-MAIT and MAIT cells gated within PBMC as shown above. Expression of granzyme B (e) and perforin (f) were assessed in resting non-MAIT and MAIT cells gated within PBMC as shown above.

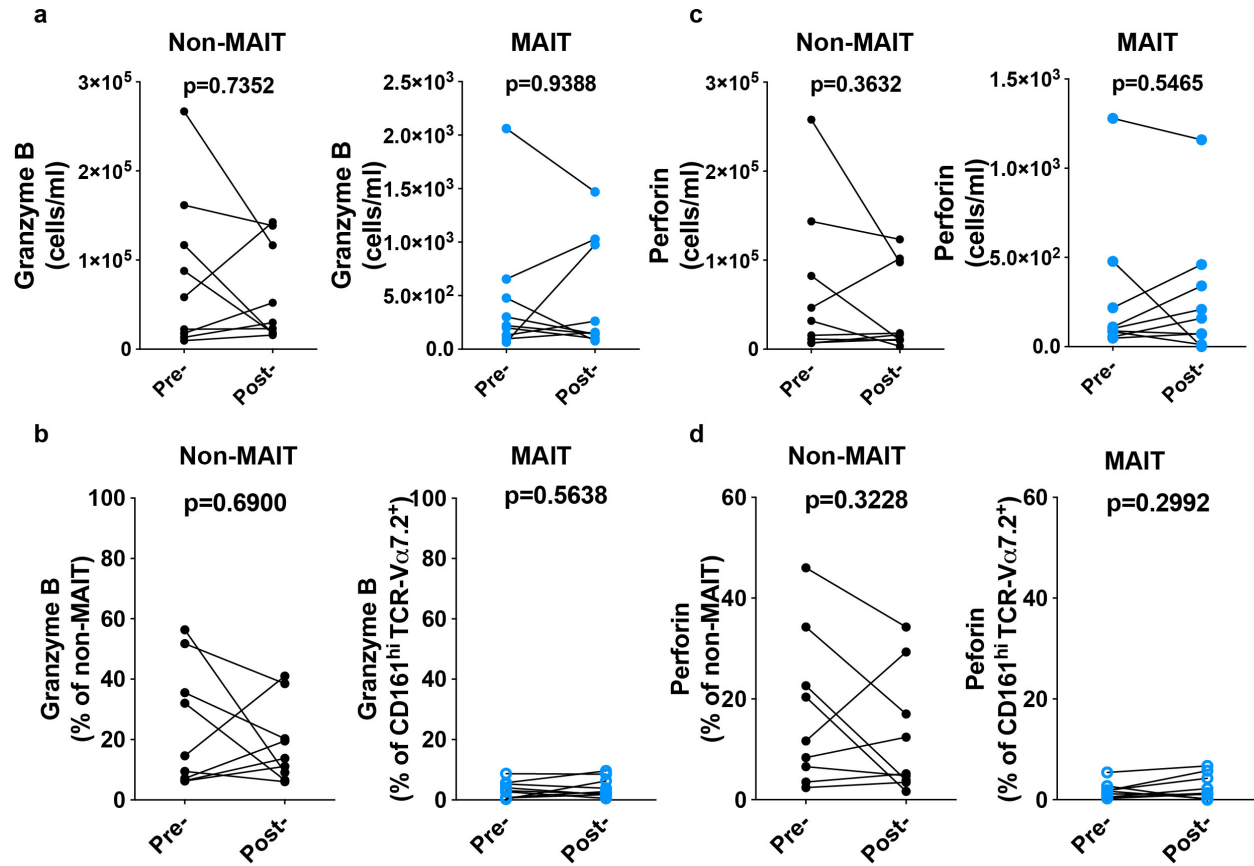


Figure S6. CD8⁺ T cell cytotoxic profile is not impacted after B cell depletion. CD8⁺ T cell populations were quantified within PBMC obtained prior to (Pre) and after (Post) B cell depletion in MS patients. Absolute cell counts per volume of (a) granzyme B as well as (b) perforin expressing non-MAIT (CD161^{-int} TCR-V α 7.2^{+/+}) and MAIT (CD161^{hi} TCR-V α 7.2⁺) cells were quantified in n=9 donors. P-values were assessed two-tailed ratio paired t-test.

Supplemental Table 1. Patient characteristics

Characteristics	N= 9
Age (median, range)	42 (22-66)
Female (% , number)	45 (4/9)
Duration of MS (mean, range)	2.0 (0-9)
Previously treated (% , number)	0 (0/9)
EDSS score at baseline (median, range)	2.5 (1-4.5)

Supplemental Table 2. Immune phenotyping panels.

Laser	Blue (488nm)		Red (460nm)			Violet (405nm)					Yellow-Green (561nm)			UV (355nm)	
Filter	530/30	695/40	660/20	730/45	780/60	450/40	525/50	660/20	710/50	780/60	575/26	610/20	780/60	379/28	820/860
FC	FITC	PerCP-Cy5.5	APC	APC-R700	APC-H7	BV421	Aqua	BV650	BV711	BV786	PE	PE-CF594	PE-Cy7 (PE-Vio770)	BUV395	BUV805
Panel 1	CD45RA	CD57	CCR7	CD8	CD20	CD28	L/D	CD27	CD3	HLA-DR	Ki-67	KLRG1	CD95	CD38	CD4
Panel 2	<u>GzK</u>	TCR-Va7.2	CCR7	CD8	CD20	Perforin	L/D	CD56	CD3	CD45RA	<u>GzA</u>	<u>GzB</u>	CD161	NKG2C	CD4
Panel 3	TCR-Va7.2		CCR6	CD8	TNF	CCR2	L/D	IL-17	CD3	CD45RA	GM-CSF	CCR5	CD161	IFN-g	CD4

Supplemental Table 3. Staining reagents used in immunophenotyping

Antibody	Fluorochrome conjugation	Clone	Source
CD3	BV711	UCHT1	BD Biosciences
CD4	BUV805	SK3	BD Biosciences
CD8	APC-R700	RPA-T8	BD Biosciences
CD20	APC-H7	2H7	BD Biosciences
CD27	BV650	M-T271	BD Biosciences
CD28	BV421	CD28.2	BD Biosciences
CD38	BUV395	HB7	BD Biosciences
CD45RA	FITC	HI100	BD Biosciences
CD45RA	BV786	HI100	BD Biosciences
CD56	BV650	NCAM16.2	BD Biosciences
CD57	PerCP-Cy5.5	HNK-1	Biolegend
CD95	PE-Cy7	DX2	BD Biosciences
CD161	PE-Vio700	REA631	Miltenyi Biotec
CD197	Alexa-Fluor 647	3D12	BD Biosciences
GM-CSF	PE	BVD2-21C11	BD Biosciences
Granzyme A	PE	CB9	Biolegend
Granzyme B	PE-CF594	GB11	BD Biosciences
Granzyme K	FITC	GM26E7	Biolegend
HL-A-DR	BV786	G46-6	BD Biosciences
IFN-gamma	BUV395	B27	BD Biosciences
IL-17	BV650	N49-653	BD Biosciences
Ki-67	PE	Ki-67	Biolegend
KLRG1	PE-Vio615	REA261	Miltenyi Biotec
NKG2C	BUV395	134591	BD Biosciences
Perforin	BV421	$\delta G9$	BD Biosciences
TCR-Va7.2	PerCP-Cy5.5	3C10	Biolegend
TCR-Va7.2	FITC	3C10	Biolegend

TNF	APC/Cy7	MAb11	Biolegend
LIVE/DEAD Fixable Aqua Dead Cell Stain	N/A	N/A	Invitrogen

Supplementary Table 4. Cell subset counts pre- and on-treatment with anti-CD20

Cell subset	Pre (SEM)	On-treatment (SEM)	P-value
Total CD3⁺ T cells	1.252e+006 (170109)	1.423e+006 (202085)	0.3297
CD8⁺ T cells	331222 (62566)	333278 (49585)	0.9307
Naïve CD8⁺ T cells	133144 (25112)	169244 (35200)	0.1608
Central memory CD8⁺ T cells	42856 (6707)	36833 (5763)	0.2480
Effector memory CD8⁺ T cells	93611 (34722)	67911 (20333)	0.1736
Terminal effector CD8⁺ T cells	67944 (20644)	61600 (19358)	0.4369
Non-MAIT cells	316667 (61943)	322211 (49545)	0.8605
MAIT cells	13751 (2360)	10670 (1744)	0.0284
IFN-γ⁺ non-MAIT cells	171711 (50784)	128956 (35796)	0.0918
IFN-γ⁺ MAIT cells	11552 (1939)	7689 (1445)	0.0099
GM-CSF⁺ non-MAIT cells	67089 (12237)	51644 (9329)	0.0415
GM-CSF⁺ MAIT cells	7857 (1649)	5730 (1255)	0.0047
TNF⁺ non-MAIT cells	105378 (23300)	72456 (14074)	0.0472
TNF⁺ MAIT cells	11696 (2018)	8666 (1535)	0.0472
Granzyme B⁺ non-MAIT cells	83892 (28849)	61646 (18253)	0.7352
Granzyme B⁺ MAIT cells	468 (209)	484 (175)	0.9388
Perforin⁺ non-MAIT cells	67080 (28162)	43638 (16233)	0.3632
Perforin⁺ MAIT cells	274 (133)	276 (121)	0.5465

Mean and standard error of the mean for cell counts (cell/ml) of T cell subsets pre- and on-treatment are shown for n=9 donors. Ratio-paired t-test was used for statistical analysis.

Supplementary Table 5. Cell subset frequencies pre- and on-treatment with anti-CD20

Cell subset	Pre (SEM)	On-treatment (SEM)	P-value
Total CD3⁺ T cells	63.07 (0.9922)	72.54 (2.982)	0.0083
CD8⁺ T cells	16.89 (1.863)	17.88 (2.476)	0.7890
Naïve CD8⁺ T cells	41.52 (7.509)	48.33 (7.803)	0.0076
Central memory CD8⁺ T cells	14.47 (2.203)	13.08 (2.335)	0.1183
Effector memory CD8⁺ T cells	25.68 (4.398)	21.65 (4.055)	0.0105
Terminal effector CD8⁺ T cells	18.33 (3.697)	16.88 (3.578)	0.2266
Non-MAIT cells	95.04 (0.8097)	95.98 (0.7238)	0.0189
MAIT cells	4.78 (0.8433)	3.86 (0.7173)	0.0472
IFN-γ⁺ non-MAIT cells	51.76 (6.40)	39.64 (5.60)	0.0918
IFN-γ⁺ MAIT cells	85.00 (2.80)	79.26 (2.30)	0.1104
GM-CSF⁺ non-MAIT cells	23.10 (3.36)	18.29 (3.04)	0.0235
GM-CSF⁺ MAIT cells	55.16 (2.93)	49.52 (4.29)	0.0954
TNF⁺ non-MAIT cells	35.87 (5.92)	26.02 (4.62)	0.0472
TNF⁺ MAIT cells	85.38 (1.57)	79.59 (2.36)	0.0984
Granzyme B⁺ non-MAIT cells	24.40 (6.69)	18.44 (4.37)	0.6900
Granzyme B⁺ MAIT cells	3.47 (0.93)	4.12 (1.08)	0.5638
Perforin⁺ non-MAIT cells	17.33 (4.98)	12.45 (4.02)	0.3228
Perforin⁺ MAIT cells	1.77 (0.53)	2.51 (0.83)	0.2992

Mean and standard error of the mean for cell counts (cell/ml) of T cell subsets pre- and on-treatment are shown for n=9 donors. Ratio-paired t-test was used for statistical analysis

Chapter 4: Discussion, conclusion and future directions

4.1 General discussion

In this thesis, I set out to study human B-cell functions of potential relevance to the common CNS inflammatory disease multiple sclerosis (MS). I focused on methods that would facilitate the study of functionally distinct (and particularly cytokine-defined) B cell subpopulations and on studies of antibody-independent functions of B cells (particularly B cell interactions with CD8⁺ T cells). Following Chapter 1 (Introduction into MS pathophysiology), in Chapter 2, I optimized an approach for the isolation of viable human cytokine-secreting B cells that avoids the need for intracellular cytokine staining (which requires killing the cells), making it an exciting tool for investigating viable cytokine-secreting B cells in a range of applications. In Chapter 3, I showed that B cells can exert two opposing functions in their interactions with distinct CD8⁺ T cell subsets, including interactions with MAIT cells, which may be relevant to MS pathophysiology and to the therapeutic mode of action of B cell depleting therapy in MS.

4.2 Human cytokine-defined B cells – novel therapeutic targets in MS?

B cell cytokine production is undoubtedly involved in regulating adaptive and innate immune responses in host response to infection and inflammatory/chronic diseases^{271,343}. B cells can secrete pro- and anti-inflammatory cytokines, and certain B cell populations possess a higher propensity to produce particular cytokines, such that human naïve and immature B cells can secrete higher levels of IL-10 than memory B cells^{271,281,283,377}. Moreover, we and others have documented an imbalance between the production of pro- and anti-inflammatory cytokines by human B cells in MS patients, typified by an increased frequency of GM-CSF⁺ B cells concomitant with a decreased frequency of IL-10⁺ B cells^{271,281,282}. Despite the relevance of cytokine-producing B cells to human diseases, there remain gaps in our understanding of their development and functions, in part due to a lack of unique cell surface markers, alone or in combination, which selectively encompass these cells. Our work presented in chapter 2 establishes a methodology that will serve as a foundation for further interrogating cytokine-secreting B cell subpopulations. This optimized approach for the isolation of viable and highly purified cytokine-defined human B cells will enable subsequent analyses such as next-generation sequencing and functional assays, which rely on intact, viable cells. We expect these studies will lead to the identification of transcriptional networks (including master transcriptional factors) and metabolic pathways that contribute to the regulation of GM-CSF or IL-10 expression in B cells. These future studies focusing on

interrogating cytokine-defined B cells should provide a platform for the development of more selective, and even personalized, therapeutics for patients with MS and beyond.

Even though anti-CD20 antibody therapy has proven highly efficacious in reducing new disease activity in MS, the long-term safety of such broad B cell depletion is not known^{273,274}. Anti-CD20 rather non-selectively depletes both pathogenic and regulatory B cell sub-populations as well as other subsets required for host immunity against pathogens^{271,278,279,281,283}. It is therefore conceptually more appealing to generate therapies that more selectively target pathogenic B cell sub-populations, such as those producing GM-CSF, while sparing other B cell subsets. One hopes that our new approach for isolating cytokine-secreting human B cells will facilitate discovery and development of such selective therapies.

For example, future work could examine whether distinct cytokine-producing B cell subsets utilize distinct metabolic pathways. Recent work has highlighted the differing metabolic requirements for effector and regulatory T cells⁵⁹³ which has offered a therapeutic opportunity to selectively manipulate the balance between these subsets in anti-tumor immunity. The same could potentially be done with B cells in the context of MS and autoimmune diseases. In fact, dimethyl fumarate and dihydroorotate dehydrogenase inhibitor (teriflunomide), both approved therapies for MS, have recently been found to modulate T cell metabolic pathways in a way that reduces pro-inflammatory responses and prunes high-affinity T cells in MS patients^{594,595}. It remains unknown if the metabolic demands of distinct B cell cytokine-producing subsets are similar to T cell subsets. If so, it might provide greater insights into the biology of cytokine-defined B cells and guide novel therapeutic targeting of key metabolic pathways that could restore the imbalance between pro- and anti-inflammatory T and B cell responses in multiple sclerosis.

4.3 Dual B cell functions: regulatory and helper cells

As part of our ongoing investigation of B cell antibody-independent functions, my PhD work has identified two novel roles for B cells in modulating conventional and innate-like CD8⁺ T cell effector functions. In chapter 3, we found that, *in vitro*, B cells provided helper factors to MAIT cells, thereby enhancing their expansion, pro-inflammatory cytokine production, and cytotoxic potential. Therefore, we coin the term “MAIT-cell helper B cells” to describe the role of B cells in

this interaction. Our attempts to uncover these so-called helper factors have so far been unsuccessful, though my experiments indicate that they involve soluble factors that are generated as a result of cross-talk between the B cells and the MAIT cells.

My work assessing the effects of *in vivo* anti-CD20 treatment of MS patients revealed that B cell depletion therapy resulted in reduced circulating MAIT cell numbers and frequencies as well as IFN γ production, mirroring my *in vitro* observations. This favors a model wherein B cells engage in an *in vivo* productive interaction with MAIT cells to stimulate their expansion and pro-inflammatory effector functions. We recently reported that the MAIT cell frequency as well as their propensity to produce the proinflammatory cytokines IFN γ and IL-17 are abnormally elevated in the circulation of children with multiple sclerosis compared to children with monophasic CNS inflammatory disorders or normal controls¹⁵⁰. Taken together, we speculate that B cells from multiple sclerosis patients instigate aberrant MAIT cell expansion and pro-inflammatory effector functions. The consequences of such interaction between B cells and MAIT cells may be relevant to propagating MS disease activity both in the periphery and within the CNS (where B cells and MAIT cells appear to occupy similar niches and are therefore likely to interact⁴¹³) and may represent part of therapeutic mode of action of the highly effective B cell depleting approach in patients.

A reduction in MAIT cell numbers after anti-CD20 therapy in MS patients could alternatively be due to the expression of CD20 on T cells. In our preliminary experiments, we found that <5% of MAIT cells expressed CD20 *ex-vivo* in a cohort of normal controls, and that those cells produced higher levels of pro-inflammatory cytokines (data not shown). Future experiments could aim at investigating the expression of CD20 on MAIT cells in MS, the functional profile of CD20⁺ MAIT cells including TCR-repertoire analysis, cytokine and cytotoxic molecule expression and its relevance to the depletion profile found in ocrelizumab-treated patients. These efforts would complement published work that documented CD20 expression on T cells in normal controls and MS patients. In fact, CD20 is found on a minor CD4⁺ and CD8⁺ T cell populations enriched for memory cells⁵⁹⁶⁻⁵⁹⁸. In MS, the frequency of circulating CD20⁺ CD8⁺ T cells is elevated compared to normal controls, and those cells can also be found within the CSF⁵⁹⁶⁻⁵⁹⁸. Further, two recent reports suggested that CD20⁺ T cells may recognize myelin antigens, and display a Th1/Tc1

phenotype^{598,599}. Though this data represents an intriguing phenomenon, it remains that the relevance of CD20⁺ T cells to MS pathogenesis is uncertain.

In chapter 3, we also uncovered a regulatory role for B cells in modulating CD8⁺ non-MAIT cell proliferation and cytokine production (GM-CSF and TNF). Our data indicates that B cell-derived soluble factors generated in cross-talk with CD8⁺ T cells can increase the TCR activation threshold of non-MAIT cells. B cells exerted their suppressive effects on non-MAIT cells independently from IL-10, PD-1, adenosine, and IL-2 signaling (Appendix Figure 1) and without impacting on the survival of the non-MAIT cells (Appendix Figure 2). Further, a greater degree of suppression was exerted by transitional and naïve B cells than memory cells in keeping with published reports²⁷¹. The molecular wiring that underlie the acquisition of suppressive functions by transitional and naïve B cells has not been investigated, as is the state of B cell regulation in MS.

One challenge in further extending our current observations into an *in vivo* model of CNS neuroinflammation such as classical MOG-induced EAE is the dependence of disease initiation on CD4⁺ T cells with a less prominent role for CD8⁺ T cells⁹⁵. Nonetheless, work by Goverman's group have shown that TCR-transgenic CD8⁺ T cells, in conjunction with other immune cells such as CD4⁺ T cells, can mediate inflammation within the CNS, which is aided by concurrent viral infections^{448,452,459}. Whether B cells can impact disease course in those models through antibody-independent functions has not been explored. Similarly, infection with Theiler's encephalomyelitis virus can instigate CNS-localized inflammation in which CD8⁺ T cells play dual roles – viral clearance and subsequent tissue injury⁹⁵. B cell depletion results in a worsened disease course, associated with viral persistence within the CNS⁶⁰⁰. Thus, despite its relevance in dissecting aspects of CNS inflammation, the experimental model EAE does not mirror all aspects of the human disease, including relevant interactions among CD8⁺ T cells and B cells.

In a similar vein, the relative contribution of MAIT cells to CNS inflammation remains uncertain. *Croxford et al.* hinted to a regulatory function for MR1-restricted T cells in EAE, however, these observations require further validation⁶⁰¹. In addition, the advent of MR1-tetramer has greatly helped charting MAIT cell development and functions *in vivo*, bypassing the use of Va19 transgenic mice^{513,542}. Thus, it would now be ideal to characterize MAIT cell functional phenotype

during EAE clinical course in B cell replete and deficient mice, and conversely utilize MAIT cell-depleted mice (in MR1^{-/-} or Traj33^{-/-} mice) to infer their role(s) in this disease. An additional layer of complexity is the diversity of the gut microbiota and its influence on MAIT cells and EAE course. MAIT cell abundance is tightly linked to the presence of a diverse microbial community, such that germ-free mice are devoid of MAIT cells, and specific-pathogen free mice housed in different cages have varying numbers of MAIT cells^{501,547,548}. It is interesting to note that It is also the case that germ-free mice exhibit a reduced EAE clinical score^{261,263}. The intersection between those observations is unknown, as would be the effect of the microbiota on the functional phenotype of MAIT cells in MS patients.

4.4 B cell: CD8⁺ T cell interactions beyond MS

An emerging body of work suggests that MAIT cells can be found within the cellular infiltrate in human colon adenocarcinomas and esophageal adenocarcinomas, likely in response to local tissue inflammation^{602,603}. MAIT cells may promote tumor immunity via release of pro-inflammatory and cytotoxic molecules in a bystander fashion⁵⁰⁵. Could B cells help promote MAIT cell effector functions within the tumor microenvironment? In fact, there is an increased recognition of an important role for B cells in tumor surveillance that can extend from their inherent capacity to secrete immunoglobulin – these functions can promote or inhibit productive tumor immunity³⁸⁴. Indeed, *Shalapour et al.* found that IgA⁺ plasma cells induced upon chemotherapy intervention can impede CD8⁺ T cell activation and effector functions in a prostate cancer mouse model⁵⁷⁶. Further, an increased B cell:CD8⁺ T cell ratio was associated with tumor metastasis in prostate cancer patients. Similarly, IgA⁺ plasma cells can promote CD8⁺ T cell exhaustion in hepatocellular carcinoma mouse model, in an IL-10 and PD-L1 dependent mechanism⁵⁷⁷. While these studies demonstrate the acquisition of regulatory roles by B cells within the tumor microenvironment, more recent observations suggest that the relationship between B cells and CD8⁺ T cells is more nuanced. In fact, the co-presence of B cells and CD8⁺ T cells, as well as the formation of tertiary lymphoid structures, within the tumors of metastatic melanoma patients treated with checkpoint blockade was associated with improved prognosis at baseline^{604,605}. Parallel observations were made in soft-tissue sarcoma and lung cancer, in that the formation of tertiary lymphoid structures can predict improved patient survival and/or immunotherapy response⁶⁰⁶⁻⁶⁰⁸. The phenotype of tumor-infiltrating B cells is heterogeneous across different tumors, with B cells in tertiary lymphoid structures up-regulating known molecules such as Ki-67 and CXCR5⁶⁰⁸. These studies

hint to a positive role for B cells in tumor immunity, that may include antibody-dependent and independent functions. The extent and nature of any cellular interactions between B cells and other immune cells, including CD8⁺ non-MAIT and MAIT cells, require further investigation. In sum, those observations serve to highlight the influence of the tissue microenvironment, disease context and treatment modality on B cell: T cell interaction(s), and the importance of studying biospecimen from patients to inform on novel insights that can be further dissected *in vitro* or otherwise.

4.5 Conclusion and future directions

B cells have emerged as an important cellular contributor to the pathogenesis of multiple sclerosis, in part by orchestrating other cellular responses via the production of cytokines. As mentioned above, the identity of cytokine-producing B cells remains enigmatic, and future studies should focus on deciphering their transcriptional programs using next-generation sequencing and interrogating their functions *in vitro* and *in vivo*. Our studies have added a potential new dimension to the cellular network involved in MS. We have shown that human B cells can modulate both innate (MAIT) and conventional CD8⁺ T cell effector functions *in vitro* and *in vivo*. It will be important to define the signals involved in this cross-talk and to further characterize such interactions in healthy individuals and in untreated MS patients. It would be equally important to investigate the regulation of B cell functions by CD8⁺ T cell subsets, as history has taught us that cellular immune interactions are rarely uni-directional.

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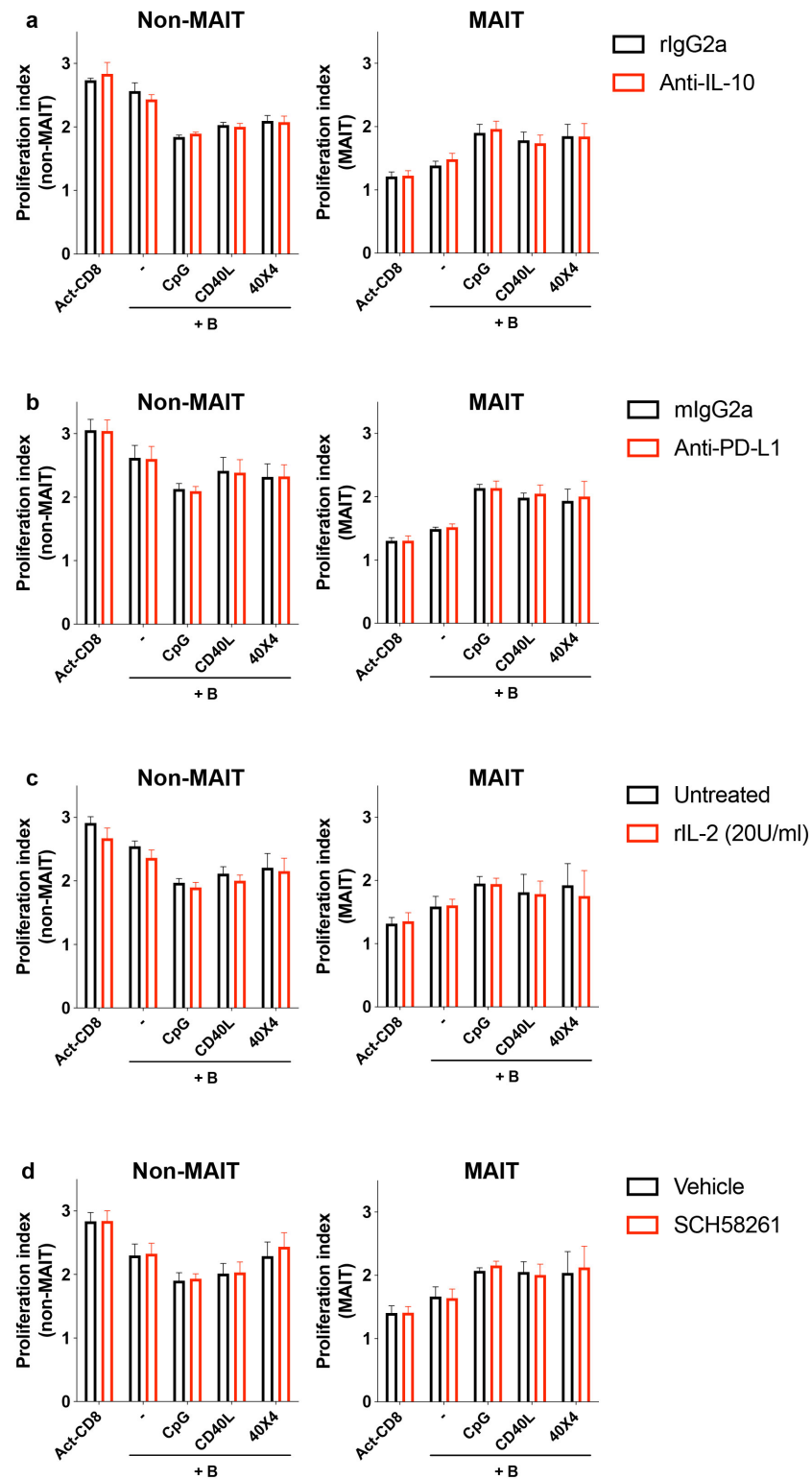
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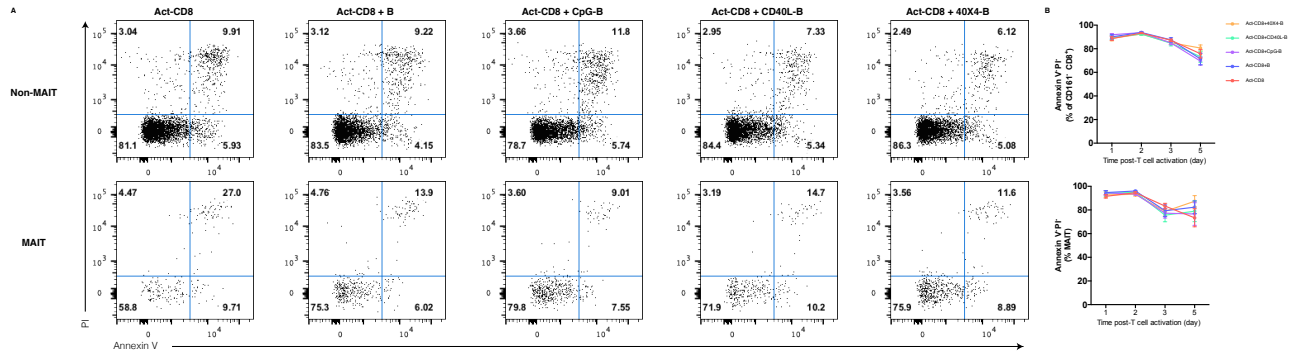
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Appendix figure 1



Appendix figure 1. B cells regulate non-MAIT cell proliferation independent of IL-10, PD-1, adenosine, IL-2 signaling. MACS-sorted CD8⁺ T cells were activated with beads coated with anti-CD2, anti-CD3 and anti-CD28 and co-cultured with autologous MACS-sorted B cells (unstimulated or pre-activated with CpG, CD40L or CD40L + anti-IgM + IL-4) for 5 days before assessing T cell proliferation by flow cytometry. Anti-IL-10 antibody, anti-PD-L1 antibody, SCH58261, and IL-2 or appropriate controls were added at the start of cell co-culture. B cells maintained their suppressive effect on non-MAIT cells and maintained their helper effect on MAIT cells independent of IL-10 (A), PD-1 (B), IL-2 (C) and adenosine (D), signaling (n=3-5). All values are represented as mean $\pm$ SEM.

Appendix figure 2



Appendix figure 2. B cells do not impact CD8⁺ T cell subset survival. MACS-sorted CD8⁺ T cells were activated with beads coated with anti-CD2, anti-CD3 and anti-CD28 and co-cultured with autologous MACS-sorted B cells (unstimulated or pre-activated with CpG, CD40L or CD40L + anti-IgM + IL-4) for up to 5 days before assessing T cell survival by flow cytometry. The presence of B cells in co-culture with T cells does not induce significant changes in cell survival quantified using Annexin V and PI, as shown in (A) a representative experiment, and (B) summarized for n=5 independent experiments. All values are represented as mean $\pm$ SEM.