

**ON THE ROLE OF CD24 IN THE PATHOGENICITY OF MYELIN ANTIGEN  
SPECIFIC T CELLS**

**DISSERTATION**

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## ABSTRACT

CD24 is a glycosylphosphatidylinositol (GPI) anchored cell surface glycoprotein that is expressed in hematopoietic cells and cells of the central nervous system (CNS). Although CD24 is commonly used as a maturation marker for T lymphocytes, its role in thymocyte development is not clear. CD24 has been reported to function as a co-stimulatory molecule independent of CD28 and is required for the induction of experimental autoimmune encephalomyelitis (EAE), an animal model for multiple sclerosis (MS). Bone marrow chimera experiments suggest that CD24 expression on both bone marrow-derived cells and CNS cells are required for EAE development. Studies of single nucleotide polymorphisms (SNPs) suggest that CD24 is related to the risk and progression of MS. We have used a series of genetic models to delineate the role of CD24 in the pathogenesis of EAE.

It has previously shown that CD24 is required for the induction of EAE. In CD24<sup>-/-</sup> mice, normal levels of myelin oligodendrocyte glycoprotein (MOG) specific T cells were primed, however these T cells were non-pathogenic. To understand this issue, we bred CD24<sup>-/-</sup> mice with 2D2 TCR transgenic mice, which bear TCR specific to MOG, and generated 2D2 TCR transgenic mice with or without CD24. Here I show that 2D2 TCR transgenic mice with CD24-deficiency (2D2<sup>+</sup>CD24<sup>-/-</sup>) have remarkably withered thymi. In peripheral lymphoid organs,

transgenic T cells from 2D2<sup>+</sup>CD24<sup>-/-</sup> mice have an immature phenotype (CD4<sup>-</sup>CD8<sup>-</sup>), do not respond to MOG peptide stimulation, and fail to cause autoimmune inflammation in the CNS and optical nerves. In contrast, OTII TCR transgenic mice with CD24 deficiency (OTII<sup>+</sup>CD24<sup>-/-</sup>), which bear TCR specific to chicken ovalbumin (OVA), have normal thymi and their peripheral T cells have a normal response to OVA peptide. These data suggest that CD24 inhibits thymic deletion of myelin antigen, but not foreign antigen-reactive T cells.

To understand the role of CD24 on the resident cells in the CNS during EAE development, I created CD24 bone marrow chimeras and transgenic mice in which CD24 expressions was under the control of a glial fibrillary acidic protein promoter (GFAP) denoted Astro<sup>CD24</sup>. I showed that mice lacking CD24 expression on the CNS resident cells developed a mild form of EAE, but mice with over-expression of CD24 in the CNS developed severe EAE. Compared with nontransgenic mice, the CNS of Astro<sup>CD24</sup> mice had higher expression of cytokine genes such as IL-17; the CNS of Astro<sup>CD24</sup> mice accumulated higher numbers of Th17 and total CD4<sup>+</sup> T cells, whereas CD4<sup>+</sup> T cells underwent more proliferation during EAE development. Expression of CD24 in CD24-deficient astrocytes also enhanced their co-stimulatory activity to myelin oligodendrocyte glycoprotein-specific, TCR-transgenic 2D2 T cells. Thus, CD24 on the resident cells in the CNS enhances EAE development via co-stimulation of encephalitogenic T cells.

The role of CD24 in the thymic generation and pathogenicity of myelin antigen specific T cells provides a novel explanation for its control of genetic susceptibility to autoimmune diseases in mice and humans.

## **DEDICATION**

To my mother and father, Laurie G. and Joseph W. Carl, who through their love and support, help me to be the best man I can be. And to my son, Adam Joseph Carl, who has inspired me to be the best man I can be.

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## FIELDS OF STUDY

Major Fields: Immunology

## TABLE OF CONTENTS

ABSTRACT.....	ii
DEDICATION .....	v
ACKNOWLEDGMENTS.....	vi
VITA .....	ix
LIST OF FIGURES.....	xiii
ABBREVIATIONS .....	xv
INTRODUCTION.....	1
1.0 PATHOGENESIS OF EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS AND MULTIPLE SCLEROSIS .....	4
2.0 THE ROLE OF CD24 IN MULTIPLE SCLEROSIS AND EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS.....	11
2.1 CD24 Molecular Genetics .....	11
2.2 CD24 and MS.....	13
2.3 CD24 and EAE.....	14
2.4 Goals of this study.....	15
MATERIALS AND METHODS.....	17
3.1 Mice.....	17
3.2 Production of Astro <sup>CD24</sup> mice .....	17
3.3 Antibodies and Flow Cytometry .....	18
3.4 Bone Marrow Chimeras .....	18
3.5 Real Time RT-PCR .....	19
3.6 BrdU Incorporation Assay .....	20
3.7 Proliferation Assay .....	21
3.8 Purification of 2D2 T cells from 2D2 <sup>+</sup> CD24 <sup>+/+</sup> or 2D2 <sup>+</sup> CD24 <sup>-/-</sup> mice .....	21
3.9 Induction and Assessment of EAE.....	22
3.10 Histology .....	23
3.11 Immunofluorescence and Confocal Laser Scanning Microscopy .....	23
3.12 Preparation of Astrocytes from Newborn Mice and Proliferation Assay .....	24

CD24 AND THYMIC GENERATION OF MYELIN ANTIGEN SPECIFIC T CELLS.....	26
4.1 Thymic clonal deletion of MOG-specific T cells in CD24-deficient mice .....	26
4.2 Restoration of CD24 on thymocytes is insufficient to rescue clonal deletion of autoreactive T cells; CD24 on radio-resistant thymic stromal cells is necessary .....	27
4.3 CD24-deficiency does not alter development of T cells specific for foreign antigen .....	33
4.4 CD24-deficiency increases the efficiency of clonal deletion of viral super antigen (VSA)-reactive T cells in the thymus .....	35
4.5 CD24-deficiency nullifies pertussis toxin-induced experimental autoimmune encephalomyelitis .....	37
CD24 ON THE CENTRAL NERVOUS SYSTEM ANTIGEN PRESENTING CELLS ENHANCES EFFECTOR FUNCTION OF MYELIN ANTIGEN SPECIFIC T CELLS. ..	42
5.1 Over-expression of CD24 in the CNS enhances EAE progression .....	42
5.2 Enhanced EAE progression in Astro <sup>CD24</sup> mice is associated with increased expression of pro-inflammatory cytokines in the CNS. ....	46
5.3 Over-expression of CD24 enhances local T cell proliferation in the CNS .....	50
CONCLUSIONS AND DISCUSSION .....	53
6.1 CD24 controls thymic generation of self reactive T cells.....	53
6.2 The cellular basis of CD24 inhibition of negative selection .....	53
6.3 Signal pathway of CD24 action in the thymus .....	54
6.4 A hypothetical model of CD24 action in the thymic generation of autoreactive T cells .....	54
6.5 The role of CD24 in the CNS in EAE development .....	55
6.6 A hypothetical model of CD24 action in the CNS during EAE development .....	56
6.7 Significance .....	57
LIST OF REFERENCES .....	60

## LIST OF FIGURES

Figure 1: A four checkpoint model for EAE pathogenesis .....	6
Figure 2: CD24 molecular genetics – DNA to mRNA to protein.....	12
Figure 3: CD24 inhibits thymic deletion of MOG-specific T cells. ....	27
Figure 4: Restoration of CD24 on 2D2 T cells in CD24-deficient mice does not prevent its thymic deletion.....	28
Figure 5: CD24 on radio-resistant thymic stromal cells is necessary but not sufficient for the generation of mature CD4 T cells specific for MOG peptide. ....	30
Figure 6: Expression of CD24 and MOG in thymic stromal cells.....	32
Figure 7: CD24 expression is not required for the thymic generation of CD4 T cells specific for ovalbumin (OVA). ....	34
Figure 8: Frequencies of viral super antigen reactive T cells are reduced in CD24 <sup>-/-</sup> BALB/c mice. ....	36
Figure 9: Phenotype analysis of 2D2 T cells in the peripheral lymphoid organs of mice with or without CD24.....	38
Figure 10: V $\alpha$ 3.2 <sup>+</sup> V $\beta$ 11 <sup>+</sup> cells in the peripheral lymphoid organs of 2D2 <sup>+</sup> CD24 <sup>-/-</sup> mice failed to proliferate in response to their cognate peptide antigen.....	39
Figure 11: CD24-deficiency prevents EAE in 2D2 TCR transgenic mice. ....	41
Figure 12: Production of Astro <sup>CD24</sup> mice.....	43
Figure 13: Astro <sup>CD24</sup> mice had enhanced EAE progression .....	45
Figure 14: Assessment of cytokine gene expression in the spinal cords of Astro <sup>CD24</sup> mice and controls by real-time PCR.....	47

<b>Figure 15: Th1 and Th17 cells in the spinal cords of Astro<sup>CD24</sup> mice .....</b>	<b>49</b>
<b>Figure 16: Over-expression of CD24 in the CNS enhances CD4 T cell proliferation in the CNS .....</b>	<b>51</b>
<b>Figure 17: Transgenic expression of CD24 in CD24-deficient astrocytes promotes their co-stimulatory activity to MOG-specific T cells.....</b>	<b>52</b>
<b>Figure 18: CD24 expression on Thymic Epithelial Cells Provides a Signal to Developing T Cells Inhibiting Apoptosis. ....</b>	<b>55</b>
<b>Figure 19: CD24 Expression on Central Nervous Systems Antigen Presenting Cells Provides a Co-stimulatory Signal to T cells Enabling the Proliferation and Survival of Effectors Cells.....</b>	<b>57</b>

## ABBREVIATIONS

2D2 – Name of transgenic mice with TCR specific for MOG<sub>35-55</sub>

aa – Amino Acid

APC – Antigen Presenting Cell

Astro<sup>CD24</sup> – Name of transgenic mice with CD24 expression under control of glial fibrillary acidic protein promoter

BBB – Blood Brain Barrier

CFA – Complete Freund's Adjuvant

CNS – Central Nervous System

DMEM – Delbecco's Modified Eagle's Medium

DN – Double Negative

DP – Double Positive

EAE – Experimental Autoimmune Encephalomyelitis

ER – Endoplasmic Reticulum

FCS – Fetal Calf Serum

GFAP – Glial Fibrillary Acidic Protein

GPI – glycosylphosphatidylinositol

H&E – Hematoxylin and Eosin

HPRT – hypoxanthine-guanine phosphoribosyltransferase

HSA – Heat Stable Antigen

i.p. – Interaperitoneal

i.v. – Intravenous

mTEC – Medulary Thymic Epithelial Cells

MBP – Myelin Basic Protein

MHC – Major Histocompatibility Complex

MOG – Myelin Oligodendrocyte Glycoprotien

MS – Multiple Sclerosis

OTII – Name of transgenic mice with TCR specific for OVA<sub>323-333</sub>

OVA – Ovalbumin

PBS – Phosphate Buffered Saline

PCR – Polymerase Chain Reaction

PLP – Proteolipid Protein

RT-PCR – Real Time PCR

s.c. – Subcutaneous

SNP – Single Nucleotide Polymorphism

SP – Single Positive

TEC – Thymic Epithelial Cells

TCR – T Cell Receptor

UTR – Untranslated Region

VSA – Viral Super Antigen

WT – Wild Type

## INTRODUCTION

Multiple Sclerosis (MS) is an autoimmune disease of the central nervous system (CNS) affecting 1/1000 Caucasians (1). Although the etiology of MS is not known, genetic, gender, and environmental triggers are factors that affect the risk of contracting the disease as well as of its progression. Most people are diagnosed with MS between the ages of 20 and 40 with women being affected twice as often as men. According to the National MS Society, about 400,000 Americans are known to have MS, with 200 new diagnoses each week. Currently there is no cure for MS, although there are therapies that target the immunological checkpoints of MS development.

MS is a complex disease associated with an inflammatory process in the CNS comprised of infiltrating lymphocytes and activated macrophages/microglia resulting in the demyelination of axons, as well as axonal damage and destruction (2-4). While the sequence of events that initiates MS is unknown, experimental autoimmune encephalomyelitis (EAE), the best animal model for MS (5, 6), has been instrumental in characterizing the pathological progression.

The EAE model was first developed in monkeys by Rivers, *et al.* (7), and shares many features of MS pathology (2, 8). EAE can be induced in mice by active

immunization with CNS antigens such as myelin basic protein (MBP), proteolipid protein (PLP), or myelin oligodendrocyte glycoprotein (MOG). EAE can also be induced by passively injecting purified activated auto-reactive T cells into healthy syngeneic mice. In both methods of EAE induction, *B. Pertussis* toxin is also utilized as another adjuvant to initiate T cell accumulation at the blood brain barrier (BBB) (9, 10), allowing activated T cells access to the CNS. Like MS, EAE is a CD4<sup>+</sup> T cell mediated disease (5, 6), and activated CD4<sup>+</sup> T cells pass through the permeable BBB secreting Th1 cytokines, such as IFN $\gamma$  and TNF $\alpha$  (11). These cytokines subsequently induce the creation of lesions that destroy the myelin sheath that normally insulates and protects nerve fibers. Lesions are commonly found in the optic nerve, periventricular white matter, brain stem, cerebellum, and spinal cord white matter (12).

It has been reported (13-15) that targeted mutation of CD24 abrogates the development of EAE induced with MOG-peptide immunization and adoptive transfer. CD24<sup>-/-</sup> mice had levels of MOG-peptide specific T cell responses similar to those found in WT mice that displayed EAE. However, CD24-deficient MOG-specific T cells were not encephalitogenic upon adoptive transfer. This observation suggests that the MOG-responsive T cells generated in CD24-deficient mice are functionally defective. Adoptive transfer studies also demonstrate that MOG-peptide specific T cells generated from WT mice can only transfer EAE to CD24<sup>+/+</sup> but not to CD24<sup>-/-</sup> recipients. These data suggest that encephalitogenic T cells need help from the host cells in order for them to

expand and persist in the CNS. Indeed, bone marrow chimera experiments suggest that both bone marrow-derived non-T and non-B cells or radiation-resistant cells of CD24<sup>+/+</sup> genotype can provide such help (15). Recently using a series of genetic models to study the role of CD24, I have found that CD24 contributes to both thymic generation and effector function of myelin antigen specific T cells.

**CHAPTER 1:**  
**PATHOGENESIS OF EXPERIMENTAL AUTOIMMUNE**  
**ENCEPHALOMYELITIS AND MULTIPLE SCLEROSIS**

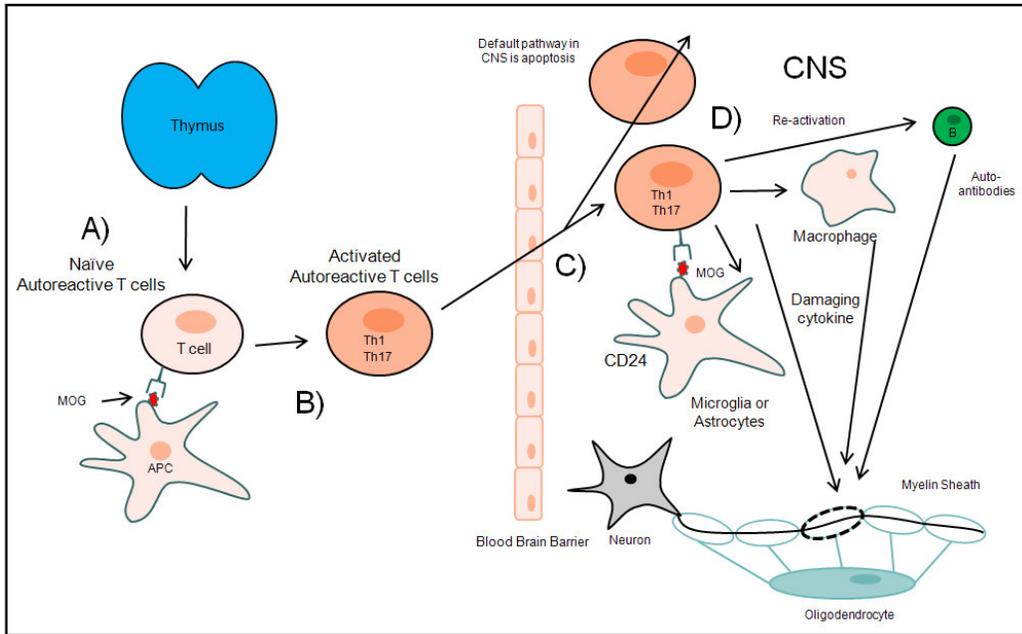
EAE serves as a model for the pathogenesis and progression of MS, and has enabled the development of therapies based on the checkpoints identified by this model. Understanding the checkpoint model of EAE pathogenesis will be useful in following the experimental design discussed in this study. I will describe a 4 checkpoint model (**Figure 1**) of EAE/MS pathogenesis consisting of 1) generation of naïve autoreactive T cells, 2) activation of naïve T cells in the peripheral lymphoid organs and differentiation of activated T cells into pathogenic effector subsets, 3) migration of activated T cells into the CNS, and 4) reactivation and survival of T cells in the CNS.

The thymus is a primary lymphoid organ responsible for the selection and development of T cells (16). It is a bi-lobed structure located on the anterior side of the heart in the pericardial mediastinum (17). A normal thymus is comprised of a cortex and a medulla enclosed by thin capsular tissue. Bone marrow-derived precursors enter the thymus via an artery at the cortico-medullary junction. The artery ramifies into fenestrated capillaries in the medulla and rarely fenestrated capillaries in the cortex (18). The lack of fenestration on the capillaries in the cortex forms a blood-thymus barrier

prohibiting entry of perivascular lymphocytes and circulating antigenic molecules. The cortex contains small immature lymphocytes, sparse epithelial cells, and phagocytic macrophages (19). The medulla contains more mature T cells, prominent epithelial cells, Hassall's corpuscles, phagocytic macrophages, non-phagocytic dendritic cells and B lymphocytes(20). Stroma in the thymus play an important role in central tolerance by expressing tissue specific antigens (21). Expression of tissue specific isoforms and doses of myelin components in the thymus determine the efficacy of central tolerance. Several studies suggest that in some strains of mice, thymic expression of myelin components, such as PLP and MBP, contribute to the resistance to EAE induction (22, 23). For example, the SJL strain of mice predominantly express an alternatively spliced form of PLP, which may contribute to the increased frequency of autoreactive T cells in the periphery (22, 23). Central tolerance shapes the repertoire of TCRs, and the existence of autoreactive T cells is the first checkpoint in the EAE model of pathogenesis (**Figure 1 – Checkpoint A**).

The developing lymphocytes are categorized by the expression of CD4 and CD8. The bone marrow-derived precursors express no CD4 or CD8 and are called double negative (DN) cells. The next stage of development is a double positive (DP) (24) cell expressing both CD4 and CD8, followed by maturation to a single positive (SP) cell expressing CD4 or CD8. The TCR genes are formed in the DN stage of development. The stepwise stages of somatic recombination events in

DN cells can be correlated by the expression of the cell surface markers CD44 and CD25.



**Figure 1: Four checkpoints model of EAE pathogenesis**

A) Generation of naïve autoreactive T cells in the thymus is the first checkpoint. B) Activation of naïve T cells by antigen presenting cells and differentiation into pathogenic effector subsets such as Th1 or Th17 is the second checkpoint. C) Migration of activated T cells to the CNS and crossing the BBB is the third checkpoint. D) The fourth checkpoint is reactivation and survival of T cells in the CNS

The earliest cells to arrive from the bone marrow are CD44 positive and CD25 negative denoted DN1 and are found primarily at the cortico-medullary junction. Lymphocytes that will become  $\gamma\delta$  cells begin to rearrange the  $\delta$  D-D and V-D gene segments in the DN1 stage. DN1 cells develop into CD44 positive and CD25 positive cells called DN2 and are found throughout the cortex. DN2 cells rearrange  $\delta$  D-J segments and  $\gamma$  segments (25). Lymphocytes that are destined to become  $\alpha\beta$  cells begin to rearrange the  $\beta$  D-J segment in the DN3 stage. DN3

cells no longer express CD44 and are concentrated in the outermost part of the thymus just below the capsule (26). DN3 cells then develop into DN4 cells and  $\beta$  VDJ recombination completes and is expressed on the cell surface with a pre $\alpha$ TCR. DN4 cells express neither CD25 nor CD44 and will become DP cells. Autoreactive T cells specific for CNS antigens are normally controlled by peripheral tolerance mechanisms such as anergy (27) or functional regulatory cells (28).

The activation and clonal expansion of autoreactive T cells is the second checkpoint in the EAE model of pathogenesis. Active induction of EAE utilizes CNS antigens suspended in an adjuvant such as complete Freund's adjuvant (CFA) and injected subcutaneously (s.c.) in the hind quarters, followed by an intravenous (i.v.) tail vein injection of *B. pertussis*. The activation mechanism of naïve CD4<sup>+</sup> T cells follows the "two-signal model" in which the interaction of the TCR with a peptide/MHC complex must be accompanied by a second co-stimulatory signal. Normally the co-stimulatory signal is CD28 on the T cell with B7 family molecules on APCs (14, 29, 30). The activation of CD4<sup>+</sup> T cells specific for CNS antigens is the second checkpoint in EAE. Concurrent with the activation of autoreactive T cells is their differentiation into effector cells. CD4<sup>+</sup> T cells differentiate into two major subtypes of effector cells defined by the cytokines they release. The two effector subtypes are denoted Th1 and Th2 (31). Th1 is associated with cell mediated immunity and release the cytokines IL2, TNF $\alpha$  and IFN $\gamma$  (31), while Th2 is associated with humoral mediated immunity and release

IL4, IL5, IL6, IL10 and IL13 (31). A recently identified subset of T cells (Th17) cells has also been shown to be correlated with EAE susceptibility (32, 33). Thus, the development of EAE can be regulated by factors that control the differentiation of Th subsets (5, 34). MS as well as EAE is generally accepted to be mediated by Th1 helper cells. In the CNS Th2 type cytokines play a role in down regulating Th1 responses and macrophage activation (35). The differentiation into Th1/Th17 helper cells is a second checkpoint in EAE (**Figure 1 – Checkpoint B**).

Once activated, the T cells must cross the BBB. The BBB is formed by highly specialized endothelial cells, which inhibit transcellular molecular trafficking (36), and astrocyte foot processes (37-39). The blood vessels on the CNS side of the BBB are ensheathed by astrocytes (40) forming a barrier. During inflammation, the BBB endothelium upregulate traffic signals that aid T cell arrest and transmigration (41-43). Infiltrating activated leukocytes accumulate in the perivascular spaces (44), while non-activated leukocytes do not, because T cells are able to cross the BBB based on their activation state, not TCR specificity (45). Additionally T lymphocytes vary in degree in their ability to enter different sites of the CNS, with higher levels of entry in the spinal cord and lowest levels at the cerebrum (46). The process of migration to the CNS and crossing the BBB is a third checkpoint in the progression of EAE (**Figure 1 – Checkpoint C**).

Once the activated autoreactive T cells cross the BBB, to become reactivated, they must encounter the CNS antigen epitope presented on MHC molecules as expressed by CNS antigen presenting cells (5, 47-49) such as microglia,

astrocytes, or dendritic cells and become reactivated. In addition to the two well-defined cytokine profiles Th1 and Th2, a third profile, associated with autoimmune diseases, has been identified and denoted Th17 (32, 33).

Reactivated T cells will induce the production of cell mediated destruction of myelin on axons (50). Activation of microglia, infiltrating macrophages, and B cells will induce these cells to release damaging cytokines or antibodies which result in the destruction of myelin on axons (51-53). Myelin is necessary for the proper conduction of electrical signals along axons.

Generally, T cells find the CNS an inhospitable environment for their survival, and will undergo apoptosis (54) unless rescued by supporting cells co-stimulation (55). Microglia constitute the tissue specific macrophage of the CNS (56), regularly engulfing material in their environment and helping to maintain the integrity of the brain (57). Under inflammatory conditions microglia up-regulate MHC class molecules and can promote the reactivation of T cells in the CNS (58).

Astrocytes influence the formation and maintenance of the BBB (59). Under inflammatory conditions they will up-regulate adhesion molecules facilitating leukocyte transmigration. The ability of astrocytes to present antigens is a controversial one; *in situ* and *in vivo* evidence supports the expression of MHC-II and co-stimulatory molecules (60), yet other studies indicate that astrocytes do not present antigens to prime T cells (61, 62). It is clear that astrocytes do not normally express MHC-II but its expression can be induced in inflammatory conditions (63). Furthermore human astrocytes do not express B7-1 or B7-2

either constitutively or due to inflammatory stimuli (64), while murine astrocytes do express B7 molecules under inflammatory conditions (60). Under inflammatory conditions, CNS APCs will upregulate MHC-II and co-stimulatory molecules. Activated T cells that have crossed the BBB will encounter CNS APCs and become reactivated. Mechanism of reactivation by CNS APC constitutes a fourth checkpoint in EAE (**Figure 1 – Checkpoint D**).

## **CHAPTER 2:**

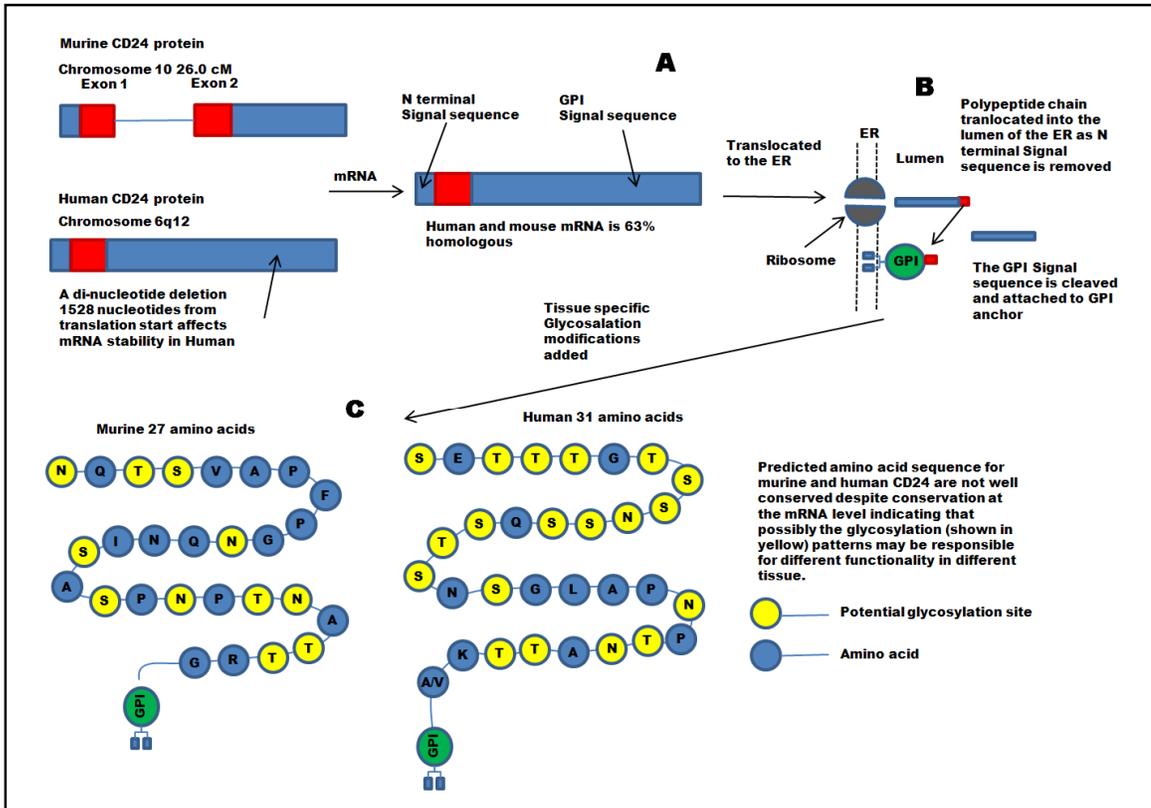
### **THE ROLE OF CD24 IN MULTIPLE SCLEROSIS AND EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS**

Springer (65) identified CD24 in 1978 while searching for lymphocyte differentiation markers. Because of its resistance to heat, it was called Heat Stable Antigen (HSA). CD24 is a glycosylphosphatidylinositol (GPI) link protein expressed on numerous cells of the immune system, including T cells (66, 67), dendritic cells (68), B cells (69), macrophages (70), neutrophils (71), as well as cells of the CNS (13, 72, 73). CD24 has been shown to be expressed on a broad range of epithelial cells such as hair follicles (74) and intestine (75) but the significance is not clear. Expression kinetics of CD24 are best understood on T cells and B cells, while expression on developing neuronal cells is still a field of ongoing study.

#### **2.1 CD24 Molecular Genetics**

First identified in the mouse using two rat antibodies M1/69 and M1/75 (65), CD24 can also be recognized by other antibodies (76-78). Located on the mouse chromosome 10 26.0 cM as two exons and on the human chromosome 6q21 as a single exon, the resulting transcripts share 63% homology (**Figure 2A**). Other intronless pseudogenes at 3p26, 15q12, 15q22, 20q11.2 and Yq11.1 exist and

most likely they do not encode for CD24 proteins (79); however, care needs to be taken when utilizing PCR to analyze gene products.



**Figure 2: CD24 molecular genetics – DNA to mRNA to protein**

A) Murine HSA (CD24) is located on Chromosome 10 26.0 cM, while Human CD24 is located on chromosome 6q12. There is a 63% homologue between the mouse mRNA and human mRNA. B) The mRNA translocates to the ER and the GPI signal sequence is cleaved as the nascent protein is attached to a GPI anchor. C) The resulting protein is 27 amino acids (aa) in length in the mouse and 31 aa in the human. The yellow aa's are predicted glycosylation sites

The mRNA contains a 5' terminal signal sequence directing the mRNA to the endoplasmic reticulum (ER) where the signal sequence is removed as it is translated. Because of its GPI anchor, the nascent protein has a GPI signal sequence associated with the long untranslated 3' region. Through mechanisms

still under investigation, the nascent protein is translated fully into the lumen of the ER, where CD24 protein is removed from the GPI anchor signal sequence and subsequently attached to a GPI anchor (68, 80) (**Figure 2B**). Numerous tissue specific N- and O- glycosylations (variations not completely elucidated) are added (81) in the ER and then trans-located to the cell surface (**Figure 2C**).

## **2.2 CD24 and MS**

At least four polymorphisms have been identified in the human CD24 coding regions, one of which results in a SNP associated with an increased risk of MS (82). The other three polymorphisms are found in the 3' untranslated region, one of which is associated with an increased protection of MS (reducing the risk by a factor of 2) and systemic lupus erythematosus (79). The replacement of alanine with valine at amino acid 31 results in an increased expression of CD24 on the cell surface (82) , possibly by facilitating the insertion of the GPI anchor. The increased expression of CD24 due to this SNP raises the relative risk of MS by two-fold, while at the same time increases the risk of rapid progression of MS. Fifty percent of the patients with a homozygous valine SNP reached an expanded disability score of 6.0 within 5 years compared to 16 years for heterozygous and 13 years for those with homozygous alanine SNP (82). The protective risk modification of CD24 reduction supports the hypothesis that increased CD24 expression increases the risk of MS. The di-nucleotide deletion of an amino acid at position 1527 from the mRNA translation start site affects the stability of the mRNA (79). The reduced stability of the mRNA produced two-fold less CD24

mRNA compared to wild-type alleles. The reduced expression of CD24 due to this di-nucleotide deletion reduced the relative risk of MS by greater than two-fold. Additionally, MS patients who have this di-nucleotide deletion have a slower progression (79).

### **2.3 CD24 and EAE**

It has been reported (13-15) that targeted mutation of CD24 abrogates the development of EAE induced with MOG-peptide immunization and adoptive transfer. CD24<sup>-/-</sup> mice had levels of MOG-peptide specific T cell responses similar to those found in WT mice that displayed EAE. However, CD24-deficient MOG-specific T cells were not encephalitogenic upon adoptive transfer. This observation suggests that the MOG-responsive T cells generated in CD24-deficient mice are functionally defective.

Adoptive transfer studies also demonstrate that MOG-peptide specific T cells generated from WT mice can only transfer EAE to CD24<sup>+/+</sup> but not to CD24<sup>-/-</sup> recipients. It was found (15) that upon adoptive transfer, activated MOG-specific CD24<sup>+/+</sup> T cells can infiltrate the CNS of both CD24<sup>+/+</sup> and CD24<sup>-/-</sup> recipients. However, donor T cells remained in the perivascular area of the CD24<sup>-/-</sup> recipients and did not cluster in the CNS parenchyma, in contrast to CD24<sup>+/+</sup> recipients. In addition, proliferation of the donor T cells was lower in CD24<sup>-/-</sup> recipients and the number of T cells in the CNS rapidly declined within 20 days in the CNS of CD24<sup>-/-</sup> mice. The number of T cells in the CNS of CD24<sup>+/+</sup> mice increased for 20 days and then declined, remaining detectable at 40 days after

adoptive transfer. These data suggest that encephalitogenic T cells need help from the host cells in order for them to expand and persist in the CNS. Indeed, bone marrow chimera experiments suggest that both bone marrow-derived non-T and non-B cells or radiation-resistant cells of CD24<sup>+/+</sup> genotype can provide such help (15). We hypothesize that CD24 on antigen presenting cells (such as bone marrow-derived dendritic cells and CNS local microglia and astrocytes) provide a co-stimulatory signal to CNS infiltrating T cells. Indeed, it was shown that astrocytes and microglia from CD24<sup>-/-</sup> mice have a 4-fold and 10-fold, respectively, reduced ability to stimulate proliferation of MOG-reactive T cells. Over-expression of CD24 in the CNS significantly enhanced EAE development, via accumulation of high numbers of Th17 cells in the CNS (13). These data suggest that APCs in the CNS contribute to the expansion and persistence of encephalitogenic T cells in the CNS via co-stimulation of CD24.

#### **2.4 Goals of this study**

The first goal of this study was to determine the role of CD24 in the pathogenicity of myelin antigen specific T cells. While CD24-deficient mice are resistant to the induction of EAE, CD24 deficient mice can generate MOG specific helper T cell response, but the T cells are not encephalitogenic suggesting that the CD24 deficient, MOG specific T cells are defective in some manner. To investigate this issue, I crossed CD24 deficient mice with myelin specific TCR transgenic mice (2D2) to produce CD24 deficient 2D2 mice. I used this model to determine if CD24 deficiency affects pathogenicity of MOG specific T cells.

The second goal was to assess the role of CD24 in the CNS. The Bai lab created transgenic mice which over-expressed CD24 on astrocytes, driven by the GFAP promoter element. I used this model to determine if CD24 on the resident cells of the CNS can affect T cell pathogenicity in EAE development.

## **CHAPTER 3:**

### **MATERIALS AND METHODS**

#### **3.1 Mice**

C57BL/6 mice were purchased from the Jackson Laboratory or National Cancer Institute. 2D2 TCR transgenic mice (83) were kindly provided by Dr. V.K. Kuchroo (Harvard Medical School). CD24-deficient mice in the C57BL/6 background have been described (14, 15). OTII TCR transgenic mice were purchased from the Jackson Laboratory. Transgenic mice expressing CD24 exclusively on T cells have been described (67). Mice with CD24 over-expression in the CNS (designated Astro<sup>CD24</sup>) were generated as I describe below. All mice were bred and maintained in a specific pathogen-free animal facility of The Ohio State University. The animal facilities are fully accredited by the American Association for Accreditation of Laboratory Animal Care.

#### **3.2 Production of Astro<sup>CD24</sup> mice**

The transgenic construct used for microinjection of C57BL/6 oocytes was generated based on the transgenic construct pGfa2-cLac (84) (provided by Dr. M. Brenner, University of Alabama, Birmingham, AL). The construct contains a 2.2kb DNA fragment of the human FGAP promoter sequence (84-86), a fragment of the mouse protamine-1 gene that supplies an intron to stabilize 3' untranslated region (UTR) and polyadenylation signal. We used the full-length

mouse CD24 cDNA (1.8kb) to replace the *LacZ* gene in the original vector. After excising the vector backbone, the full-length DNA fragment used for microinjection was 4.6kb. Oocytes were injected using conventional microinjection technology by the core facilities of The Ohio State University.

### **3.3 Antibodies and Flow Cytometry**

The following antibodies were used in the experiments according to the manufacturer's recommendations: purified, FITC-, PE- PerCP-, or biotin-labeled anti- CD4 (GK1.4), CD8 $\alpha$  (53-6.7), CD24 (M1/69), CD25 (7D4), CD44 (IM7), CD45 (30-F11), CD62L (Mel-14), CD69 (H1.2F3), V $\alpha$ 2 (B20.1) V $\alpha$ 3.2 (RR3-16), V $\beta$ 3 (KJ25), V $\beta$ 5.1/5.2 (MR9-4), V $\beta$ 8 (F23.1), V $\beta$ 11 (RR3-15), V $\beta$ 12 (MR11-1) and anti-rat IgG2a (RG7/1.30) These antibodies were purchased from either BD Pharmingen (San Diego, CA) or eBioscience (West San Diego, CA). For flow cytometry analysis, cells were incubated with antibodies on ice for 30 min followed by extensive washing; Cells were analyzed on a FACSCalibur cytometer (Becton Dickinson, Mountain View, CA, USA).

### **3.4 Bone Marrow Chimeras**

Bone marrow cells were prepared by flushing donor mice femur and tibia bones with Phosphate Buffered Saline (PBS). Recipient mice were lethally irradiated (1000 rads) and reconstituted with  $10 \times 10^6$  bone marrow cells by intravenous injection. Engraftment took place over a six to eight week period. For the thymic experiments I used 2D2 TCR transgenic mice as a basic model and generated three types of bone marrow chimeras.  $2D2^+CD24^{-/-} > CD24^{-/-}$  : bone

marrow cells from  $2D2^+CD24^{-/-}$  mice were injected into irradiated  $CD24^{-/-}$  mice resulting in bone marrow-derived (macrophages, dendritic cells, and T cells) and thymic stroma cells deficient in CD24 expression.  $2D2^+CD24^{-/-} > CD24^{+/+}$ : bone marrow cells from  $2D2^+CD24^{-/-}$  mice were injected into irradiated  $CD24^{+/+}$  resulting in bone marrow-derived cells devoid of CD24 while thymic stroma expressed CD24.  $2D2^+CD24^{+/+} > CD24^{-/-}$ : bone marrow cells from  $2D2^+CD24^{+/+}$  mice were injected into irradiated  $CD24^{-/-}$  resulting in bone marrow-derived cells expressing CD24 while thymic stroma do not. For the CNS experiments we used  $CD24^{-/-}$  mice as our basic model and generated two types of bone marrow chimeras  $WT > CD24^{-/-}$ : bone marrow-derived cells from WT mice were injected into irradiated  $CD24^{-/-}$  mice resulting in bone marrow-derived cells devoid of CD24 while CNS expressed CD24.  $WT > WT$ : bone marrow-derived cells from WT mice were injected into irradiated WT mice resulting in CD24 on both bone marrow-derived cells and the CNS.

### **3.5 Real Time RT-PCR**

Total RNA was isolated from thymi or stroma enriched thymi using the Trizol method (Invitrogen). The first strand cDNA of each sample was synthesized using a reverse transcription kit (Invitrogen). Quantitative real time PCR was performed using an ABI Prism 7900-HT sequence system (PE Applied Biosystems) with the QunatiTect SYBR Green PCR kit (Qiagen) in accordance with the manufacturer's instructions. The following primers were used: mMOG.F: 5'-GCAGCACAGACTGAGAGGAA-3'; mMOG.R: 5'-CAGATGATCAAGGCAACCAG-3';

IL4.F: 5'-TGT ACCAGGAGCCATATCCA-3'; IL4.R: 5'-TTCTTCGTTGCTGTGAGGAC-3';  
IL10.F: 5'-ACAGCCGGGAAGACAATAAC-3'; IL10.R: 5'-CAGCTGGTCCTTTGTTTGAA-  
3'; IL12b.F: 5'-TTGCTGGTGTCTCCACTCAT-3'; IL12b.R: 5'-  
GGGAGTCCAGTCCACCTCTA-3'; IL17.F: 5'-CCTCCAGAATGTGAAGGTCA-3';  
IL17.R:5'-CTATCAGGGTCTTCATTGCG-3'; IFN $\gamma$ .F: 5'-AGCTCTTCCTCATGGCTGTT-3';  
IFN $\gamma$ .R, 5'-TTTGCCAGTTCCTCCAGATA-3'; TNF $\alpha$ .F: 5'-ATGAGAAGTTCCCAAATGGC-  
3'; and TNF $\alpha$ .R: 5'-CTCCACTTGGTGGTTTGCTA-3'; NG2.F: 5'-  
GCTGAGGTAAATGCTGGGA-3'; NG2.R: 5'-GCATCGAAAGACACCATCAC-3'; DCX.F:  
5'-CCTTGGATGAGAATGAATGC-3', DCX.R: 5'-TGAGTCAGCTGGAGACTTGC-3'; P8.F:  
5'-AGACGGAGCTGGAGATAAGG-3', P8.R: 5'-AGGCCTAGGTCCTGCTTACA-3';  
HPRT.F: 5'-AGCCTAAGATGAGCGCAAGT-3'; and HPRT.R: 5'-  
TTACTAGGCAGATGGCCACA-3'. The hypoxanthine-guanine

phosphoribosyltransferase (HPRT) gene was amplified and served as endogenous control. PCR was performed using an optimal condition. 1  $\mu$ l of first strand cDNA product was amplified with platinum Taq polymerase (Invitrogen) and gene-specific primer pairs. Each sample was assayed in triplicate and experiments were repeated twice. The relative amounts of mRNA were calculated by plotting the Ct (cycle number), and average relative expression was determined by the comparative method ( $2^{-\Delta\Delta Ct}$ ).

### **3.6 BrdU Incorporation Assay**

At day 19 after EAE induction, mice were given an interaperitoneal i.p. injection of 1mg of BrdU (BD Pharmingen) . Brains and spinal cords of recipient mice were

harvested 12 hrs later. The CNS-infiltrating monocleular cells were isolated and stained for cell surface makers, followed by intracellular stained with anti-BrdU ab (BD Pharmingen).

### **3.7 Proliferation Assay**

Splenocytes from each strain of TCR transgenic mice (2D2, OTII) with or without CD24 were stimulated with titrated peptide antigens in 96-well U-bottomed plates. In some experiments, we purified CD4 cells from spleen and lymph nodes and stimulated them with peptide antigens and irradiated (2000 rad) syngenic APCs. <sup>3</sup>H-Thymidine was added into the culture at 48 h and harvested 12 h later. <sup>3</sup>H-incorporation was measured with a scintillation counter. The OVA peptide antigen used in the assay (OVA<sub>323-333</sub>) was purchased from Sigma (St. Louis, MO). MOG peptide (MOG<sub>35-55</sub>) (MEVGWYRSPFSRVVHLYRNGK) was purchased from Genemed Synthesis, Inc (South San Francisco, CA).

### **3.8 Purification of 2D2 T cells from 2D2<sup>+</sup>CD24<sup>+/+</sup> or 2D2<sup>+</sup>CD24<sup>-/-</sup> mice**

2D2 T cells were purified by negative selection. Briefly, spleen and lymph node cells from 2D2 TCR transgenic mice were incubated with a cocktail of mAbs (anti-CD8, mAb TIB210, anti-FcR mAb 2.4G2 and anti-CD11c mAb N418). After removing the unbound antibodies, the cells were incubated with anti-Ig coated magnetic beads (DynaL Biotech). A magnet was used to remove the Ab-coated cells. The remaining cells were CD4<sup>+</sup> or CD4<sup>-</sup>CD8<sup>-</sup> T cells. The purified 2D2 T cells were used for the proliferation assay.

### 3.9 Induction and Assessment of EAE

The immunogen, myelin oligodendrocyte glycoprotein (MOG) peptide 35-55 (MEVGWYRSPFSRVVHLYRNGK), was purchased from Genemed Synthesis.

C57BL/6 Mice of 8-12 wks of age were immunized s.c. with 200 µg of MOG peptide in CFA (containing 400 mg of *Mycobacterium tuberculosis*) in a total volume of 100µl. They received 200 ng of pertussis toxin (List Biological Laboratories) in 200 µl of PBS in the tail vein immediately after the immunization and again 48 hr later. 2D2 TCR transgenic mice (8 – 12 weeks of age) of different CD24 genotypes received 200 ng of Pertussis toxin (List Biological, Campbell, CA, USA) in 200 µL PBS in the tail vein at day 0 and again 48 hours later. Adoptive transfer induction of EAE was accomplished by immunizing s.c. 8 – 12 wk C57BL/6j mice with 100 µg of MOG peptide in CFA in a total volume of 100 µl.

Ten days after immunization, draining lymph nodes were harvested and stimulated at a density of  $2 \times 10^6$ /ml in Click's Eagle's Hanks' amino acid medium supplemented with 15% Fetal Calf Serum (FCS), 20 ng /ml rIL-12 and 50 µg/ml MOG peptide for 4 days. MOG-activated lymphoid cells measuring  $30 \times 10^6$  were injected i.p. into each recipient mouse that had been irradiated (350 rad) 1 hr earlier. The mice were observed every day and were scored on a scale from 0 – 5 with graduations of 0.5 for intermediate scores: 0 – no clinical signs; 1 – loss of tail tone; 2 partial paralysis of hind leg; 3 – hind limb paralysis; 4 – moribund; and 5 – death.

### **3.10 Histology**

Mice were sacrificed by inhaling CO<sub>2</sub>. Spinal cords, cerebellum and optical nerves were removed and fixed in 10% formalin/PBS. Paraffin sections were prepared and stained by the histology core facilities of the Department of Pathology (The Ohio State University) for hematoxylin and eosin (H&E) and luxol fast blue (myelin staining). To calculate the extent of spinal cord pathology in mice, an interactive digital analysis system and camera lucida attached to a photomicroscope (Zeiss) were used. The percentages of spinal cord inflammation and demyelination per mouse were calculated by first determining the total white matter area for all spinal cord sections by manually tracing the regions. Next the areas of spinal cord inflammation were determined by manually tracing each of the sections. Pathological changes of each spinal cord were scored as follows: 0 – no changes; 1 – focal area involvement; 2 – less than 5% total myelin area involvement; 3 – 5% to 10% of total myelin area involvement; 4 – 10% to 20% of total myelin area involvement; and 5 – greater than 20% of total myelin area involvement.

### **3.11 Immunofluorescence and Confocal Laser Scanning Microscopy**

The Abs used for immunofluorescence staining of spinal cord sections were the following: biotinylated CD24 (M1/69: BD Pharmingen); Alexa-633-streptavidin (Molecular Probes); FITC-rat anti-mouse CD24 (M1/69: BD Pharmingen); Alexa-488-GFAP (Molecular Probes); Alexa-488-Mouse-anti-neuron Nuclei (Molecular Probes); Alexa-488-IB4 (Molecular Probes); and biotinylated anti-CNPase

(Chemicon International). Spinal cord sections were harvested and frozen in Tissue-Tek OCT medium (Sakura Finetek), and 10  $\mu$ m thick slices were cut. Tissue sections were fixed in 1% paraformaldehyde and were blocked with 10% normal mouse serum for 1 hr at 24°C. Sections were then stained with the corresponding fluorescent Abs for another 2 hr at 24°C. After washing with PBS, slides were mounted with Fluoromount G mounting medium (Southern Biotechnology Associates) and were examined on a confocal laser-scanning microscope (Zeiss 510)

### **3.12 Preparation of Astrocytes from Newborn Mice and Proliferation**

#### **Assay**

Primary glial cell cultures were prepared from brains of newborn Astro<sup>CD24</sup> or CD24<sup>-/-</sup> mice as described previously (15, 87, 88). After removal of the meninges, the brains were dissociated mechanically by nylon sieves. The cells were seeded in Delbecco's Modified Eagle's Medium (DMEM) containing 20% FCS in 75cm<sup>2</sup> tissue culture flasks. On day 4, the medium was replaced with DMEM containing 10% FCS and subsequently changed every 3 days thereafter. The firmly adherent cells were stained with anti-GFAP ab to confirm their identity as astrocytes. To assess the Ag-presenting functions of cultured astrocytes, the purified MOG-specific 2D2 T cells were used as a responder. In brief, irradiated (3000 rad) astrocytes were cultured in round-bottom microtiter plates in 200  $\mu$ l of DMEM containing 10 U/ml IFN $\gamma$ . Three days later, the medium was removed, and 5x10<sup>4</sup> T cells in Click's Eagle's Hanks' amino acid medium and the indicated

concentrations of MOG peptide were added into each well. After 48 hr, the cultures were pulsed with 1  $\mu\text{Ci}/\text{well}$   $^3\text{H}$  for another 12 hr and incorporation for  $^3\text{H}$  was measured in a liquid scintillation beta plate counter.

### **3.13 Statistical Analysis.**

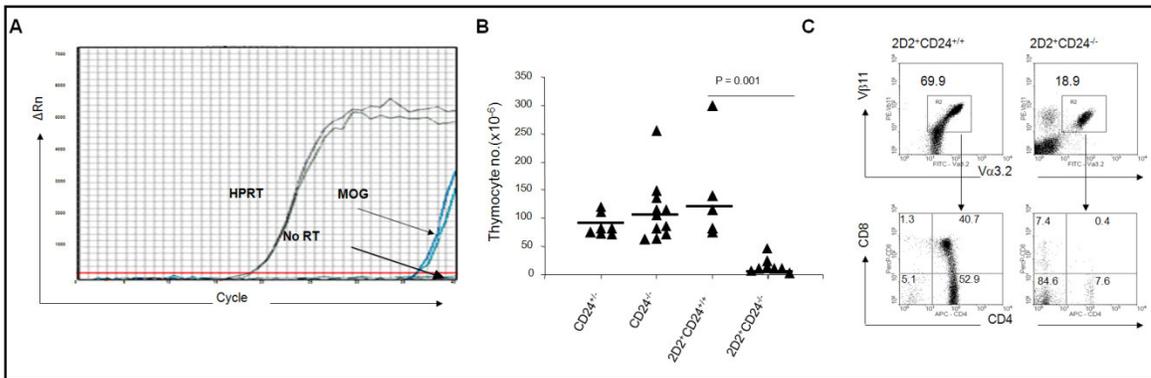
Statistical analysis was conducted using Microsoft Excel 2007 software. Cell quantity comparison was analyzed by the Student's t test. Differences were considered significant at  $P \leq 0.05$ , and P values are shown where applicable.

## CHAPTER 4:

### CD24 AND THYMIC GENERATION OF MYELIN ANTIGEN SPECIFIC T CELLS

#### 4.1 Thymic clonal deletion of MOG-specific T cells in CD24-deficient mice

Kuchroo and colleagues(83) have produced 2D2 TCR transgenic mice, whose TCR recognizes MOG<sub>35-55</sub>, the pathogenic epitope in the C57BL/6 mice. Since MOG specific transgenic T cells developed normally in C57BL/6 mice, and other groups have demonstrated MOG mRNA expression in the thymus (89, 90) or thymic epithelial cells (91), we tested if MOG is ectopically expressed in the thymus of C57BL/6 mice. Significant expression of MOG mRNA was detected in the thymus by real time PCR (**Figure 3A**). Thus, 2D2 T cells have escaped clonal deletion despite expression of MOG in the thymus. Furthermore, the targeted mutation of CD24 caused a massive reduction of thymic cellularity in the 2D2 transgenic mice but not in CD24<sup>+/-</sup> or CD24<sup>-/-</sup> mice without 2D2 TCR transgene (**Figure 3B**). To determine whether the thymus reduction was related to age, we examined young mice (18-20 days after birth) and observed similar thymus size reduction in 2D2<sup>+</sup>CD24<sup>-/-</sup> mice (data not shown). Correspondingly, numbers of  $\alpha\beta$ -positive 2D2 T cells and the CD4<sup>+</sup>CD8<sup>+</sup> and CD4<sup>+</sup>CD8<sup>-</sup> populations were dramatically reduced in the thymi of the 2D2<sup>+</sup>CD24<sup>-/-</sup> mice compared with that of the 2D2<sup>+</sup>CD24<sup>+/+</sup> mice (**Figure 3C**).



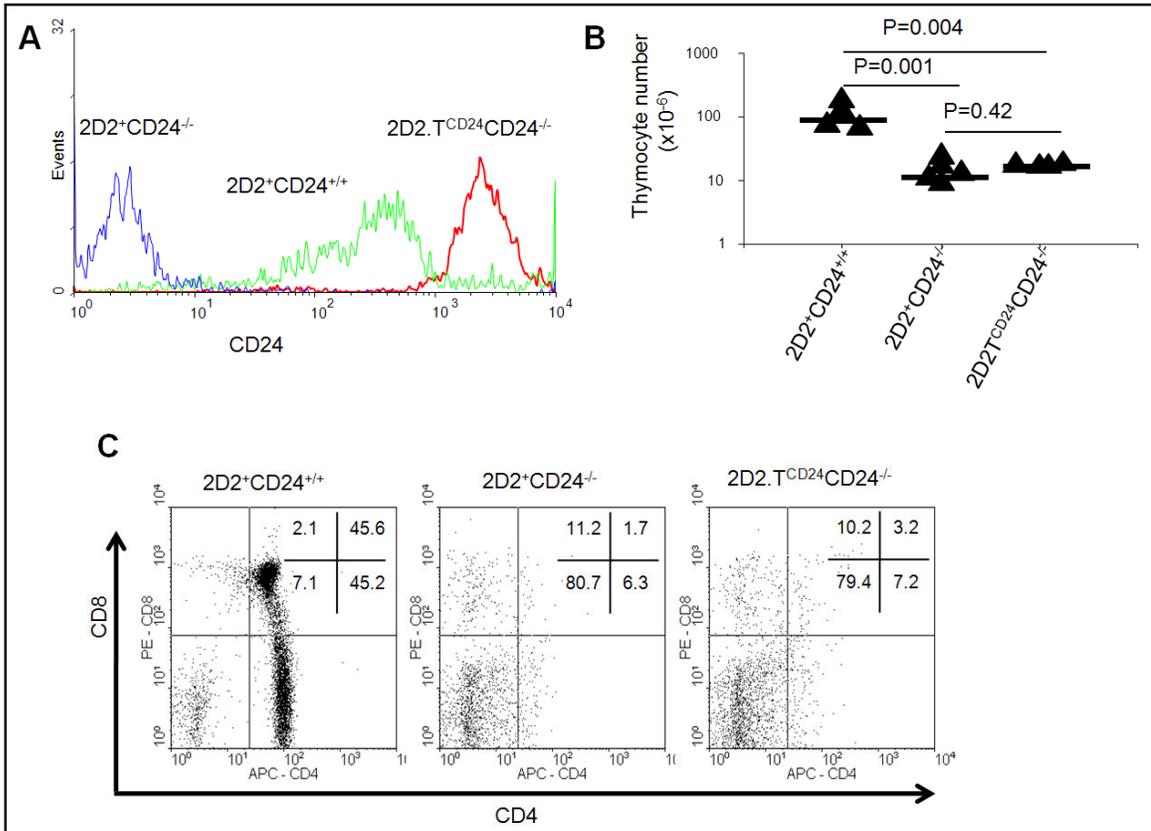
**Figure 3: CD24 inhibits thymic deletion of MOG-specific T cells.**

A) MOG antigen is expressed in the thymi of C57BL6 mice. A standard 40-cycle realtime PCR was used to detect MOG mRNA expression in the thymus. Data shown represent three experiments with similar results. B) Thymocyte cellularity. Each triangle represents the value from a single mouse. Thick lines represent median numbers of each group of mice. Student's t test was used for the comparison. C) Impact of CD24-deficiency on the development of 2D2 TCR transgenic mice. Thymocytes from 2D2<sup>+</sup>CD24<sup>-/-</sup> and 2D2<sup>+</sup>CD24<sup>+/+</sup> mice were stained for V $\alpha$ 3.2, V $\beta$ 11, CD4 and CD8. The thymi from 2D2<sup>+</sup>CD24<sup>-/-</sup> mice had dramatically reduced V $\alpha$ 3.2<sup>+</sup>V $\beta$ 11<sup>+</sup> populations and failed to generate CD4<sup>+</sup>CD8<sup>+</sup> and CD4<sup>+</sup>CD8<sup>-</sup> T cells compared with that of 2D2<sup>+</sup>CD24<sup>+/+</sup> mice. Data represent at least five experiments with similar results.

#### 4.2 Restoration of CD24 on thymocytes is insufficient to rescue clonal deletion of autoreactive T cells; CD24 on radio-resistant thymic stromal cells is necessary

Since the majority of thymocytes expressed high levels of CD24, we tested the possibility that CD24 expressed on thymocytes may be responsible for the enhanced clonal deletion. We generated 2D2<sup>+</sup>CD24<sup>-/-</sup> mice that express CD24 under the control of proximal Ick promoter. The Ick promoter was known to be active in the thymocytes, starting at the DN3 stage (92). Essentially all 2D2 TCR-expressing thymocytes in the CD24 transgenic mice expressed high levels of CD24 (**Figure 4A**). Nevertheless, the thymic cellularity (**Figure 4B**) and the

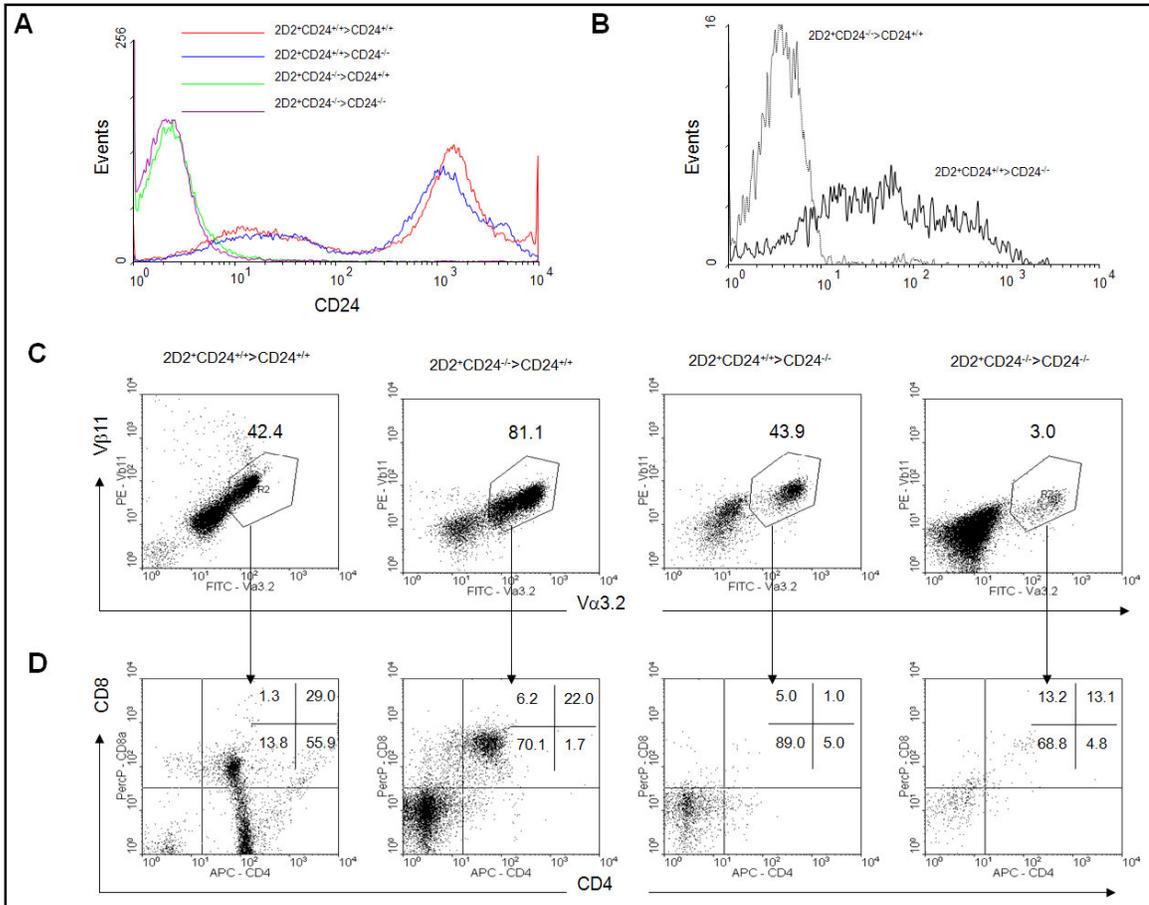
distribution of T cell subsets (**Figure 4C**) were unaffected by CD24 expression in the thymocytes. These results demonstrate that lacking CD24 in the thymocytes is not solely responsible for enhanced clonal deletion.



**Figure 4: Restoration of CD24 on 2D2 T cells in CD24-deficient mice does not prevent its thymic deletion.**

We produced double transgenic mice by breeding 2D2<sup>+</sup>CD24<sup>-/-</sup> mice with T<sup>CD24</sup>CD24<sup>-/-</sup> mice (mice with CD24 expression on T cells only) and produced CD24 deficient mice with CD24 expression on T cells alone (2D2.T<sup>CD24</sup>CD24<sup>-/-</sup> mice). A) Phenotypes of three different mice identified by flow cytometry. Single cell suspensions of thymocytes were stained for CD24 and Vα3.2 markers followed by flow cytometry analysis. Data shown were gated on Vα3.2-positive thymocytes. B) Thymocyte numbers in mice with different genotypes. No significant difference was observed between 2D2<sup>+</sup>CD24<sup>-/-</sup> mice with 2D2.T<sup>CD24</sup>CD24<sup>-/-</sup> mice. C) Thymocytes from 2D2.T<sup>CD24</sup>CD24<sup>-/-</sup> mice show a phenotype similar to that seen in 2D2<sup>+</sup>CD24<sup>-/-</sup> mice.

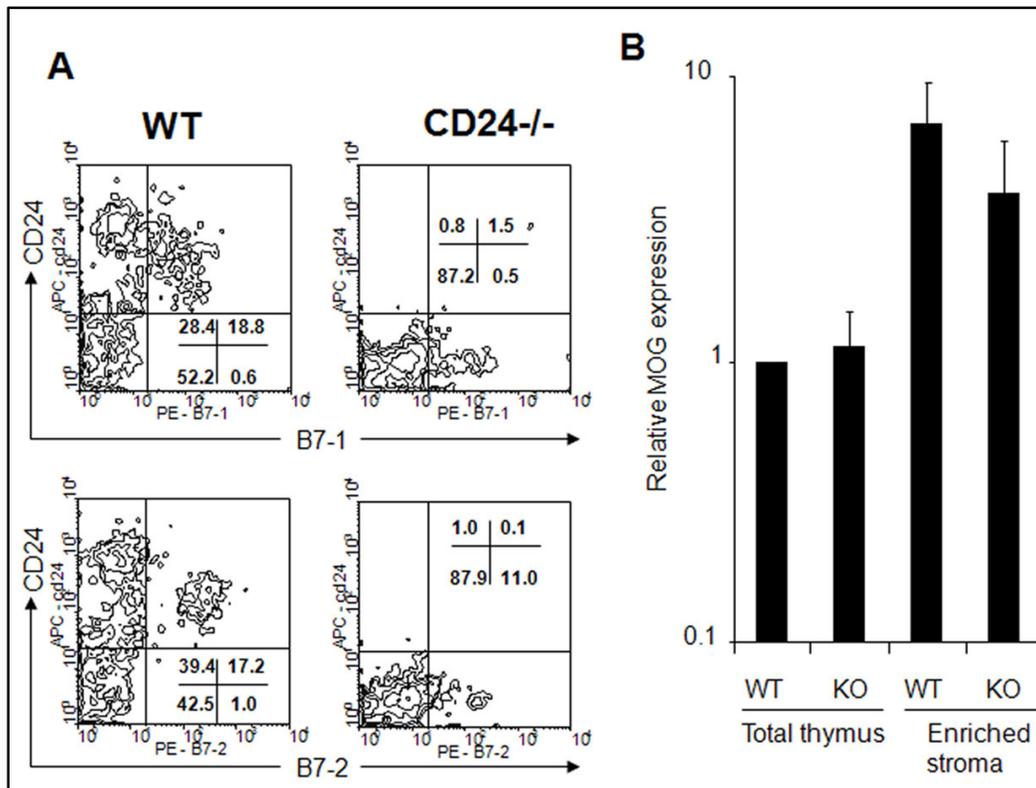
To determine whether CD24 expressed on bone marrow-derived or non-bone marrow-derived stromal cells is responsible for the enhanced clonal deletion, we established chimeras using bone marrow from 2D2<sup>+</sup>CD24<sup>+/+</sup> or 2D2<sup>+</sup>CD24<sup>-/-</sup> mice to reconstitute lethally irradiated WT or CD24-deficient mice. CD24 expression on thymocytes in chimeric mice that received BM from CD24 deficient donors (**Figure 5A** red (2D2<sup>+</sup>CD24<sup>+/+</sup> > CD24<sup>+/+</sup>) and blue (2D2<sup>+</sup>CD24<sup>+/+</sup> > CD24<sup>-/-</sup>) lines) indicates a nearly complete replacement of the hematopoietic compartment in the chimera mice. In spleens of mice, we detected intermediate to high levels of CD24 expression on CD11c<sup>+</sup> cells from 2D2<sup>+</sup>CD24<sup>+/+</sup> > CD24<sup>-/-</sup> chimeras but not on CD11c<sup>+</sup> cells from 2D2<sup>+</sup>CD24<sup>-/-</sup> > CD24<sup>+/+</sup> chimeras (**Figure 5B**). Thus, the chimeric mice can be used to evaluate the contribution of CD24 in clonal deletion of 2D2 T cells. Mature 2D2 T cells (CD4-single positive) were generated in 2D2<sup>+</sup>CD24<sup>+/+</sup> > CD24<sup>+/+</sup> chimeras but not in 2D2<sup>+</sup>CD24<sup>-/-</sup> > CD24<sup>-/-</sup> chimeras (**Figure 5C & D**, left and right panels). CD24 expression on the radio-resistant stromal cells (**Figure 5C & D**, middle left panel), but not on bone marrow-derived cells (**Figure 5C & D**, middle right panel), rescued transgenic TCRαβ<sup>+</sup> cells at the CD4<sup>+</sup>CD8<sup>+</sup> stage; however, since no mature CD4<sup>+</sup> 2D2 T cells were generated (**Figure 5D**, middle left), it is likely that CD24 expression on radio-resistant thymic stromal cells alone is not sufficient for rescuing 2D2 T cell deletion. Thus, these bone marrow chimera data suggest that CD24 expression on radio-resistant stromal cells inhibits deletion of transgenic T cells at the CD4<sup>+</sup>CD8<sup>+</sup> stage.



**Figure 5: CD24 on radio-resistant thymic stromal cells is necessary but not sufficient for the generation of mature CD4 T cells specific for MOG peptide.**

CD24<sup>-/-</sup> and CD24<sup>+/+</sup> mice were lethally irradiated (1000-Rad) and reconstituted with 2D2<sup>+</sup>CD24<sup>-/-</sup> or 2D2<sup>+</sup>CD24<sup>+/+</sup> donor bone marrow cells. A) CD24 expression on the thymocytes from different bone marrow chimeric mice. B) CD24 expression on splenic CD11c<sup>+</sup> cells from different bone marrow chimeras. Splenocytes were digested with collagenase IV, and the resulting mononuclear cells were stained for CD11c and CD24 followed by flow cytometry analysis. Data shown were gated on CD11c-positive cells. C) Generation of 2D2 T cells in the thymi of bone marrow chimeras. Thymocytes were stained for Vα3.2, Vβ11, CD4 and CD8 followed by flow cytometry analysis. D) 2D2 T cell subsets in bone marrow chimeras. Data shown were gated on Vα3.2<sup>+</sup>Vβ11<sup>+</sup> thymocytes. The result shown represents three independent experiments with similar results.

Since thymic epithelial cells (TECs), especially medullary epithelial cells (mTECs), are the major non-hematopoietic cells that are involved in negative selection (91, 93-95), we analyzed expression of CD24 on TECs. More than 50% of CD45-negative thymic stromal cells express CD24 (**Figure 6A**); almost 100% of medullar epithelial cells (B7<sup>+</sup>) express CD24. These data are consistent with a role of CD24 on radio-resistant thymic epithelial cells. To determine whether CD24-deficiency effects expression of MOG antigen in the thymus, we compared MOG mRNA expression in the thymus and enriched thymic stromal cells. Similar levels of MOG-transcripts were detected in WT and CD24-deficient thymi (**Figure 6B**), regardless of whether RNA from whole thymus extract or from enriched stromal cells were compared. As such, the function of CD24 is unlikely through regulation for expression of peripheral antigens in the thymus.

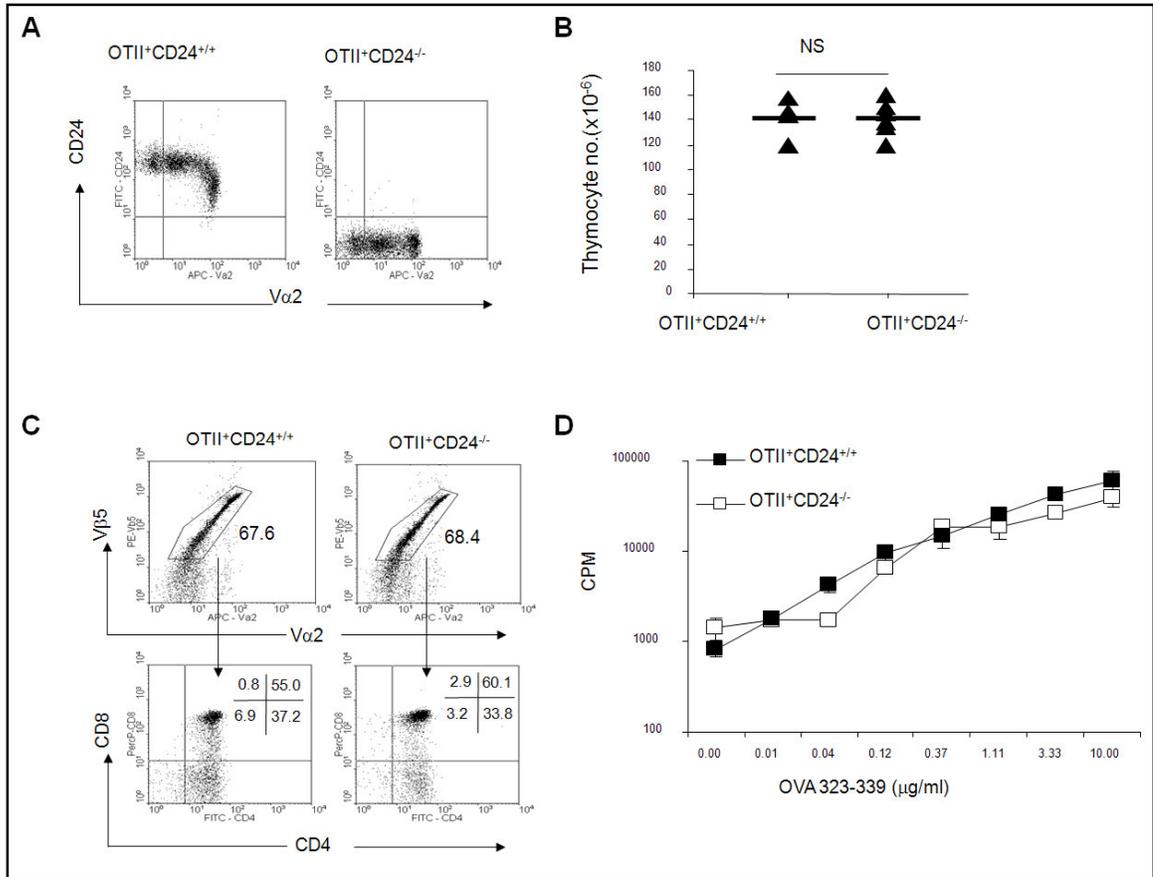


**Figure 6: Expression of CD24 and MOG in thymic stromal cells.**

A) Thymi from CD24<sup>-/-</sup> and CD24<sup>+/+</sup> C57BL6 mice were digested with collagenase, cell suspensions were enriched for stromal cells and were then stained for CD45, CD24 and B7-1 or B7-2 markers. Data shown were gated on CD45<sup>-</sup> cells. B) Real time PCR was used to examine MOG gene expression in total thymocytes and enriched thymic stromal cells. Three experiments were performed with similar results.

### **4.3 CD24-deficiency does not alter development of T cells specific for foreign antigen**

As a comparison to the development of autoreactive transgenic T cells, we also studied development of transgenic T cells specific for ovalbumin (OTII – V $\alpha$ 2 V $\beta$ 5) in WT and CD24-deficient host. The TCR distribution (**Figure 7A**), thymic cellularity (**Figure 7B**) and subset distribution (**Figure 7C**) are similar in OTII<sup>+</sup>CD24<sup>+/+</sup> and OTII<sup>+</sup>CD24<sup>-/-</sup> transgenic mice. Moreover, the OTII T cells in the periphery are fully functional (**Figure 7D**). These results demonstrate that CD24 does not have a general effect on the development of all transgenic T cells. Moreover, since the development of the OTII T cells requires positive selection (96), our data emphasize that the CD24 gene does not regulate positive selection.

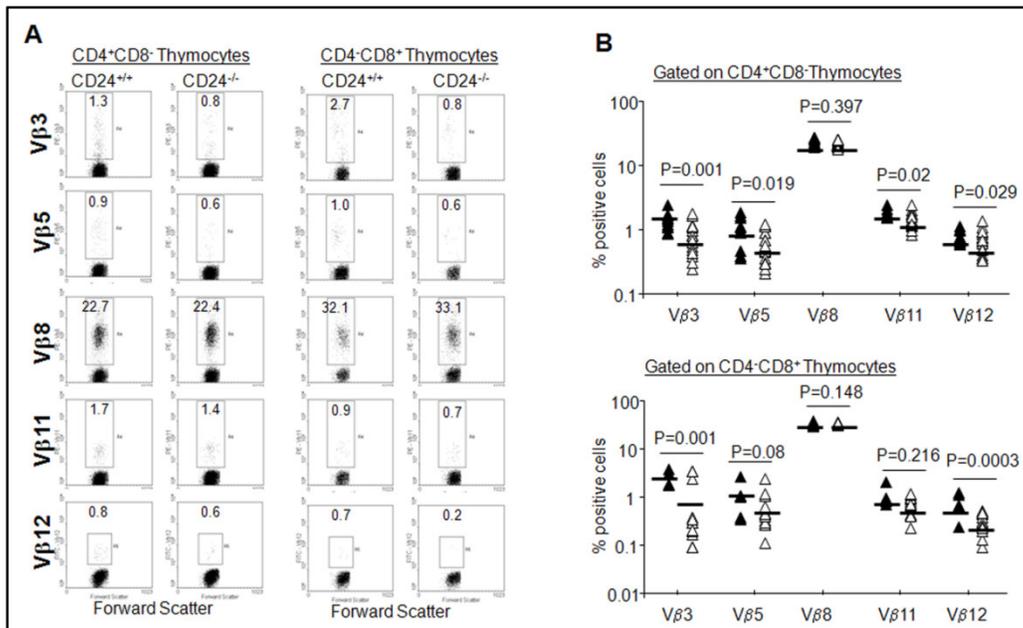


**Figure 7: CD24 expression is not required for the thymic generation of CD4 T cells specific for ovalbumin (OVA).**

OTII TCR transgenic mice were bred with CD24<sup>-/-</sup> mice for two generations. The resulting OTII<sup>+</sup>CD24<sup>-/-</sup> mice were compared with wild type mice for thymocyte development. A) CD24 expression in the thymocytes of OTII TCR transgenic mice with different genotypes. B) Summary of thymocyte numbers in mice of different genotypes. C) Flow cytometry analysis of the thymi of OTII TCR transgenic mice with or without CD24. OTII<sup>+</sup>CD24<sup>+/+</sup> and OTII<sup>+</sup>CD24<sup>-/-</sup> mice revealed similar generation of OTII T cells. D) Splenocytes from OTII<sup>+</sup>CD24<sup>+/+</sup> and OTII<sup>+</sup>CD24<sup>-/-</sup> mice show similar proliferation in response to OVA peptide. Data presented in **A**, **C** and **D** represent five independent experiments with similar results.

#### **4.4 CD24-deficiency increases the efficiency of clonal deletion of viral super antigen (VSA)-reactive T cells in the thymus**

BALB/c mice have integrated mouse mammary tumor provirus types 6, 8, and 9 into their genome and are subject to negative selection. As a result, the majority of T cells expressing V $\beta$ 3, V $\beta$ 5, V $\beta$ 11, and V $\beta$ 12 have been deleted (97, 98). The VSAs react with the variable regions of the TCR  $\beta$  chain (V $\beta$ ). Since T cells expressing any given V $\beta$  can be monitored by flow cytometry, quantitation of the frequencies of these T cells is a useful assay available to evaluate clonal deletion in mice without a transgenic TCR. We therefore generated CD24<sup>-/-</sup> BALB/c mice by five generations of marker-assisted backcross to achieve nearly 100% of the BALB/c genome. The CD24<sup>+/-</sup> BALB/c were intercrossed, and the CD24<sup>+/+</sup> and CD24<sup>-/-</sup> littermates were compared for the V $\beta$ 3, 5, 8, 11 and 12 in order to determine whether CD24-deficiency increased the efficacy of clonal deletion. VSA-reactive T cells among CD4 or CD8 single positive thymocytes from CD24<sup>+/+</sup> or CD24<sup>-/-</sup> BALB/c mice were quantitated (**Figure 8A**). We observed significantly reduced frequencies of V $\beta$ 3, 5, 11 and 12 positive CD4 single positive thymocytes (**Figure 8B**); V $\beta$ 3 and 12 positive CD8 single positive thymocytes were also significantly reduced (**Figure 8B**). These data demonstrate that CD24-deficiency increased the efficiency of clonal deletion of VSA-reactive T cells. Therefore, the function of CD24 is not limited to MOG-specific autoreactive T cells. Furthermore, it is physiologically relevant as they are not an artifact of transgenic  $\alpha\beta$  expression.

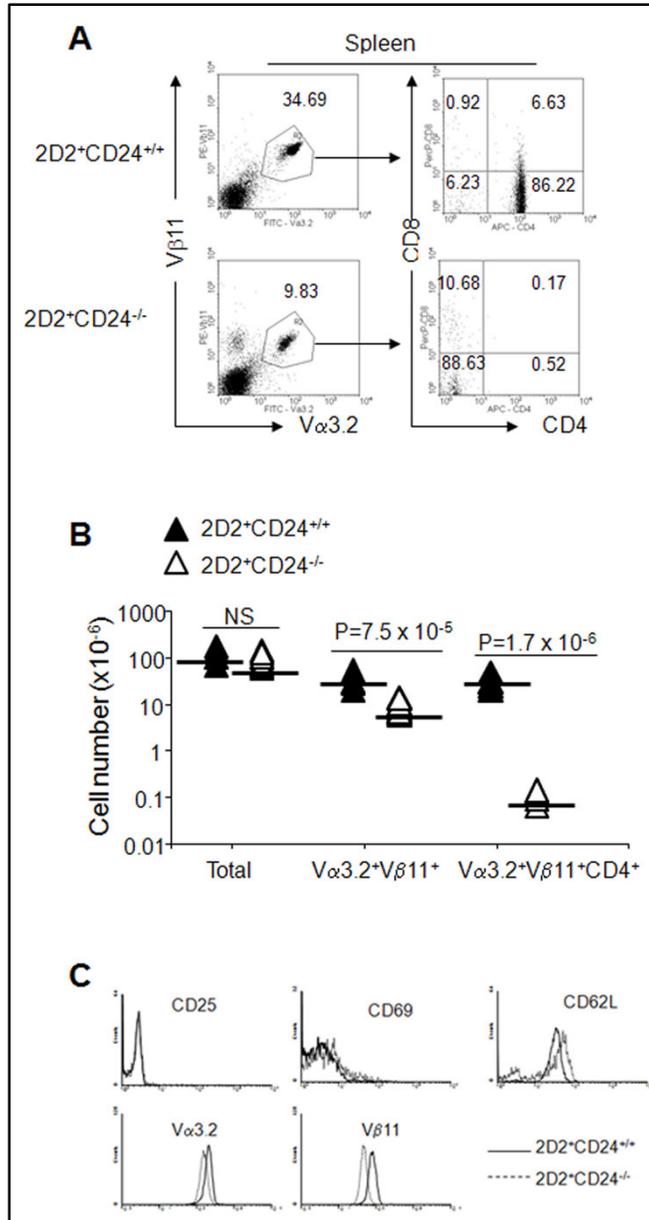


**Figure 8: Frequencies of viral super antigen reactive T cells are reduced in CD24<sup>-/-</sup> BALB/c mice.**

CD24<sup>+/-</sup> BALB/c mice were bred with CD24<sup>+/-</sup> BALB/c mice and CD24<sup>+/+</sup> BALB/c and CD24<sup>-/-</sup> BALB/c mice were generated. Thymocytes from mice (4-5 weeks old) were stained for CD4, CD8 and a single Vβ. Frequencies of each type of Vβ<sup>+</sup> cells (Vβ3, 5, 8, 11, 12) were quantitated. A total of 200,000 cells were harvested for each sample. Student's t test was used for statistical analysis. A) representative flow cytometry profile of CD4<sup>+</sup>CD8<sup>-</sup> and CD4<sup>-</sup>CD8<sup>+</sup> thymocytes from one pair of mice is shown. B) Summary of frequencies of VSAg-reactive CD4<sup>+</sup>CD8<sup>-</sup> and CD4<sup>-</sup>CD8<sup>+</sup> thymocytes. Each triangle represents a number from a single mouse. A closed triangle (▲) represents a number from CD24<sup>+/+</sup> BALB/c mouse; an open triangle (△) represents a number from CD24<sup>-/-</sup> BALB/c mouse. Student's t test was used for the comparison.

#### **4.5 CD24-deficiency nullifies pertussis toxin-induced experimental autoimmune encephalomyelitis**

In order to understand the immunological consequence of CD24-mediated clonal deletion for autoimmune diseases, we compared the function and pathogenicity of 2D2 T cells developed in the presence or absence of CD24 gene. In spleens of 2D2<sup>+</sup>CD24<sup>+/+</sup> mice, the V $\alpha$ 3.2<sup>+</sup>V $\beta$ 11<sup>+</sup> population of cells are mainly CD4<sup>+</sup>, while the V $\alpha$ 3.2<sup>+</sup>V $\beta$ 11<sup>+</sup> cells from 2D2<sup>+</sup>CD24<sup>-/-</sup> mice do not express CD4 (**Figure 9A**), thus, no mature 2D2 T cells (CD4<sup>+</sup>V $\alpha$ 3.2<sup>+</sup>V $\beta$ 11<sup>+</sup>) are present in the spleens of 2D2<sup>+</sup>CD24<sup>-/-</sup> mice (**Figure 9B**). Immunostaining of the V $\alpha$ 3.2<sup>+</sup>V $\beta$ 11<sup>+</sup> T cells from 2D2<sup>+</sup>CD24<sup>-/-</sup> mice suggests that the majority of the transgenic T cells are of a naïve phenotype, as is reflected by high expression of CD62L and low or no expression of CD25 and CD69 (**Figure 9C**). TCR expression levels on 2D2 T cells from 2D2<sup>+</sup>CD24<sup>-/-</sup> mice were down-regulated compared to 2D2 T cells from 2D2<sup>+</sup>CD24<sup>+/+</sup> mice (**Figure 9C**). Thus it is likely that those TCR-positive T cells in the peripheral lymphoid organs of 2D2<sup>+</sup>CD24<sup>-/-</sup> mice were anergic. Functional analysis suggests that splenocytes from 2D2<sup>+</sup>CD24<sup>-/-</sup> mice failed to respond to MOG peptide stimulation whereas splenocytes from 2D2<sup>+</sup>CD24<sup>+/+</sup> mice had a vigorous proliferative response to MOG peptide even at (1.0 – 10  $\mu$ g) (**Figure 10A**). This difference is not attributable to co-stimulatory activity of CD24 on APC as purified T cells from WT and CD24<sup>-/-</sup> 2D2 transgenic mice exhibit the same difference when WT APC were used (**Figure 10B**).



**Figure 9: Phenotype analysis of 2D2 T cells in the peripheral lymphoid organs of mice with or without CD24.**

A) Phenotypes of 2D2 T cells in the peripheral lymphoid organs.

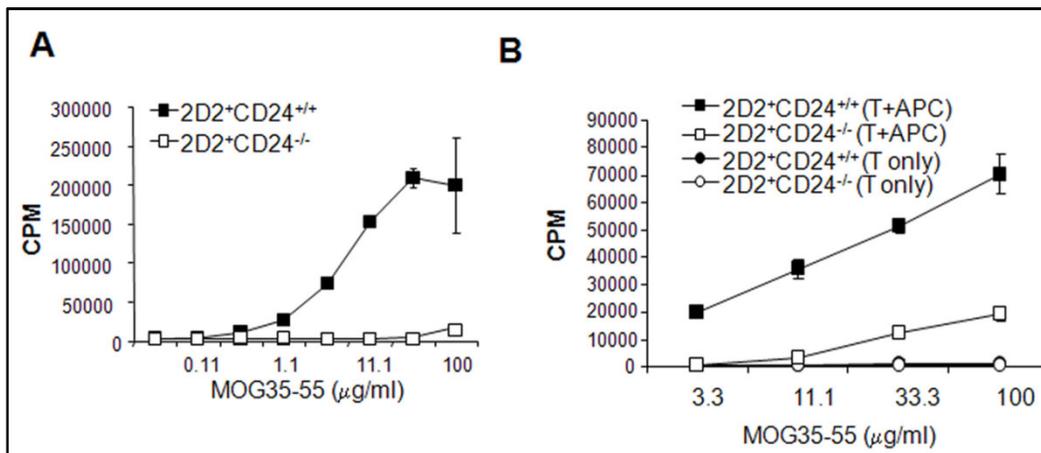
Splenocytes were stained for different cell surface markers and flow cytometry was used to analyze the stained splenocytes. Data represent at least five experiments with similar results. The Vα3.2<sup>+</sup>Vβ11<sup>+</sup> cells in the peripheral lymphoid organs of 2D2<sup>+</sup>CD24<sup>-/-</sup> mice are mainly CD4<sup>-</sup>CD8<sup>-</sup>.

B) The peripheral lymphoid organs (spleen) of 2D2<sup>+</sup>CD24<sup>-/-</sup> mice contain no mature 2D2 (CD4<sup>+</sup>Vα3.2<sup>+</sup>Vβ11<sup>+</sup>) T cells. Significant, but reduced numbers of Vα3.2<sup>+</sup>Vβ11<sup>+</sup> cells were detected in 2D2<sup>+</sup>CD24<sup>-/-</sup> mice. Splenocytes were stained for different cell surface markers and numbers of each subset of

cells were calculated. Each triangle denotes a number from one single mouse. Thick lines represent median numbers. Student's t test was used for statistical analysis. C) Vα3.2<sup>+</sup>Vβ11<sup>+</sup> cells in the peripheral lymphoid organs of 2D2<sup>+</sup>CD24<sup>-/-</sup> mice are of a naïve phenotype with down-regulated TCR expression. Cell suspensions of spleen were stained for Vα3.2, Vβ11 and one of the other cell surface markers. Data shown were gated on Vα3.2<sup>+</sup>Vβ11<sup>+</sup> cells. Three independent experiments were done with similar results.

cells were calculated. Each triangle denotes a number from one single mouse. Thick lines represent median numbers. Student's t test was used for statistical analysis. C) Vα3.2<sup>+</sup>Vβ11<sup>+</sup> cells in the peripheral lymphoid organs of 2D2<sup>+</sup>CD24<sup>-/-</sup> mice are of a naïve phenotype with down-regulated TCR expression. Cell suspensions of spleen were stained for Vα3.2, Vβ11 and one of the other cell surface markers. Data shown were gated on Vα3.2<sup>+</sup>Vβ11<sup>+</sup> cells. Three independent experiments were done with similar results.

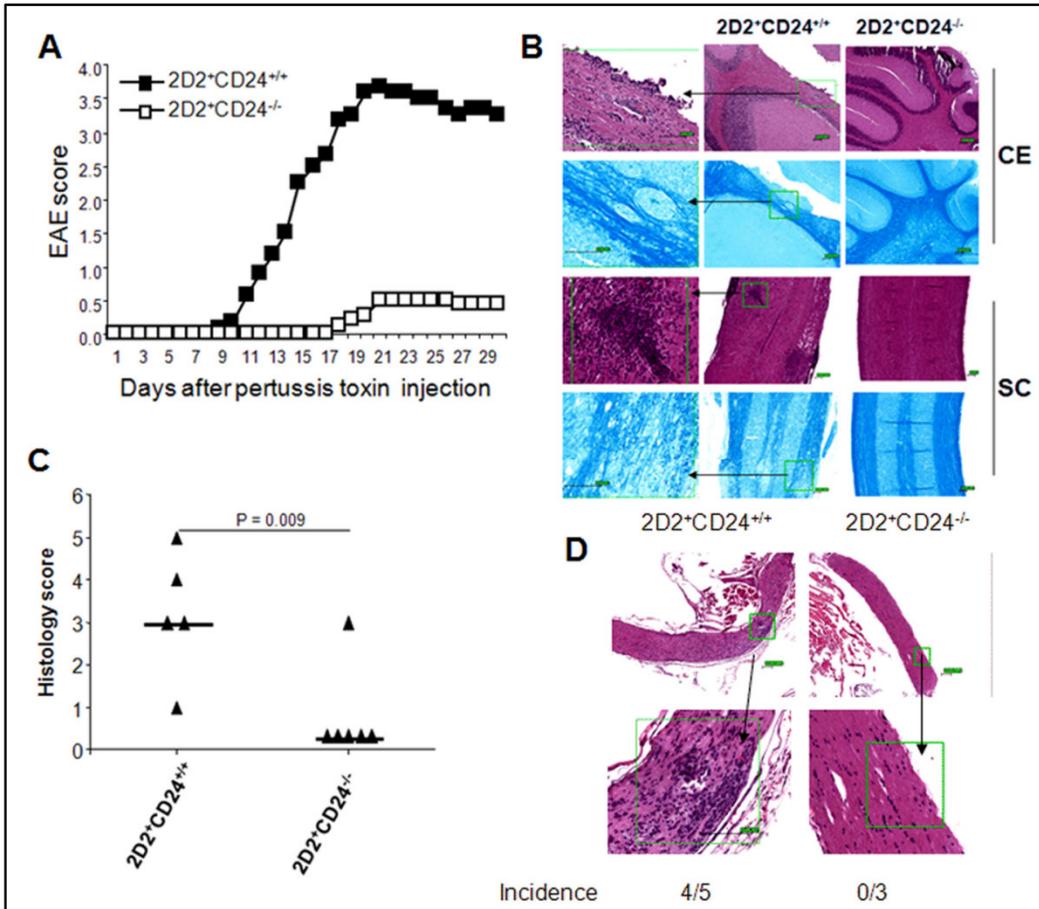
2D2 T cells are encephalitogenic, as the injection of pertussis toxin induces EAE in 2D2 TCR transgenic mice (83). We therefore used this model to determine the immunological consequence of CD24-mediated escape of autoreactive T cells. Two doses of pertussis toxin at day 0 and day 2 induced severe EAE symptoms (Figure 11A) in 7 out of 10 2D2<sup>+</sup>CD24<sup>+/+</sup> mice, with disease onset at about day 10, peaked at about day 18 and persisted over the observation period.



**Figure 10: Vα3.2<sup>+</sup>Vβ11<sup>+</sup> cells in the peripheral lymphoid organs of 2D2<sup>+</sup>CD24<sup>-/-</sup> mice failed to proliferate in response to their cognate peptide antigen**

Splenocytes from mice with different genotypes were cultured in the presence of titrated MOG peptide. <sup>3</sup>H-Tridium assay was used to quantify DNA synthesis in response to MOG peptide stimulation. A) Splenocytes from 2D2<sup>+</sup>CD24<sup>+/+</sup> mice proliferated vigorously to MOG peptide stimulation, while splenocytes from 2D2<sup>+</sup>CD24<sup>-/-</sup> mice failed to respond to MOG peptide. B) Purified 2D2 T cells from 2D2<sup>+</sup>CD24<sup>-/-</sup> mice failed to respond to MOG antigen. 2D2 T cells from 2D2<sup>+</sup>CD24<sup>-/-</sup> and 2D2<sup>+</sup>CD24<sup>+/+</sup> mice were purified from spleens by negative selection using Dynabeads. Equal numbers of purified 2D2 T cells were then used as responders, irradiated splenocytes were used as antigen presenting cells (APC). Since the two lines representing purified T cells only are overlapping, only three lines can be seen in this figure. Data presented in A and B represents three independent experiments with similar results.

In contrast, only 1 out of 10  $2D2^+CD24^{-/-}$  mice that received the same dose of pertussis toxin developed EAE. Histology analysis further revealed that inflammatory cells infiltrated the cerebellum and spinal cords of  $2D2^+CD24^{+/+}$  mice and caused demyelination, while the cerebellum and spinal cords of  $2D2^+CD24^{-/-}$  mice were largely devoid of inflammation and demyelination (**Figure 11B, C**). We also detected severe inflammation in the optic nerves of  $2D2^+CD24^{+/+}$  mice but not in optic nerves of  $2D2^+CD24^{-/-}$  mice (**Figure 11D**). Therefore, CD24-mediated escape of clonal deletion preserved autopathogenic T cells that can potentially cause autoimmune diseases under the condition of inflammatory insults.



**Figure 11: CD24-deficiency prevents EAE in 2D2 TCR transgenic mice.**

We induced EAE in mice with different genotypes by pertussis toxin injection (200 ng i.v. on day 0 and 2). A) 2D2<sup>+</sup>CD24<sup>+/+</sup> mice developed severe EAE while 2D2<sup>+</sup>CD24<sup>-/-</sup> mice show no signs of EAE, with the sole exception of one 2D2<sup>+</sup>CD24<sup>-/-</sup> mouse which became severely disabled later. B) H&E and fast blue stainings of cerebellum and spinal cords revealed severe inflammation and demyelination in 2D2<sup>+</sup>CD24<sup>+/+</sup> but not in 2D2<sup>+</sup>CD24<sup>-/-</sup> mice. Blown up sections are shown to the left. C) Summary of histology scores in each group. The median score for 2D2<sup>+</sup>CD24<sup>+/+</sup> mice was 3.0 and only one 2D2<sup>+</sup>CD24<sup>-/-</sup> mouse reached a score of 3.0. D) H&E staining of the optical nerves revealed 2D2<sup>+</sup>CD24<sup>+/+</sup> but not 2D2<sup>+</sup>CD24<sup>-/-</sup> mice have inflammation in response to pertussis toxin (bottom row shows the blow up images).

**CHAPTER 5:**

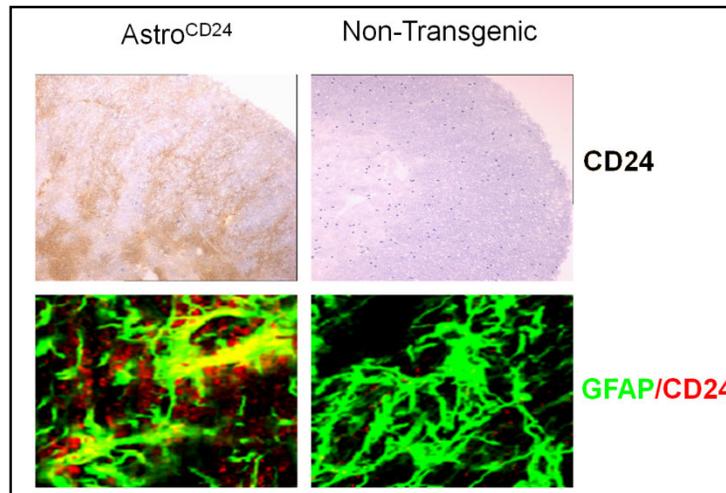
**CD24 ON THE CENTRAL NERVOUS SYSTEM ANTIGEN PRESENTING  
CELLS ENHANCES EFFECTOR FUNCTION OF MYELIN ANTIGEN SPECIFIC T  
CELLS.**

**5.1 Over-expression of CD24 in the CNS enhances EAE progression**

Studies from our lab have shown that CD24<sup>-/-</sup> mice are resistant to T cell adoptive transfer-induced EAE (15). Bone marrow chimeric mice in which CD24 deficient recipients received WT donor cells (WT > CD24<sup>-/-</sup>) become sensitive to the induction of adoptive transfer EAE, although the disease severity is significantly reduced compared to WT > WT chimeras. Both WT > CD24<sup>-/-</sup> and WT > WT chimeras developed EAE around day 10 after T cell transfer. The lower severity in WT > CD24<sup>-/-</sup> mice suggests that CD24 on the CNS parenchymal cells contributes to EAE development.

To understand how CD24 on the CNS cells contributes to EAE development, we have produced CD24-transgenic mice in which CD24 transgene expression is under the control of the GFAP promoter (Astro<sup>CD24</sup>). See Materials and Methods chapter for transgene construct information. We obtained a strain of mice with abundant expression of CD24 in the CNS (**Figure 12**), in contrast to the CNS of non-transgenic mice. CD24 expression colocalized with astrocytes (GFAP<sup>+</sup>), but

not with other CNS cells such as neurons (NeuN<sup>+</sup>), microglia (IB4<sup>+</sup>), nor oligodendrocytes (CNPase<sup>+</sup>) (data not shown).



**Figure 12: Production of Astro<sup>CD24</sup> mice**

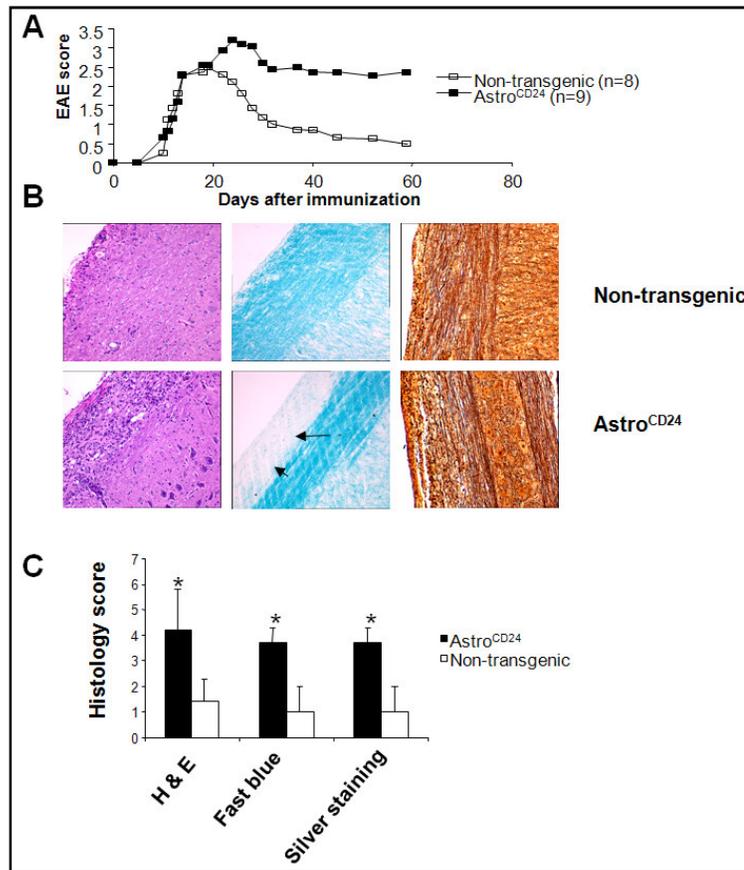
The transgenic vector contained a 2.2-kb human GFAP promoter, 1.8-kb cDNA, for mouse CD24 and a fragment of the mouse protamine-1 gene that supplies an intron to stabilize 3'-UTR and a polyadenylation signal. The DNA used for microinjection of fertilized eggs from C57BL/6 mice is a 4.6-kb fragment. Confocal microscopy verified expression of CD24 in the spinal cords of Astro<sup>CD24</sup> mice but not in non-transgenic WT mice. The Abs used for CD24 immunohistochemistry were biotinylated CD24 (M1/69; BD Pharmingen), followed by HRP-streptavidin (BD Pharmingen), and color was developed by using 3, 3'-diaminobenzidine as substrate. For confocal analysis, biotinylated CD24 and Alexa-633-streptavidin (Molecular Probes) were used to label CD24, and Alexa-488-GFAP (Molecular Probes) were used to label astrocytes. Spinal cord tissue sections (10 μm) were analyzed.

We induced EAE in Astro<sup>CD24</sup> and non-transgenic littermates with MOG<sub>35-55</sub> peptide and PTx. Disease symptoms were evident in both groups of mice within 2 weeks post immunization with MOG peptide and pertussis toxin peaking between days 17 and 25. Recover from paralysis after day 20 occurred in both groups of mice, however Astro<sup>CD24</sup> mice did not recover as well, as paralysis in

Astro<sup>CD24</sup> mice persisted throughout the observation period (**Figure 13A**). The mean accumulating scores and mean maximal scores were significantly different between these two groups ( $p < 0.05$ ), while other parameters such as mean onset days and incidences were not (data not shown). Thus, Astro<sup>CD24</sup> mice had enhanced EAE progression. Inflammatory lesions could be detected in all spinal cord histological sections in both groups of mice on day 50 (**Figure 13B**).

Inflammatory infiltration crossing the gray matter of the spinal cord was detected in Astro<sup>CD24</sup> mice (**Figure 13B – Bottom Left**), but in non-transgenic mice, infiltrates were located in proximity to meninges (**Figure 13B – Top Left**) and sometimes non-detectable in spinal cords. Large areas of demyelination could be detected in the spinal cords of Astro<sup>CD24</sup> mice (**Figure 13B – Bottom Middle**), whereas only little or focal demyelination was detected in the spinal cords of non-transgenic mice (**Figure 13B – Top Middle**). Axonal staining of the spinal cord sections suggested that broad areas of axonal damage were present in Astro<sup>CD24</sup> mice (**Figure 13B – Bottom Right**), while non-transgenic mice usually show axonal damage limited to the submeninges area(**Figure 13B – Top Right**).

Quantitation of inflammation, demyelination, and axonal degeneration areas revealed significant differences between AstroCD24 and non-transgenic (**Figure 13C**). Thus, Astro<sup>CD24</sup> mice suffered enhanced EAE progression with broad demyelination and axonal damage.



**Figure 13: Astro<sup>CD24</sup> mice had enhanced EAE progression**

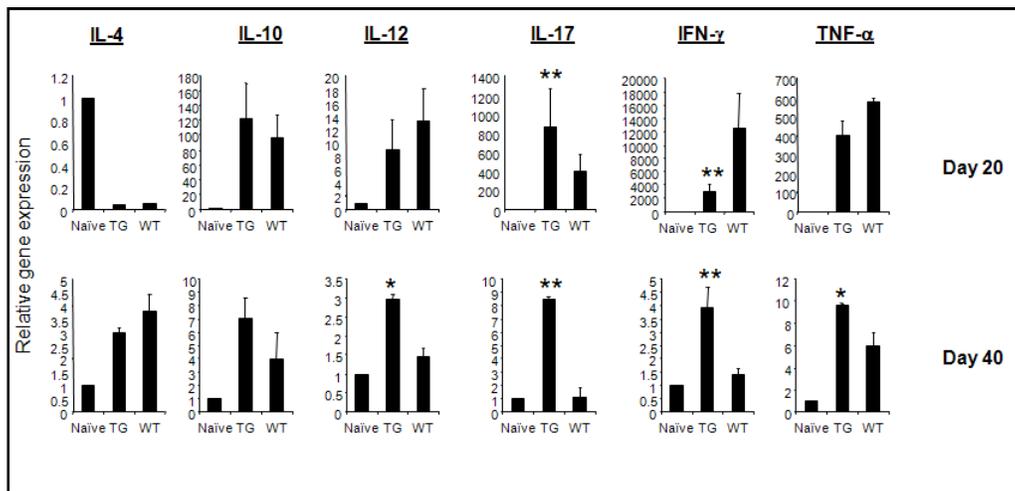
A) Astro<sup>CD24</sup> mice and their nontransgenic littermates were immunized with MOG peptide and pertussis toxin. EAE signs were scored every 2–3 days. B) Histology of spinal cords from Astro<sup>CD24</sup> mice and controls. At day 50, after EAE induction, mice were sacrificed, spinal cords were fixed in formalin, and tissues were processed for H&E (left panel), Luxol fast blue (middle panel), and Biechowsky silver stainings (right panel). Original photographs were taken at x200. C) Seminal quantitative summary of inflammation, demyelination, and axonal damage. To calculate the extent of spinal cord pathology in mice, an interactive digital analysis system and camera lucida attached to a photomicroscope (Zeiss) were used. The percentages of spinal cord inflammation, demyelination, and axonal damage per mouse were calculated by first determining the total white matter area for all spinal cord sections and by manually tracing the regions. Next, the areas of spinal cord inflammation, demyelination, and axonal damage were determined by manually tracing each of the sections. Pathological changes of each spinal cord were scored as follows: 0, no changes; 1, focal area involvement; 2, <5% of total myelin area involvement; 3, 5–10% of total myelin area involvement; 4, 10–20% of total myelin area involvement; and 5, >20% of total myelin area involvement. Inflammation was evaluated on H&E slides, TG = 5, NTG = 6; demyelination was evaluated on myelin-stained slides,  $n = 3$  for both groups; axonal damage was evaluated on silver-stained slides,  $n = 3$  for both groups. \*,  $p < 0.05$ . Mann-Whitney  $U$  test was used for the comparison.

## **5.2 Enhanced EAE progression in Astro<sup>CD24</sup> mice is associated with increased expression of pro-inflammatory cytokines in the CNS.**

To evaluate if CD24 over-expression by astrocytes results in a T cell population more optimally primed for damaging effects, we measured cytokine gene expressions at day 20 (peak of EAE), and day 40 (EAE recovery) by using real-time PCR (RT-PCR). On day 20, the spinal cords of Astro<sup>CD24</sup> mice had increases in the expression of IL17 ( $p < 0.01$ ) and decrease in the expression of IFN $\gamma$  genes ( $p < 0.01$ ) (**Figure 14**). On day 40, the spinal cords of Astro<sup>CD24</sup> mice IL17 and IFN $\gamma$  continued to be elevated ( $p < 0.01$ ), while IL12, and TNF $\alpha$  also become elevated compared to WT ( $p < 0.05$ ).

Enhanced EAE signs and myelin/axonal damage in Astro<sup>CD24</sup> mice may be a result of a more aggressive T cell population during EAE development. We compared expression of cytokine genes in the spinal cords of Astro<sup>CD24</sup> mice with non-transgenic mice at day 20 (peak of EAE) and day 40 (EAE recovery) by using realtime PCR (RT-PCR). On day 20 (**Figure 14** Top Row), dramatic up-regulation of cytokine genes, including IL-10, IL-12, IL-17, IFN- $\gamma$ , and TNF- $\alpha$ , but not IL-4, were detected in both groups of mice (**Figure 14**). IL-17 was significantly increased in the spinal cords of Astro<sup>CD24</sup> mice ( $p < 0.01$ ) compared to non-transgenic mice. Additionally IFN- $\gamma$  significantly reduced in Astro<sup>CD24</sup> mice ( $p < 0.01$ ) compared to non-transgenic mice. No significant differences were detected among other cytokine genes between Astro<sup>CD24</sup> and non-transgenic mice. On day 40 (**Figure 14** Bottom Row) after EAE induction, the majority of

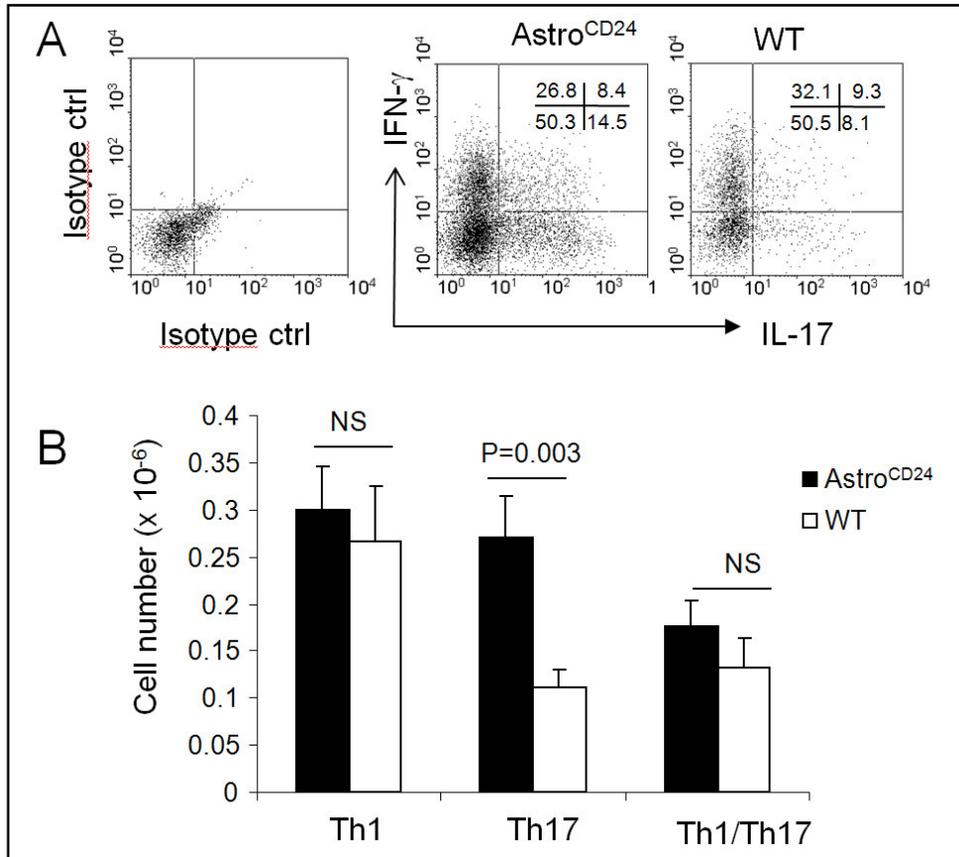
cytokine genes measured was dramatically lower compared with day 20 in both groups of mice; however, the expression of IL-12, IL-17, IFN- $\gamma$ , and TNF- $\alpha$  was still significantly higher in the spinal cords of Astro<sup>CD24</sup> mice in comparison with non-transgenic mice. Up-regulation of IL-10 and IL-4 genes was also observed in both groups of mice on day 40, but no significant differences were observed between Astro<sup>CD24</sup> and non-transgenic mice.



**Figure 14: Assessment of cytokine gene expression in the spinal cords of Astro<sup>CD24</sup> mice and controls by real-time PCR**

We first induced EAE in Astro<sup>CD24</sup> (TG) mice and their WT littermates by active immunization. On days 20 (peak of EAE) and 40 (recovery of EAE), we sacrificed mice, and total RNA was prepared from diseased mice and naive C57BL/6 mice. Real-time PCR was used to quantify cytokine gene expression. The HPRT gene was amplified and served as endogenous control. Each sample was assayed in triplicate, and experiments were repeated twice. The relative amounts of mRNA were calculated by plotting the Ct (cycle number), the average relative expression was determined by the comparative method ( $2^{-\Delta\Delta Ct}$ ), and cytokine gene expression in naive spinal cord was set as 1. Three mice per group were used and data were expressed as mean  $\pm$  SD. (\*\* P < 0.01, \* P < 0.05)

The most recent research in EAE pathogenesis has revealed that IL-17-producing T cells, but not IFN- $\gamma$  producing T cells, are linked with pathogenicity in the CNS (32, 99). Moreover, the development of Th17 cells is negatively regulated by Th1 cells (99, 100). Therefore, we directly quantitated Th1 vs Th17 cells in the CNS of Astro<sup>CD24</sup> mice and non-transgenic mice induced with EAE. On day 20, the CNS of Astro<sup>CD24</sup> mice had more Th17 cells than the CNS of non-transgenic mice. However, there was no statistical difference in Th1 cell numbers between the two groups (**Figure 15**). Thus, the intracellular cytokine-staining data correlated with real-time PCR data and suggested that over-expression of CD24 in the CNS increased Th17 but not Th1 responses. We also detected similar numbers of IFN- $\gamma$ /IL17 double-positive cells in the spinal cords of both groups of mice. IFN- $\gamma$ /IL17 double-positive cells have been detected by other groups in the spinal cords of EAE mice (101, 102); the significance of these cells remains unclear.



**Figure 15: Th1 and Th17 cells in the spinal cords of Astro<sup>CD24</sup> mice**  
 EAE was induced in Astro<sup>CD24</sup> and control mice by active immunization. On day 20 after immunization, we sacrificed mice and perfused mice with PBS (pH 7.4), and we then isolated the CNS-infiltrating cells from the brain and spinal cord of each mouse. Cells were incubated with PMA and ionomycin for 5 h. During the last 2 h of culture, Golgi<sup>Stop</sup> (BD Pharmingen) was added into the cell culture. Cells were first stained for CD4 followed by intracellular cytokine staining. We performed intracellular staining for cytokines by using a kit from BD Pharmingen. The following Abs were used for the staining: anti-CD4 FITC (GK1.4; BD Pharmingen), anti-IFN- $\gamma$  allophycocyanin (XMG1.2; BD Pharmingen), anti-IL-17 PE (TC11-18H10; BD Pharmingen), and rat IgG1 isotype control PE or allophycocyanin (BD Pharmingen). Cells were analyzed on a FACSCalibur flow cytometer. A) Example of intracellular cytokine staining. B) Quantitation of Th1, Th17, and Th1/Th17 cells among total CD4 cells. Student's *t* test was used for the statistical analysis. Four mice per group were quantitated. Data are representative of at least three experiments with similar results.

### 5.3 Over-expression of CD24 enhances local T cell proliferation in the CNS

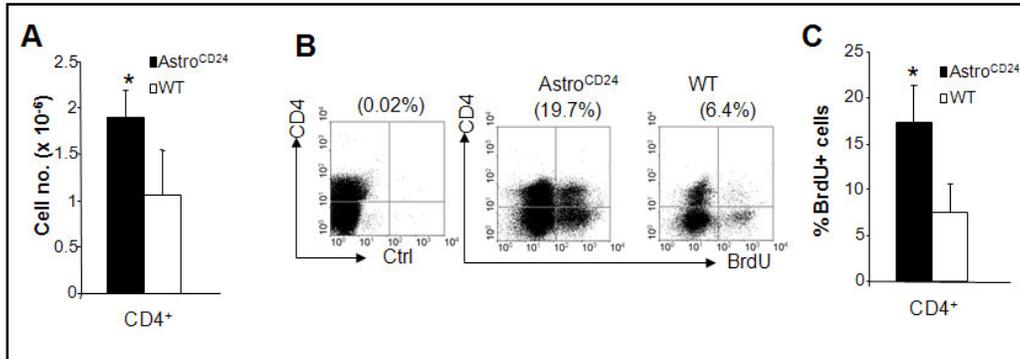
To determine if CD24 over-expression in the CNS enhances T cell proliferation, thereby increasing EAE severity, we quantitated total CD4<sup>+</sup> T cell numbers in the CNS of Astro<sup>CD24</sup> mice vs. non-transgenic mice at day 20 after of EAE induction.

We injected 1 mg of BrdU i.p. into each mouse and twelve hours later evaluated CD4<sup>+</sup> T cells in the CNS of Astro<sup>CD24</sup> and WT mice. We detected significantly increased numbers of CD4<sup>+</sup> T cells in the CNS of Astro<sup>CD24</sup> mice compared to non-transgenic mice (**Figure 16A**). The CD4<sup>+</sup> T cells in the CNS of Astro<sup>CD24</sup> mice were proliferating more vigorously (19.7% BrdU<sup>+</sup>) than in non-transgenic mice (6.4% BrdU) (**Figure 16B&C**).

To evaluate the hypothesis that CD24 expression on astrocytes is sufficient to support proliferation of T cells, we bred Astro<sup>CD24</sup> mice with CD24-deficient mice to produce Astro<sup>CD24</sup>CD24<sup>-/-</sup> mice in which CD24 is over expressed on astrocytes, but absent on all other cells. We cultured astrocytes from Astro<sup>CD24</sup>CD24<sup>-/-</sup> and CD24<sup>-/-</sup> newborn (day 2) mice, and stimulated them with IFN $\gamma$  (100 U/ml) for 72 hours. We then performed a proliferation assay with MOG peptide and purified 2D2 TCR transgenic T cells to evaluate the proliferation potential of CD24 on astrocytes. After 5 days, Astro<sup>CD24</sup>CD24<sup>-/-</sup> astrocytes were observed to support proliferation of 2D2 T cells (**Figure 17A**), while CD24<sup>-/-</sup> astrocytes did not support 2D2 T cell proliferation. Furthermore the proliferation of 2D2 T cells by

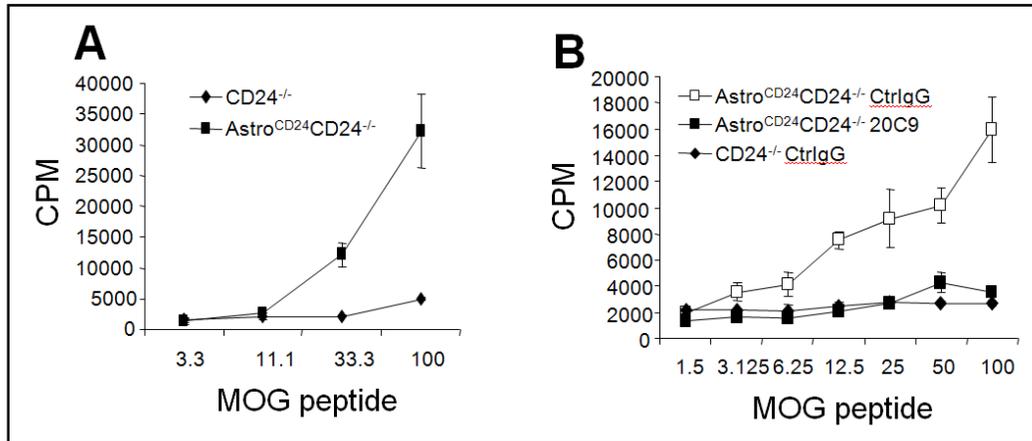
Astro<sup>CD24</sup>/CD24<sup>-/-</sup> astrocytes can be blocked by a CD24 specific antibody (20C9)

(15) (Figure 17B).



**Figure 16: Over-expression of CD24 in the CNS enhances CD4 T cell proliferation in the CNS**

A) Quantitation of total CD4<sup>+</sup> T cells in the CNS of mice with EAE. EAE was induced in Astro<sup>CD24</sup> and control mice by active immunization. On day 20 after immunization, we sacrificed mice and perfused mice with PBS (pH 7.4). We then isolated the CNS-infiltrating cells from the brain and spinal cord of each mouse. Cells were stained for CD4 marker, and total CD4<sup>+</sup> T cells were quantitated by flow cytometry. Data were expressed as mean  $\pm$  SD, with five mice per group being used. \*,  $p < 0.05$ , Student's  $t$  test was used. B) Analysis of BrdU incorporation in the CNS infiltrating cells. On day 19, we injected 1 mg of BrdU (BD Pharmingen) i.p. into each mouse. Twelve hours later, we sacrificed mice and isolated CNS-infiltrating cells from each mouse. We performed BrdU staining by using a kit from BD Pharmingen. C) Quantitation of BrdU incorporation in CD4<sup>+</sup> T cells. Data were expressed as mean  $\pm$  SD,  $n = 5$ /group. \*,  $p < 0.05$ , Student's  $t$  test was used.



**Figure 17: Transgenic expression of CD24 in CD24-deficient astrocytes promotes their co-stimulatory activity to MOG-specific T cells**

We have bred Astro<sup>CD24</sup> mice with CD24<sup>-/-</sup> mice and generated mice with CD24 expression only on astrocytes (Astro<sup>CD24</sup>CD24<sup>-/-</sup>). Astrocytes were generated from newborn (day 2) mice with CD24<sup>-/-</sup> or Astro<sup>CD24</sup>CD24<sup>-/-</sup> genotypes. A) Astrocytes from CD24<sup>-/-</sup> and Astro<sup>CD24</sup>CD24<sup>-/-</sup> mice were tested for their ability to stimulate MOG specific 2D2 T cells to proliferate in the presence of MOG peptide ([<sup>3</sup>H] thymidine incorporation assay). Data shown were after 5 days co-culture and represents four experiments with similar results. B) Anti-CD24 Ab 20C9 blocked the stimulatory effects of Astro<sup>CD24</sup>CD24<sup>-/-</sup> astrocytes. 20C9 Ab or control IgG (10 µg/ml) was used in the culture.

## **CHAPTER 6:**

### **CONCLUSIONS AND DISCUSSION**

#### **6.1 CD24 controls thymic generation of self reactive T cells**

We have demonstrated that CD24 actively inhibits clonal deletion of autoreactive T cells, as CD24 deficient mice exhibit enhanced clonal deletion. The phenomenon of enhanced deletion is observed in transgenic T cells specific for MOG as well as in polyclonal T cells specific for VSAs. These data establish that CD24 mediated active mechanisms exist to enable the selection of autoreactive T cells, and rescuing them from negative selection. The biological benefits of CD24 mediated inhibition of thymic negative selection are unclear. It is conceivable, that CD24-mediated protection of self-reactive T cells may be required for the immune system to preserve anti-tumor immunity, since the majority of tumor antigens are self antigens.

#### **6.2 The cellular basis of CD24 inhibition of negative selection**

Recent studies demonstrate that both DP and SP thymocytes are targets of negative selection (93, 94, 103, 104). mTECs can synthesize peripheral antigens and present them on MHC class II molecules thereby playing a central role in negative selection. In addition to mTECs, dendritic cells can import peripheral antigens to the thymus and present the self antigens to the immature thymocytes (105-108). Our results demonstrate the importance of TECs in

rescuing DP thymocytes, however CD4 SP thymocytes are not rescued in bone marrow chimeric mice with CD24 expression only TECs (**Figure 5**). So CD24 on dendritic cells may also provide a signal inhibiting clonal deletion, but further experiments are required to support this hypothesis.

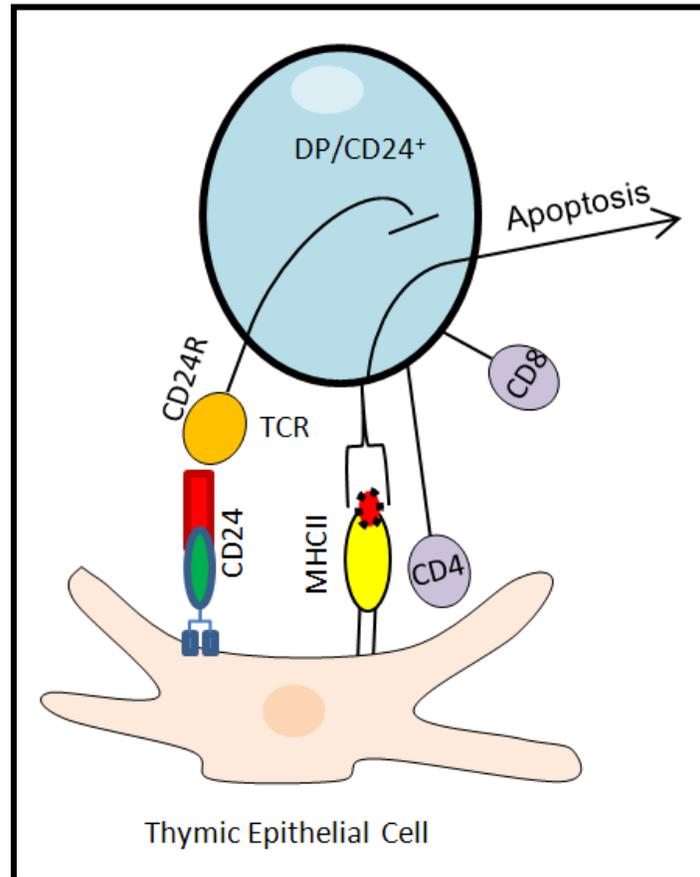
### **6.3 Signal pathway of CD24 action in the thymus**

The molecule mechanisms of how CD24 inhibits negative selection remains to be determined. Increased understanding of the signaling pathways that regulate negative selection has recently been achieved (109). c-Jun NH2-terminal kinase (JNK) is activated in DP thymocytes *in vivo* in response to signals that initiate negative selection (110). Studies have revealed that the JNK pathway is required for the deletion of DP thymocytes by apoptosis in response to TCR-derived signals (110-112). JNK is a signaling molecule downstream of kinase MINK and upstream of pro-apoptotic molecule Bim (109, 113). All three molecules have been shown to be critically involved in promoting negative selection (110, 114, 115), thus, it is interesting to determine if CD24 directly affects activation/induction of JNK/Bim signaling pathways during negative selection.

### **6.4 A hypothetical model of CD24 action in the thymic generation of autoreactive T cells**

We suggest a model (**Figure 18**) that CD24 provides a survival signal blocking apoptosis and allowing immature thymocytes differentiation and progression into mature SP T cells. A default pathway of apoptosis exists for T cells that engage their TCR with a self peptide. CD24 on APCs will interact with CD24

ligand on T cells providing an inhibitory signal to the apoptotic pathways. In the absence of CD24 signaling, DP T cells that interact with self antigen will be eliminated leaving only immature T cells to populate the periphery.



**Figure 18: CD24 expression on Thymic Epithelial Cells Provides a Signal to Developing T Cells Inhibiting Apoptosis.**

MHC II presentation of self autoantigens by TECs engages TCRs on naïve Thymocytes inducing a default pathway of apoptosis. Co-stimulation by CD24 on TECs with CD24R (unknown ligand) on naïve thymocytes provides an inhibitory signal blocking apoptosis.

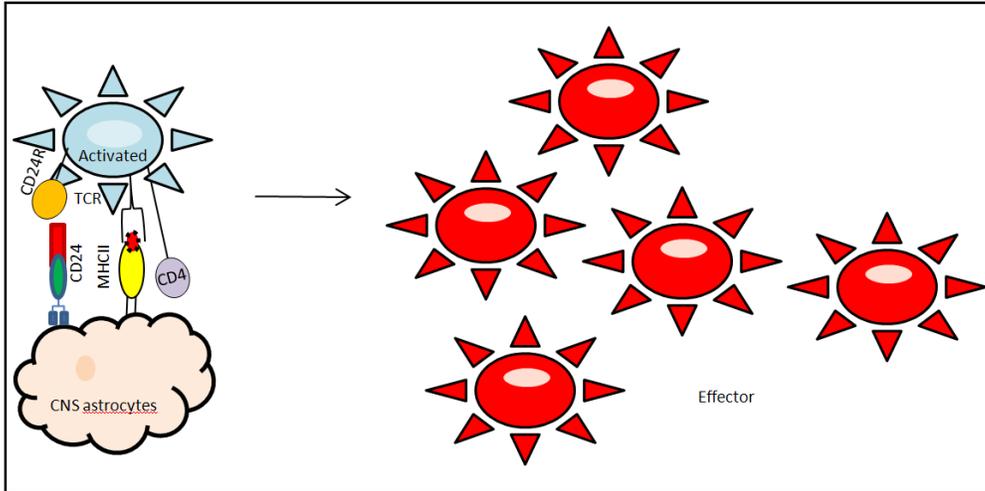
### 6.5 The role of CD24 in the CNS in EAE development

We have tested the hypothesis that abundant CD24 in the CNS co-stimulates myelin antigen specific T cells and promotes their effector function. Several lines of evidence support this hypothesis. Over-expression of CD24 on astrocytes

enhanced the progression of EAE (**Figure 13**). The Enhanced EAE progression was associated with higher expression of cytokine genes such as IL-17 in the spinal cords of Astro<sup>CD24</sup> mice compared with nontransgenic mice. The CNS of Astro<sup>CD24</sup> mice accumulated higher numbers of total CD4<sup>+</sup> T cells and Th17 cells compared with non transgenic mice. Moreover, BrdU incorporation assay revealed that CD4<sup>+</sup> T cells from the CNS of Astro<sup>CD24</sup> mice underwent more proliferation compared with that of non transgenic mice. We also showed that transgenic expression of CD24 in CD24- deficient astrocytes significantly enhanced their co-stimulatory activity to MOG-specific, TCR-transgenic 2D2 T cells *in vitro*. CD24 is not required for the differentiation of Th17 in peripheral lymphoid organs (unpublished data), however it is not clear if CD24 co-stimulation directly causes CD4<sup>+</sup> T cells to differentiate into Th17 cells in the CNS. Further studies are required to clarify this issue.

### **6.6 A hypothetical model of CD24 action in the CNS during EAE development**

We propose a model (**Figure 19**) that CNS APCs provide a necessary CD24 signal to pathogenic T cells, which allows optimal proliferation and persistence of T cells in the CNS. Over-expression of CD24 on APCs provides a stronger co-stimulatory signal enhancing the proliferation and survival of pathogenic autoreactive T cells in the CNS.



**Figure 19: CD24 Expression on Central Nervous Systems Antigen Presenting Cells Provides a Co-stimulatory Signal to T cells Enabling the Proliferation and Survival of Effectors Cells.**

Co-stimulation by CD24 on astrocytes with CD24R (unknown ligand) on activated myelin specific T cells can optimally activate CNS antigen specific T cells.

## 6.7 Significance

CD24 is a critical checkpoint for the pathogenesis of autoimmune diseases (116, 117). Mice with targeted mutation of CD24 are resistant to EAE (14, 118, 119).

Moreover, CD24 polymorphism affects risk of both organ-specific and systemic autoimmune disease in human (79, 82). Our previous studies have

demonstrated several mechanisms by which CD24 facilitates autoimmune

diseases, including expansion of autoreactive T cells in the target organ (15, 120)

and regulation of homeostatic proliferation (121, 122). Our study presented

here suggests a novel mechanism by which CD24 mediates pathogenesis of

autoimmune diseases, namely the escape of autoreactive T cells from clonal

deletion.

## 6.8 Future Prospective

Based on this study, a therapeutic that could block the signaling associated with CD24 would be beneficial to the amelioration of EAE and presumable MS in humans. CD24's ligand is currently unknown, so a soluble CD24 protein was developed, and has been shown to drastically reduce EAE symptoms when administered 8-10 days after the induction of EAE(14). The soluble CD24 protein is comprised of the mature murine CD24 protein and the signal protein fused to a human IgG1 Fc fragment denoted HSAIg. Secreted as a homodimer, HSAIg presumably will bind with the ligand of CD24 (CD24L) thus blocking CD24 associated co-stimulatory signaling. The HSAIg method of action hypothetically should mimic a CD24 deficient mouse.

During the course of MS, activation of myelin antigen specific T cells should exhaust the naïve population of potentially autoreactive T cells. The generation of a new pool of naïve autoreactive T cells would be affected by the presence of the soluble HSAIg. Based on the data presented in this study, autoreactive T cells should be eliminated and the periphery should become depleted of autoreactive T cells specific for myelin antigen. Assuming the peripheral pool of naïve autoreactive T cells is depleted, the soluble HSAIg should provide a long term protection from future relapses.

During an inflammatory process, the BBB should allow access of the soluble HSAIg into the CNS thus blocking the action of CD24 on thymocytes. CD24 deficient mice are highly resistant to the induction of EAE(14), furthermore

adoptive transfer studies indicated that activated T Cells expressing CD24 will traffic to the CNS but not become re-activated (15) and subsequently undergoing apoptosis. As shown in this study, over-expression of CD24 on astrocytes resulted in a more severe course of EAE. Taken together, one could predict that HSAIg would have a similar method of action as the CD24 deficient mice and block the activation of myelin specific T cells in the CNS. Once the short lived activated T cells are exhausted, no newly activated T cells should be generated and the inflammation response should subside. Based on the data found in this study, the HSAIg looks to be a promising therapeutic for the treatment of MS.

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