

RAGs AND REGULATION OF AUTOANTIBODIES

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■ **Abstract** Autoreactive antibodies are etiologic agents in a number of autoimmune diseases. Like all other antibodies these antibodies are produced in developing B cells by V(D)J recombination in the bone marrow. Three mechanisms regulate autoreactive B cells: deletion, receptor editing, and anergy. Here we review the prevalence of autoantibodies in the initial antibody repertoire, their regulation by receptor editing, and the role of the recombinase proteins (RAG1 and RAG2) in this process.

INTRODUCTION

Antigen receptor diversity is generated by random rearrangements between variable (V) diversity (D) and joining (J) gene segments in developing B cells and T cells (1). This receptor diversity ensures efficient immune responses to a universe of rapidly evolving potential pathogens. However, random gene reassortment can also produce self-reactive antibodies that could cause “horror autotoxicus,” as pointed out by Ehrlich (2). Burnett, Talmage, and Lederberg provided a framework for understanding how self-reactive lymphocytes might be removed from the nascent repertoire as part of the clonal selection theory (3–5): They proposed that any self-reactive antibody producing lymphocytes would be deleted during development. In the past 20 years transgenic experiments in mice have shown that at least three mechanisms account for silencing of self-reactive antibodies during B cell development in the bone marrow: receptor editing, deletion, and anergy (6–9). One of these mechanisms, receptor editing, relies on V(D)J recombination to obviate autoantibody production *in vivo*. Here we review recent work on aspects of V(D)J recombination relevant to production and regulation of autoreactive antibodies *in vivo*.

MOST NASCENT B CELLS PRODUCE AUTOANTIBODIES

How B cells produce a diverse antibody repertoire while maintaining self-tolerance has been an important question since the time of Ehrlich (2). Landsteiner's finding that the antibody repertoire is almost infinitely diverse further stressed the potential importance of avoiding self-reactivity and raised the problem of prevalence of autoantibodies in the initial repertoire (10).

A number of investigators found that the majority of nascent immature B cells are deleted before they reach the mature B cell compartment, suggesting that autoreactive B cells might be a large part of the initial repertoire (11–15). Only 10%–20% of the bone marrow immature cells reach the periphery, and as few as 3% contribute to the mature B cell pool (14, 16–18). Furthermore, deletion was not random because there was a specific shift in the representation of antibodies in the repertoire between the immature and mature B cell stages (19–21).

The number of self-reactive antibodies was determined for human B cells by single cell analysis of the bone marrow and blood (22) (Figure 1). Two types of autoreactive antibodies were measured by ELISA, antinuclear antibodies (ANAs) and antibodies to defined antigens such as DNA, insulin and LPS. Antibodies that bound to more than one of these defined antigens were considered polyreactive. The ANAs were assayed by ELISA on HEp-2 cell lysates and verified by indirect immunofluorescence. Fifty-five percent to 75% of all antibodies in the early immature B cell compartment (B cells with the surface phenotype of pre-B cells that contained in-frame Ig κ or Ig λ chains) produced self-reactive antibodies (22). The self-reactive antibodies were lost from the B cell repertoire at two discrete checkpoints in development. The first checkpoint was between the early immature B cell stage and the immature B cell stage. Nearly all antibodies (poly)reactive with defined antigens were lost in this early transition in the bone marrow. ANA antibodies were lost from the repertoire in the immature B cell compartment and also in the periphery at the transition between the immature and mature B cell pool. Therefore, the majority of nascent human B cells is self-reactive. Future experimentation should focus on understanding changes in the efficiency of autoantibody removal that might lead to increased susceptibility to autoimmunity.

RAG EXPRESSION AND ANTIBODY ASSEMBLY IN DEVELOPING B CELLS

RAG1 and RAG2 proteins catalyze V(D)J recombination and antibody gene assembly (23, 24). RAGs bind to and cleave DNA at conserved recombination signal sequences (RS) that flank immunoglobulin (Ig) and T cell receptor (TCR) gene segments (25). These proteins are essential for the recombination reaction, and loss of either one in mice or humans results in complete block of lymphocyte development (26–28).

RAG1 and *RAG2* are only coexpressed in developing lymphocytes, and the level of expression is regulated in a developmental stage-specific manner (29, 30)

(see Figure 1). The first B cells to express *RAG1* and *RAG2* are early lymphoid committed progenitors found in fraction A1 (31, 32). These cells are Lin⁻CD27⁺c-kit^{Hi}Sca^{Hi} and express low levels of RAGs and exhibit low levels of recombinase activity as measured by recombination of antibody D and J gene segments (33). RAGs are further induced in pro-B cells where Ig heavy chain gene assembly begins (31, 32, 34). Successful heavy chain gene recombination leads to expression of membrane Ig heavy chains (μ), which in turn induce clonal expansion, RAG downregulation, heavy chain allelic exclusion, and progression to the pre-B cell stage (35–40). It is essential for heavy chain allelic exclusion to be established at this stage of B cell development because persistent recombination might inactivate the productively rearranged heavy chain or produce a cell with two heavy chains and multiple antibody specificities. *RAG1* and *RAG2* downregulation is likely an important initial aspect of establishing allelic exclusion at the heavy chain locus. However, exclusion is maintained in later B cell stages by RAG-independent changes in heavy chain accessibility that appear to be induced through IL-7 (41, 42). *RAG1* and *RAG2* expression is downregulated in cycling pre-B cells but it is not known whether this downregulation is mediated at the transcriptional level or at the level of mRNA stability (43). Decreased transcription is suggested by decreased GFP expression in mice that carry YFP and GFP inserted into the *RAG1* or *RAG2* genes, respectively (32, 44). RAG protein levels are also regulated by phosphorylation of the RAG protein, which decreases the half-life of the protein (45).

A second wave of RAG expression is induced when pre-B cells stop dividing, and it is associated with onset of high levels of Ig light chain gene recombination (35, 46). Upon successful expression of an Ig light chain gene and assembly of a functional BCR, pre-B cells become immature B cells. Immature B cells are the first B cells to express surface IgM, and it is in this compartment that antibodies are initially tested for self-reactivity and that central B cell tolerance is established by receptor editing or deletion (6, 7). Immature B cells display two features that facilitate induction of central tolerance: persistent RAG expression that allows for receptor editing, and apoptosis in response to high levels of BCR cross-linking that promotes deletion (32, 44, 47, 48).

PERSISTENT RAG EXPRESSION AND RECEPTOR EDITING

Receptor editing involves replacement of self-reactive antibody V region (7, 49) genes by V(D)J recombination (6). Gene replacement by persistent V(D)J recombination was first described in B cell lines in vitro (50–52). In mice, it was noted that Ig κ transgenes did not induce high levels of allelic exclusion and that there was frequent persistent V(D)J recombination with some antibody transgenes (53, 54). However, the potential physiologic significance of secondary recombination of Ig genes in maintaining tolerance was only appreciated from studies of transgenic mice carrying anti-double stranded DNA or anti-MHC antibodies (6, 7). In these mice, immature B cells are exposed to multivalent self-antigens at early stages

of development (8, 55). Most of these B cells are deleted, but a small cohort of B cells escapes deletion and migrates to the spleen and lymph nodes where they accumulate with age (6). It was shown that while the transgenic heavy chain was present in the B cells that escape deletion, they expressed an endogenous, non-transgenic κ or λ gene, and the resulting chimera was no longer self-reactive (6, 7, 49). Thus, the nontransgenic κ or λ gene was said to “edit” the original transgenic self-reactivity.

Further insight into light chain editing came from the analysis of the transgenic mice that carry only the 3H9 heavy chain of an anti-DNA antibody (49, 56). 3H9 produces anti-DNA when combined with most light chains but a small group of light chains with low isoelectric points such as $V\kappa 12A$ block anti-DNA reactivity. Despite the high level of reactivity of 3H9 with DNA, splenic B cells from these mice did not produce anti-DNA antibodies. 3H9 peripheral B cells showed highly skewed $V\kappa$ and $J\kappa$ usage with a large number of cells expressing $V\kappa 12A$, and the majority of the $V\kappa$ genes were joined to $J\kappa 5$, indicating that multiple recombination events had occurred on the same chromosome (49). Efficient light chain “editors” differed from other κ light chains in that their CDRs are very acidic and have the capacity to prevent DNA binding by neutralizing the arginines in the CDR3 of 3H9 (57). Enhanced editing was associated with high levels of *RAG* expression, suggesting that editing induced or prolonged *RAG* expression (7).

The efficiency of editing was assessed using mice produced by gene targeting to express anti-MHC ($H-2K^{k-b}$) or anti-DNA heavy and light chains (58, 59). In contrast to the severely reduced numbers of mature B cells reported in conventional anti-MHC transgenic mice, the bone marrow and peripheral B cell compartments of these knock-in mice were nearly normal, suggesting that editing was highly efficient (58, 59).

Ig V_H genes can also be replaced by secondary V(D)J recombination through the use of cryptic recombination signal sequences embedded in the V_H gene (52, 60–62). Studies in mice and humans have shown evidence for V_H replacement in autoantibody-producing B cells (63–65). However, edited heavy chains frequently show N nucleotide addition, suggesting that this process can occur in progenitor B cells before light chain assembly (63, 66, 67). Such replacements would not be a response to self-antigen binding. Nevertheless, it has been estimated that 5%–12% of the human antibody repertoire is produced by V_H replacement (68).

SITE OF EDITING

RAG expression was believed to be upregulated for a third time in immature B cells that carry self-reactive receptors. In vitro experiments with both transgenic and wild-type B cells showed increased *RAG* mRNA levels in cultures of developing B cells following BCR cross-linking (69, 70). In addition bone marrow cells from mice that carry anti-MHC ($H-2K^{k-b}$) antibody transgenes show higher levels of *RAG* expression in the self-reactive background (71). Whether this increase in *RAG*

expression is due to increased transcription or selection for cells that express high levels of RAG remains to be determined. Immature B cells are not a homogeneous population with respect to the level of RAG or BCR expression (Figure 1). Analysis of the *RAG2*-GFP indicator mice showed that RAG levels were inversely correlated with the density of the surface B cell receptor and B cell maturation (44, 72). More mature B cells with higher levels of cell surface BCR expression showed lower levels of RAG expression, suggesting that RAG expression is gradually turned off as B cells mature (44, 72). Immature B cells that express high levels of surface IgM are also more susceptible to negative selection (47, 48). Thus, the apparent upregulation of RAG mRNA by BCR cross-linking in vitro could also be a consequence of the selective survival of the cells that expressed higher levels of RAGs and lower levels of BCR to begin with. Similarly, increased RAG expression in transgenic B cells altered B cell maturation and enrichment for less mature B cells that have lower levels of surface BCR and higher RAG expression.

To visualize the editing compartment in vivo, an *Ig κ* allelic polymorphism was created by targeted replacement of the mouse constant region gene (*mC κ*) by its human homologue (*hC κ*) (73). In mice heterozygous for both a prerecombined light chain (at the *mC κ* locus) and the *hC κ* allele, edited B cells were distinguished as those cells that lost expression of the prerecombined *mC κ* allele (73). Kinetic studies showed that B lymphocytes undergoing editing were arrested for at least two hours at the pre-BII cell stage when compared to unedited counterparts. The delayed and edited B cell population showed higher levels of RAG expression than unedited cells (73). Similar kinetic data have been obtained using mice that carry a prerecombined *V λ* gene instead of *hC κ* (74). These observations are consistent with a model where self-recognition activates secondary gene recombination by inducing a developmental arrest at a stage where *RAG1* and *RAG2* are expressed. In this model, cross-linking of the cell surface receptor by self-antigen does not reinduce but sustains *RAG1* and *RAG2* expression and allows for secondary V(D)J recombination. The model further clarifies how light chain allelic exclusion is maintained in the presence of high levels of editing: B cells expressing innocuous receptors transit rapidly from this stage to a compartment where RAG expression and V(D)J recombination are turned off. Thus, B cells with a nonself-reactive receptor are not exposed to prolonged V(D)J recombination, and the self-reactive cells that are trapped in the editing compartment remain so only until they produce a nonself-reactive receptor. In this regulated model for allelic exclusion, both *Ig κ* alleles could be accessible to the V(D)J recombinase simultaneously without interfering with allelic exclusion.

EXTENT OF EDITING

Several lines of evidence suggest that secondary gene rearrangements are a common occurrence. For example, analysis of hybridomas generated from *V κ 4J κ 4* and *V κ 8J κ 5* knock-in mice shows that both prearranged light chains are replaced by

editing in a large number of B lymphocytes (75). Likewise, the $V_{\kappa}3-83J_{\kappa}2$ light chain is edited by secondary recombination occurring at the targeted allele and this is accompanied by V(D)J recombination at the wild-type allele (58). Editing has also been examined in $Ig\lambda$ expressing nontransgenic B cells in mice and man (76, 77). Forty-seven percent of all mouse $Ig\lambda$ expressing B cells that have had their $Ig\kappa$ genes inactivated by RS rearrangements show in-frame and potentially functional $Ig\kappa$ genes (77). In man, almost all λ expressing B cells also carry a rearranged κ locus, whereas only 2% of κ expressing B cells carry rearrangement $Ig\lambda$ genes (76). Furthermore, inactivated in-frame κ joints are found in 30% of human λ expressing cells (76). However, it was not determined why the in-frame $Ig\kappa$ alleles were replaced in mouse or man.

A direct measurement of the extent of receptor editing was made using the h $C\kappa$ and $V\lambda$ knock-in alleles (73, 74). These studies revealed that on average 25% of the repertoire is the result of secondary gene replacements, indicating that editing makes an important contribution to the normal antibody repertoire.

TRANSCRIPTION AND SECONDARY V(D)J RECOMBINATION

Ig gene expression has been proposed to be essential for primary V(D)J recombination based on the direct correlation between the onset of germline transcription and antibody gene recombination (78–80). In support of this model, targeted deletion of transcription regulatory elements and some transcription factors impairs both expression and recombination of TCR and Ig genes in vivo (81–85). In addition, V(D)J recombination can only be induced in nonlymphoid cells when Ig genes are transcribed (86). However, experiments with cell lines, transgenic recombination substrates, and $Pax5^{-/-}$ B cells show that transcription does not always correlate with recombinational accessibility (87–91). Furthermore, the question of whether there is a role of transcription per se as opposed to indirect enhancement of locus accessibility has not been resolved.

The role of transcription in secondary recombination was investigated in mice mutant for the transcriptional coactivator OcaB. OcaB (also known as Bob-1 and OBF-1) (92–94) forms a ternary complex with the transcription factor Oct-1 (or Oct-2) (95) on octamer motifs present in some Ig gene promoters. This octamer/Oct-1(2)/OcaB ternary complex is thought to activate Ig gene transcription by specific interactions with the TATA-box-associated basal transcription machinery (96, 97). A direct correlation was found between light chain promoter transcription and receptor editing (98). In the absence of OcaB, the $Ig\kappa$ chromatin domain is accessible as measured by DNA demethylation, histone acetylation, promoter loading of Oct-1, and low level transcription (98). However, open chromatin and low level transcription were not sufficient for gene replacement by V(D)J recombination. Only strongly transcribed promoters were replaced (98). Thus, a specific threshold of $V\kappa$ gene transcription is required for secondary gene recombination.

TERMINATION OF RAG EXPRESSION

RAG expression was initially thought to be confined to pro-B, pre-B, and immature B cells in the bone marrow. However, several reports showed RAG mRNA and protein expression in germinal centers and in vitro activated B cells (99, 100). RAG1 and RAG2 mRNAs were detected in IgD⁺ B cells cultured in the presence of CD40 (or lipopolysaccharide) and IL4, whereas splenic, Peyer's patches, or lymph node germinal center B cells showed abundant RAG1 protein expression as determined by immunostaining (99, 100). Unlike most peripheral B cells, RAG⁺ lymphocytes (in both mice and humans) expressed several cell surface markers characteristic of pro-B or pre-B cells such as $\lambda 5$, VpreB, TdT, GL7, low levels of B220, and IL7R (99, 101–105). Ongoing recombination in these peripheral cells was implied by the presence of DNA double-stranded break V(D)J intermediates (106–108) and de novo formation of V $\lambda 1$ -J $\lambda 1$ signal joints. However, the similarities between bone marrow and peripheral RAG⁺ B cells raised the possibility that these cells might in fact represent B cell precursors. Experiments with transgenic and GFP knock-in mice supported this hypothesis (44, 72). In both cases, GFP expression in developing B and T cells mimics endogenous RAGs with the caveat that the GFP expression level in the transgenic mice was one order of magnitude higher than in the knock-in mice. Despite this, the results obtained with both models were similar in that they showed that RAG-GFP expression in spleens was restricted to immature new immigrant B cells (44, 72). Furthermore, adoptive transfer experiments showed that mature B cells could not be induced to re-express RAGs during an immune response in vivo or by culturing them in the presence of LPS and IL4 (44, 72). Interestingly, the RAG⁺ immature B cell compartment in the spleen was increased in animals immunized with antigen, infectious agents, or adjuvant only at late stages of the immune response (44, 72, 109, 110). Increase in production and export of immature B cells from the bone marrow (109, 110) accounted for accumulation of these RAG⁺ immigrants with kinetics similar to germinal center formation (99, 100).

The levels of RAG expression in developing B cells decreased as they acquired higher levels of surface IgM expression (see above). New immigrant B cells in the periphery express substantially lower levels of RAG than immature B cells in the bone marrow (44, 72). Nevertheless, alterations in the kinetics of immature B cell migration to the periphery under conditions of immunization might explain reports on RAG expression in peripheral B cells even in the absence of reinduction.

FROM EDITING TO DELETION

Termination of RAG expression prevents further V(D)J recombination and receptor editing. To maintain tolerance, B cells that cannot edit self-reactive receptors must be deleted or rendered anergic.

The idea that self-reactive clones are deleted during development was put forward by Joshua Lederberg as a refinement of the clonal selection theory (5). This

concept was confirmed by experiments in which mice were treated with anti-Igs from birth and were found to be B cell depleted (111). The assumption linking this result to tolerance was that anti-IgM antibodies must mimic autoantigens by cross-linking the cell surface receptor. Likewise, bone marrow B cells challenged in vitro with anti-IgM antibodies downregulate surface Ig and undergo apoptosis (11, 13, 15, 19). In transgenic mice, expression of certain self-specificities also induced clonal B cell deletion (8, 55, 112–114). In anti-MHC expressing B cells exposure to antigen induced a developmental block that was concurrent with secondary VL gene recombination and replacement of cell surface receptors (48, 69, 70). Cells that failed to undergo successful editing were destined for death by apoptosis. This idea was confirmed in experiments with *RAG*-deficient mice that carried anti-DNA or self-MHC antibodies (115, 116). In the absence of secondary recombination all autoreactive B cells were deleted and there were no peripheral B cells (115, 116). Thus, antigen-induced apoptosis is a relatively late event in bone marrow B cell development that is preceded by an editing permissive stage that appears to be dependent on the bone marrow microenvironment (21, 48, 117).

CIS REGULATION OF *RAG* EXPRESSION

Highly regulated *RAG* expression is required for successful assembly of Ig and TCR genes and normal lymphocyte development. On the other hand, silencing *RAG*s in mature lymphoid cells is necessary in order to ensure genomic stability.

The *RAG* locus is peculiar in that *RAG1* and *RAG2* are adjacent but convergently transcribed genes that entered the vertebrate genome at the time of emergence of jawed fish (23–25, 118, 119). This unusual evolutionarily conserved genomic organization and the finding that *RAG* proteins can mediate transposition in vitro lead to the hypothesis that these genes originate from a mobile element that entered the vertebrate genome at the time of emergence of jawed fish (120, 121). Regulation of *RAG* expression has been studied by transfection in cell lines in vitro and in vivo using bacterial artificial chromosome (BAC) transgenic mice, using green or yellow fluorescent protein (GFP or YFP) as reporters in reconstitution experiments with transfected ES cells, and by gene targeting. The disadvantage of the transfection systems is that the transfected cells represent static stages in B or T cell development and therefore the dynamic aspects of *RAG* regulation in developing lymphocytes cannot be explored. Nevertheless, much has been learned about the chromatin structure and transcription factors that bind the murine and human *RAG1* and *RAG2* TATA-less promoters in vitro (122–126). The *RAG1* promoter is not active or tissue specific in transient transfections in the absence of a heterologous enhancer such as the Ig E μ (125). In contrast, the murine *RAG2* promoter is active in transient transfection experiments in B and T cell lines, and the activity is dependent on PAX5 and GATA3 (127, 128). However, stable transfectants showed little activity for either *RAG1* or *RAG2* promoters in the absence of exogenous enhancers (129).

A second method used to evaluate *RAG* regulation was *RAG2*^{-/-} blastocyst reconstitution by transfected *RAG2* transgenes (130). These experiments suggested

that all of the information required for *RAG2* regulation was found in an 18 kb genomic fragment extending from 9 kb upstream of the *RAG2* promoter to 2.4 kb 3' of the untranslated region because it rescued thymocyte development (130). Similar rescue of *RAG2*^{-/-} mice was also obtained with a yeast artificial chromosome (*RYAC*) that contained both functional *RAG* genes and 12 kb of DNA 5' of *RAG2* (131). The double positive (DP) compartment was fully reconstituted, and mature CD4⁺CD8⁻ and CD4⁻CD8⁺ thymocytes were present at one third of normal levels in the *RYAC/RAG2*^{-/-} mice (131). However, this reconstitution of the DP and single positive (SP) stage differed significantly from the normal wild-type T cell development in that the mature cells were reduced by up to 70% and that the TCR α rearrangements were restricted to only the initial recombination at the 5' end of the *J α* locus (131). Reconstitution was nonphysiological because *RYAC* failed to induce detectable *RAG1* or *RAG2* transcription in DP T cells. Thus, neither the 18 kb genomic fragment (130) nor the *RYAC* contained sequences required for *RAG* expression in DP T cells (131), and the *RAG2*^{-/-} blastocyst reconstitution is not a sensitive assay to study *RAG* regulation in vivo.

Transgenic mouse and gene targeting experiments have confirmed the requirement for distal enhancers in regulating *RAG* expression in vivo. Two elements with *RAG* promoter-enhancing activity have been identified: One element is active in B cells and the second in DP T cells (32, 129, 131). Both of these elements are on the *RAG2* side of the locus, and both elements have effects on *RAG1* and on *RAG2* promoters, suggesting a mechanism for achieving coordinate regulation of the two genes by one set of genetic elements (32).

The B cell specific element is found in a 2.3 kb area located approximately 22 kb 5' of *RAG2*. In cell lines this element enhances transcription over background levels in a highly variegated manner (36% of the transfected cells show no expression at all and only 10% of the clones show high levels of expression) (129). Nevertheless, enhancement is found only in pro-B cells and is absent from T, adult B, or nonlymphoid cell lines. Targeted deletion of this element from the mouse genome leads to a B cell specific tenfold and a twofold decrease in *RAG1* and *RAG2* mRNA levels, respectively, with no effect on *RAG* expression in DN or DP cells (129). Although the targeted deletion shows that this element is required for complete regulation, no ectopic or developmentally aberrant expression is reported in its absence. It remains to be determined whether this element is sufficient to drive tissue-specific and developmentally regulated expression of *RAG*, as is the case for other enhancers such as the *Ig μ* enhancer.

The T cell specific element was identified in transgenic experiments with bacterial artificial chromosomes (BACs) that carry fluorescent protein indicator genes in place of the *RAG* genes (32). These experiments showed that the transcription of both *RAG1* and *RAG2* in DP thymocytes is coordinated by one or more cis element(s) located between 32 and 87 kb 5' of *RAG2*. In addition to regulating expression in DP thymocytes, this region was also required to prevent position effect variegation in developing T cells and B cells. Therefore, an element (or elements) in this region is a required part of a traditional locus control region (132, 133).

Like developing B cells, thymocytes express RAGs in two waves. V(D)J recombination is initiated with the first wave of RAG expression at the TCR β locus in CD4⁻CD8⁻ (DN) T cells. The TCR β locus is analogous to the Ig heavy chain locus, and DN T cells are analogous to pro-B cells (134). Once a TCR β chain is expressed, it combines with pre-T α and CD3 components to produce the pre-TCR (135, 136). Similar to the pre-BCR, the pre-TCR downregulates RAG expression and induces T cells to mature to the CD4⁺CD8⁺ double positive (DP) stage. Upon entering the DP stage there is a second wave of RAG expression and progressive V(D)J recombination along the J α locus (29, 131, 137–139). V(D)J recombination is only turned off in DP cells when they express a TCR that recognizes self-MHC with an affinity that allows for positive selection (140, 141). Thus, TCR cross-linking in DP T cells is the signal that extinguishes RAG expression. This is different from pre-B cells where receptor cross-linking delays extinction of RAG expression and prolongs recombination leading to receptor editing (73).

We speculate that the separate B cell and DP T cell specific elements for RAG regulation may provide a molecular explanation for why T cells turn off RAG expression upon TCR cross-linking, whereas immature B cells prolong RAG expression and induce receptor editing upon BCR cross-linking.

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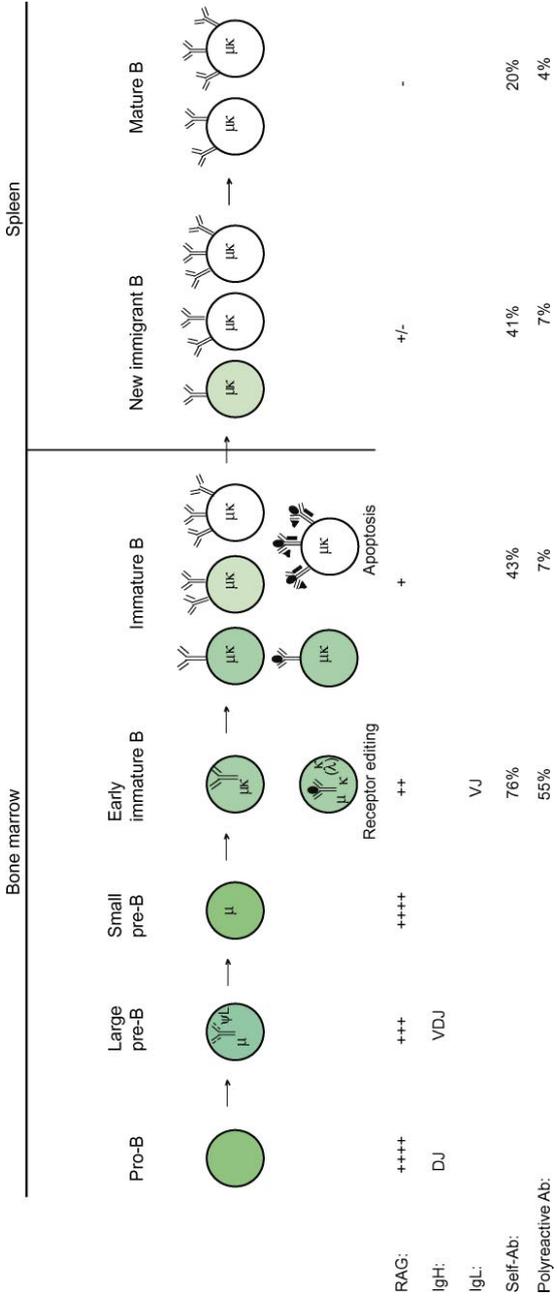


Figure 1 B cell development. Stages, status of the immunoglobulin heavy (IgH) and light chain (IgL) loci, expression of the RAG proteins (the shades of green represent the intensity of expression of the RAG2 protein in mouse RAG2-GFP indicator strains). Expression of the pre-B and B cell receptors, induction of receptor editing, and apoptosis by self-antigens.