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## Impaired B cell tolerance checkpoints promote the development of autoimmune diseases and pathogenic autoantibodies

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### Summary:

A role for B cells in autoimmune diseases is now clearly established both in mouse models and humans by successful treatment of multiple sclerosis and rheumatoid arthritis with anti-CD20 monoclonal antibodies that eliminate B cells. However, the underlying mechanisms by which B cells promote the development of autoimmune diseases remain poorly understood. Here we review evidence that patients with autoimmune disease suffer from defects in early B cell tolerance checkpoints and therefore fail to counter-select developing autoreactive B cells. These B cell tolerance defects are primary to autoimmune diseases and may result from altered B cell receptor signaling and dysregulated T cell/regulatory T cell compartment. As a consequence, large numbers of autoreactive naïve B cells accumulate in the blood of patients with autoimmune diseases and may promote autoimmunity through the presentation of self-antigen to T cells. In addition, new evidence suggests that this reservoir of autoreactive naïve B cells contains clones that may develop into CD27<sup>+</sup>CD21<sup>-/lo</sup> B cells associated with increased disease severity and plasma cells secreting potentially pathogenic autoantibodies after the acquisition of somatic hypermutations that improve affinity for self-antigens.

### Keywords

B cell development; immune tolerance checkpoint; autoimmune disease; autoantibodies

### Introduction

Millions of individuals worldwide are affected by autoimmune disorders but their etiologies remain poorly understood. Defects in B cell tolerance are associated with most autoimmune diseases and are illustrated by the production of autoantibodies that target self-antigens. Some of these autoantibodies are pathogenic because they interfere with the function of the molecules they recognize, such as the acetylcholine receptor (AChR)/ muscle-specific tyrosine kinase (MuSK) in myasthenia gravis (MG) and aquaporin-4 water channel (AQP4)

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in neuromyelitis optica spectrum disease (NMOSD) <sup>1,2</sup>. Others target nucleic acids or their associated proteins, allowing the formation of immune complexes that deposit in various organs of patients with systemic lupus erythematosus (SLE) and induce organ damage <sup>3</sup>. These immune complexes also allow the activation of myeloid cells expressing both FcRs binding autoantibodies and Toll-like receptors (TLRs), such as TLR7, TLR8, and TLR9, that recognize autoantibody-bound nucleic acids and lead to cell activation and foster inflammation <sup>4</sup>. However, the relevance of the various autoantibodies in the pathophysiology of type 1 diabetes (T1D) is unclear and their identification in patients with multiple sclerosis (MS) is elusive. While B cells have been shown to be essential for the development of diabetes in the NOD mouse model, additional investigations revealed that B cells promote diabetes by recognizing self-antigens with their autoreactive antibodies and presenting self-antigens via MHC class II molecules to T cells <sup>5-12</sup>. Hence, these data suggest that self-antigen presentation by autoreactive B cells that escaped tolerance may initiate the development of autoimmune diseases. The identification of impaired B cell tolerance checkpoints in patients with autoimmune diseases and the recent identification of pathogenic anti-AQP4 clones originating from unmutated autoreactive naïve B cells in patients with NMOSD agree with this scenario and will be presented and discussed in this review.

### **Central and peripheral B cell tolerance checkpoints shape the human naïve B cell repertoire**

Self-tolerance is achieved by silencing self-reactive lymphocytes that are generated during either B cell development in the bone marrow or B cell activation in the periphery <sup>13</sup>. Engineered models using transgenic and knock-in mice have revealed that developing B cells expressing self-reactive receptors can be silenced by one of three mechanisms: 1. clonal deletion; 2. clonal unresponsiveness to antigen or anergy; 3. “receptor editing” or antigen receptor gene replacement by continued V(D)J recombination catalyzed by the recombinase-activating genes (RAGs) <sup>13-16</sup>. However, the frequency of self-reactive antibodies that arise during unmanipulated B cell development could neither be assessed using these mice, nor could it be determined when such antibodies were actually removed from the repertoire under physiologic circumstances.

To determine the proportion of autoreactive B cells that were removed from the nascent repertoire and how central B cell tolerance was established in humans, we assessed the frequencies of autoreactive clones in sequential subsets of B cells during their early B cell development in the bone marrow and the blood of healthy donors <sup>17</sup>. This approach was dependent on a method that allows Ig gene amplification, cloning, and expression *in vitro* of recombinant antibodies initially produced by single human B cells <sup>17</sup>. By testing the reactivity of recombinant antibodies against double-stranded DNA, insulin, and LPS in ELISAs or immunofluorescence on slide-coated HEP-2 cells, we previously established that a first step for immature B cell selection removes the vast majority of developing B cells that express polyreactive and anti-nuclear antibodies in bone marrow and is referred to as the central B cell tolerance checkpoint <sup>17,18</sup>. In addition, using a second ELISA test in which plates are coated with HEP-2 cell lysates, we found that a peripheral B cell tolerance checkpoint further eliminates autoreactive new emigrant/transitional B cells that

escaped central tolerance before they entered the mature naïve B cell compartment<sup>17</sup>. This bimodal removal of autoreactive clones from the initial B cell repertoire generated by random V(D)J recombination may result from B cell exposure to self-antigens first in the bone marrow where B cell production takes place in adults and then in the periphery when immature B cells migrate out of the bone marrow and encounter a new set of self-antigens. This model is supported by our recent observations showing that autoimmune regulator (AIRE)-deficient patients display specific defects in the peripheral B cell tolerance checkpoint caused by a failure of AIRE-mediated T cell/regulatory T cell (Treg) selection that normally prevents the expansion of autoreactive naïve B cells recognizing peripheral self-antigens<sup>19</sup>. The mechanisms by which T cell/Tregs may control the peripheral selection of B cells continuously produced by the bone marrow are not well characterized at this point, but specific defects in this checkpoint have been observed in FOXP3-deficient, immune dysregulation, polyendocrinopathy, enteropathy, X-linked (IPEX) patients who lack functional Tregs<sup>20</sup>. In addition, decreased Treg frequencies and/or impaired Treg suppressive function in patients with ADA-, CD40L-, DOCK8-, MHC class II, and WASp-deficiency as well as the absence of T cells in either CD3D- or CD3E-deficient patients also resulted in the specific accumulation of autoreactive clones in the mature naïve B cell compartments of these patients, further suggesting the B cell extrinsic regulation of this peripheral checkpoint<sup>19,21–24</sup>.

In contrast, central B cell tolerance is not affected by decreased Treg frequencies or suppressive function and appears instead to be regulated by intrinsic B cell pathways<sup>21,25–28</sup>. Indeed, mutations in genes that encode molecules belonging to the BCR and TLR pathways such as Bruton's tyrosine kinase (BTK), Adenosine deaminase (ADA), Wiskott-Aldrich syndrome protein (WASP), MYD88, IRAK-4, Transmembrane Activator and CAML Interactor (TACI), and Activation induced cytidine deaminase (AID) affected central B cell tolerance, thereby revealing a B cell intrinsic regulation of this checkpoint<sup>21,24,26–29</sup>. These studies suggest that, in addition to BCRs, TLRs, especially those binding to nucleic acids and expressed in B cells such as TLR7 and TLR9, contribute to the induction of B cell tolerance as also demonstrated in mice<sup>30</sup>. This may be especially important for membrane-bound self-antigens that may be co-expressed with nucleic acids at the surface of apoptotic cells or cellular debris and therefore co-engage BCR and TLRs in developing B cells and inducing tolerance mechanisms such as receptor editing and eventually lead to the expression of AID, which results in the deletion of autoreactive clones<sup>30–33</sup>. Our data, consistent with this hypothesis, showed that p53 inhibition increased the proportion of AID-expressing B cells in the bone marrow of humanized mice and abrogated central B cell tolerance, likely by rescuing developing autoreactive B cells from apoptosis<sup>34</sup>. These collective analyses of patients with primary immunodeficiencies revealed that the regulation of central B cell tolerance in humans requires proper BCR and TLR signaling and function, whereas the peripheral B cell tolerance checkpoint depends on T cells/Tregs to prevent the accumulation of autoreactive naïve B cells.

### **Defective early B cell tolerance checkpoints in patients with autoimmune diseases**

Autoantibody production is a characteristic of most autoimmune diseases including SLE, T1D, MG, NMOSD, and rheumatoid arthritis (RA)<sup>35,36</sup>. Autoantibodies appear in the

serum many years before the onset of the clinical disease, which suggests an early break in B cell tolerance<sup>37,38</sup>. The underlying mechanisms that account for autoreactive B cell and autoantibody production in patients with autoimmune diseases remain elusive. We sought to determine the stage of B cell development at which B cell tolerance was broken in patients with autoimmune diseases. Two non-exclusive scenarios could be considered: first, B cell tolerance may not be established properly during early B cell development, resulting in the accumulation of autoreactive naïve B cell clones in the periphery; alternatively, early B cell tolerance checkpoints may be functional and B cells present in a normal repertoire may receive signals from T cells to develop into clones secreting high affinity self-reactive antibodies.

To determine whether early B cell tolerance checkpoints were functional in patients with autoimmune diseases, we assessed the frequencies of autoreactive clones in new emigrant and mature naïve B cells isolated from the blood of untreated patients with SLE, RA, T1D, Sjögren's syndrome (SjS), MS, MG, and NMOSD. Despite the broad age range and duration of disease, we found that three out of three pediatric SLE patients, ten out of ten RA patients, six out of six T1D patients, five out of five SjS patients, three out of three MG patients, and three out of three NMOSD patients displayed elevated frequencies of new emigrant/transitional B cells expressing autoreactive/polyreactive antibodies when compared to healthy donors<sup>39-45</sup> (Fig. 1). These collective findings demonstrate that central B cell tolerance is not functional in these patients. In addition, these patients also displayed elevated frequencies of autoreactive and polyreactive mature naïve B cells that accumulated in their blood, suggesting that their peripheral B cell tolerance checkpoint may also not be functional<sup>39-45</sup> (Fig. 2). Indeed, we have previously reported that a functional peripheral B cell tolerance checkpoint can decrease the frequencies of autoreactive B cells in the mature naïve B cell compartment of asymptomatic subjects who display defective central B cell tolerance induced by heterozygous *TNFRSF13B* gene mutation that encodes TACI<sup>29</sup>. A recent study utilizing an alternative method to assess the frequency of autoreactive clones confirmed the impairment of early B cell tolerance checkpoints in SLE patients<sup>46</sup>. In contrast, the establishment of B cell tolerance in MS patients differs from other patients with autoimmune diseases in that five out of seven patients with MS displayed normal central B cell tolerance<sup>45</sup> (Fig. 1). However, seven out of seven MS patients displayed an impaired peripheral B cell tolerance checkpoint, which resulted in the peripheral accumulation of autoreactive and polyreactive mature naïve B cells<sup>45</sup> (Fig. 2). Principal component analysis of the collective checkpoint assay data demonstrates a conspicuously distinct grouping between healthy donors as a first cluster and patients with autoimmune disease and healthy donors carrying the *1858T PTPN22* risk allele associated with many autoimmune diseases as another big cluster (Fig. 3)<sup>47</sup>. Interestingly, MS patients cluster into a third group distinct from both healthy donors and other autoimmune patients, demonstrating the unique B cell tolerance defect in this disease (Fig. 3).

Some of these autoreactive naïve B cells and mostly polyreactive clones expressed unmutated antibodies that could recognize the RA-specific antigens IgG and cyclic citrullinated peptides, extracts of human brain white matter affected in MS and SjS-targeted Ro52/SS-A self-antigen with low affinity<sup>40,41,45</sup>. However, somatic hypermutation during autoimmune B cell responses may increase their affinity for self-antigens (see below). We

conclude that patients with autoimmune diseases suffer from defective early B cell tolerance checkpoints which increases the proportion of autoreactive naïve B cells in their blood and which may favor the development of autoimmunity by increasing the incidence of autoreactive B cells that can present self-antigens to T cells.

### Origins of the impaired early B cell tolerance checkpoints in patients with autoimmune diseases

The analysis of patients with primary immunodeficiencies suggests that the impaired central B cell tolerance that characterizes most patients with autoimmune diseases—except MS—may result from defective/hyporesponsive BCR/TLR pathways. Hence, risk alleles associated with autoimmune diseases that affect BCR/TLR function may alter the establishment of B cell tolerance. Genome wide association studies (GWAS) have identified the *1858T* polymorphism in the *PTPN22* gene (*PTPN22 T*) to be one of the strongest genetic risk factors after the MHC, and is associated with the development of many autoimmune diseases including RA, T1D, and SLE, but not MS<sup>47</sup>. This polymorphism encodes PTPN22 phosphatases with a tryptophan at position 620 (620W PTPN22) instead of an arginine in the common 620R PTPN22 variant. This missense mutation abrogates PTPN22 interaction with CSK tyrosine kinase and results in decreased T cell receptor (TCR) and B cell receptor (BCR) signaling<sup>48–51</sup>.

In agreement with our observations in primary immunodeficiencies, in which defective BCR/TLR function induces a defective central B cell tolerance, we reported that the presence of a *PTPN22 T* allele is sufficient to induce central and peripheral B cell selection defects in healthy donors similar to those in patients with autoimmune diseases (Fig. 1, 2 and 3)<sup>28</sup>. Hence, a single *PTPN22 T* risk allele has a dominant effect on impairing autoreactive B cell counterselection before onset of autoimmunity. In agreement with this hypothesis, we demonstrated that a lentiviral-driven expression of 620W PTPN22 variant in human B cells that developed in humanized mice was sufficient to abrogate central B cell tolerance, whereas the expression of the common 620R PTPN22 had no impact on the functionality of this tolerance checkpoint<sup>52</sup>. In addition, the substitution of the conserved arginine by a tryptophan at the equivalent position, 619, in murine Ptpn22 (called PEP) also promotes autoimmunity in knock-in mice<sup>53</sup>. Furthermore, the same study also showed that the restricted expression of 619W PEP to only B cells was sufficient to impair immune tolerance and to produce anti-dsDNA autoantibodies<sup>53</sup>.

Collectively, these observations demonstrate an essential role for PTPN22 and its 620W variant in the development of autoimmunity by regulating autoreactive B cell selection, differentiation, and activation, which may explain why the *PTPN22 T* risk allele confers a high risk of developing many autoimmune diseases with the exception of MS<sup>47</sup>. GWAS studies analyzing polymorphisms associated with MS identified gene variants that may affect more specifically APCs, such as monocytes, and T cells—notably Tregs—in addition to B cells<sup>54,55</sup>. These findings are in agreement with the specific impairment in the peripheral B cell tolerance checkpoint in MS that resemble those associated with defective Treg function. Indeed, Tregs from MS patients display defective suppressive function and abnormally produce IFN $\gamma$ <sup>56,57</sup>. Many other risk alleles identified by GWAS and associated

with autoimmune diseases such as BLK and BANK1 also belong to the BCR signaling pathway and may also alter the establishment of B cell tolerance<sup>47</sup>. However, the analysis in our labs of more than 110 subjects who did not carry the *PTPN22* T allele failed to identify a single individual with impaired central B cell tolerance, which suggests that other common variants associated with autoimmune diseases identified by GWAS and with a frequency greater than 5% are unlikely to interfere with the establishment of central B cell tolerance impaired in most patients with autoimmune diseases. What could then interfere with the removal of developing autoreactive B cells? We do not exclude the involvement of B cell extrinsic factor that may alter BCR/TLR function in patients with autoimmune diseases, but we previously reported that suppressing inflammation with either methotrexate or anti-TNF $\alpha$  reagents did not correct early B cell tolerance checkpoints in RA patients<sup>42</sup>. In addition, the engraftment of humanized mice with hematopoietic stem cells (HSCs) isolated from an RA patient or a T1D patients led to the production of human B cells containing a high frequency of autoreactive clones that were similar to those in the patients<sup>58</sup>. These findings point toward a genetic or epigenetic origin of early B cell tolerance checkpoint defects. In line with this hypothesis, B cell depletion therapy mediated by rituximab that eliminates B cells also failed to restore the functionality of early B cell tolerance checkpoints in early onset T1D patients<sup>59</sup>. As a consequence, newly generated B cells after rituximab treatment contain many autoreactive clones, which may explain the relapse that occurs in many autoimmune patients after B cell depletion therapy.

In addition to altered BCR signaling induced by the *PTPN22* T allele, we recently reported defects in TLR9 function in B cells from untreated SLE patients that may also account for the impaired central B cell tolerance in these patients<sup>60,61</sup>. TLR9 exerts tolerogenic function as evidenced by lupus-prone *Thr9* KO mice which display exacerbated autoimmune disease<sup>62</sup>. While TLR9 ligands activate B cells, co-crosslinking of BCR and TLR9 that mimics autoreactive B cell stimulation by dsDNA-containing self-antigen induces cell death by apoptosis after transient B cell expansion and therefore prevents anti-dsDNA autoantibody production<sup>63,64</sup>. These data demonstrate that TLR9 plays an important role in limiting the peripheral activation of autoreactive B cells. Decreased TLR9 function in SLE B cells is associated with the downregulation of CD19/CD21 expression on the surface of these cells, but the molecular mechanisms associated with altered CD19/CD21 expression or TLR9 function remain unknown at this point. Decreased CD19 expression was also reported in mice humanized with T1D-derived and RA-derived HSCs and associated with the production of autoreactive B cells<sup>58,65</sup>. Since CD19 is important for both BCR and TLR signaling and function, decreased CD19 expression may therefore affect the removal of developing autoreactive B cells<sup>66,67</sup>. It also remains to be determined if TLR9 function may also be affected in B cells from patients with other autoimmune diseases in which tolerance to self-antigens interacts with dsDNA such as topoisomerase I and centromere proteins in systemic sclerosis (SSc). Altogether, our data suggest that patients with autoimmune diseases may often display altered BCR and TLR9 function in B cells associated with an impaired central B cell tolerance that may promote the emergence of autoimmune manifestations.

## Tolerance checkpoint defects alter the naïve B cell repertoire

We showed that autoreactive naïve B cells escape counterselection by defective early B cell tolerance checkpoints in patients with autoimmune diseases. As a consequence, the naïve BCR repertoire includes clones that would otherwise have been eliminated. Thus, deviations from the repertoire established in healthy controls may be conspicuous. Earlier studies of single B cells isolated from the blood of RA and SLE patients, in which tolerance checkpoints are impaired, demonstrated that characteristics of the Ig kappa (Ig $\kappa$ ) repertoire from new emigrant/transitional B cells that recently emigrated from the bone marrow, and to a lesser extent mature naïve B cells, differed from those in healthy control counterparts<sup>39,40,68</sup>.

Light chain Ig $\kappa$  secondary recombination that may mediate receptor editing, which is the main mechanism of central B cell tolerance, occurs through secondary recombination in which incoming V $\kappa$  genes delete pre-existing V $\kappa$ J $\kappa$  genes by recombining with downstream J $\kappa$ s<sup>16,69</sup>. Ig $\kappa$  secondary recombination therefore results in increased utilization of upstream V $\kappa$ s and downstream J $\kappa$ s. We found that about a third of RA patients (RA Group I) displayed new emigrant/transitional B cells that express BCRs with Ig $\kappa$  gene segments characterized by decreased secondary recombination events, whereas the rest of RA patients (RA Group II) did not show evidence of dysregulated secondary recombination<sup>40,68</sup>. Indeed, new emigrant/transitional B cells from Group I RA patients expressed an Ig $\kappa$  repertoire with a dearth in upstream V $\kappa$  and downstream J $\kappa$ 3–4–5 genes combined to increased J $\kappa$ 1 usage and suggesting a lack of secondary recombination events in these immature B cells that exited the bone marrow<sup>40,68</sup>. This pattern of Ig light chain antibody rearrangements, potentially characteristic of a defective regulation of secondary recombination, was also reported in B cells from SLE patients<sup>70–72</sup>. In addition, inefficient receptor editing in T1D is also evidenced in NOD mice and patients<sup>73–75</sup>. However, our recent studies revealed that the altered Ig $\kappa$  repertoire in B cells from Group I RA patients may originate from decreased or impaired ataxia-telangiectasia mutated (ATM) expression and function<sup>68</sup>. Indeed, both AT patients and NSG humanized mice injected with an ATM inhibitor displayed an Ig $\kappa$  repertoire with a lack of breadth of V $\kappa$ -J $\kappa$  rearrangements similar to that in group I RA patients<sup>68</sup>. Since ATM controls the repair of RAG-mediated DNA double-strand breaks and regulates cell-cycle checkpoints, novel RAG-mediated DNA lesions in immature B cells undergoing Ig $\kappa$  secondary recombination may fail to be properly repaired these when the ATM function is defective, leading to genomic instability and cell loss<sup>76</sup>. The increased frequency of immature B cells undergoing apoptosis in the bone marrow of NSG humanized mice injected with ATMi supports this scenario<sup>68</sup>. It remains to be determined if the altered B cell repertoire induced by decreased ATM function in some RA patients may contribute to disease pathogenesis or if it is solely a byproduct of improper ATM expression in developing B cells.

The restricted size of Ig gene sequencing of antibodies cloned from single B cells analyzed during B cell tolerance checkpoint studies, which can include up to several hundred unique BCR sequences, limited the identification of wider repertoire abnormalities between individuals with or without functioning B cell tolerance, especially for the heavy chains encoded by the recombination of numerous V<sub>H</sub>, D and J<sub>H</sub> gene segments. In contrast,

adaptive immune receptor repertoire sequencing (AIRR-seq) generates considerably larger BCR libraries, often reaching over 1,000,000 unique sequences. Since the circulating peripheral repertoire in humans includes up to  $10^{11}$  B cells<sup>77</sup>, AIRR-seq provides the depth necessary to adequately depict such large populations and therefore affords a comprehensive evaluation of BCR repertoire properties. An increasing compilation of AIRR-seq studies including both total and sorted B cell populations from patients with autoimmunity revealed altered BCR repertoires in MS<sup>78</sup>, SLE<sup>79</sup>, and celiac disease<sup>80</sup>.

We more specifically applied AIRR-seq to analyze the BCR repertoire of naïve B cells from AChR and MuSK MG patients that are enriched in autoreactive clones due to impaired central and peripheral B cell tolerance checkpoints in MG and compared them to those of healthy donors (HD) to potentially identify naïve BCR repertoire features associated with autoimmunity<sup>81</sup>. Our initial study focused on determining whether the naïve BCR repertoires in MG included skewed immunoglobulin gene usage and physiochemical properties<sup>81</sup>. In agreement with a previous study, the naïve B cell repertoires obtained from multiple healthy control subjects displayed highly consistent IGH variable (IGHV) gene usage with limited variability<sup>82</sup>. In contrast, naïve BCR repertoires from MG patients were highly diverse among individuals and may reflect dysregulation B cell development in these patients<sup>81</sup>. Biased usage of IGHV gene segments were observed in naïve B cells from MG patients as illustrated by decreased usage of IGHV3 family gene segments and increased in IGHV1 and IGHV4 family gene usage<sup>81</sup> (Fig. 4). Other studies offer similar findings regarding differential variable region gene segment expression. Systemic sclerosis (SSc), or scleroderma, is a rare chronic autoimmune disease that leads to tissue fibrosis and vasculopathy<sup>83</sup>. Antinuclear antibodies (ANA) are detectable in 90–95% of patients, indicative of immune, and particularly B cell, abnormalities. An AIRR-seq investigation revealed that differential expression of IGHV genes in the repertoires from SSc cohorts relative to a healthy cohort are present in the IgD/IgM compartment<sup>84</sup>. These collective data therefore show that defective early B cell tolerance checkpoints in patients with autoimmune diseases alter the generation of the BCR repertoires of naïve B cells associated with inadequate counter-selection of developing autoreactive clones.

### **Impaired early B cell tolerance checkpoints likely favor the production of circulating atypical CD19<sup>hi</sup>CD27<sup>hi</sup>CD21<sup>-/lo</sup> B cells in some autoimmune diseases**

Several groups have now reported that CD19<sup>hi</sup>CD27<sup>hi</sup>CD21<sup>-/lo</sup> B cells that are scarce in the blood of healthy donors are enriched in various patients with autoimmune diseases including SLE, RA, and SjS<sup>85–88</sup>. This circulating atypical CD19<sup>hi</sup>CD27<sup>hi</sup>CD21<sup>-/lo</sup> B cell subset is also expanded in the blood of patients with chronic viral infection such as HIV and HCV and in patients with malaria, suggesting that ongoing immune responses driven by some self-antigens or chronic exposure to pathogens may favor the production of these B cells<sup>89–91</sup>. Indeed, we found that CD19<sup>hi</sup>CD27<sup>hi</sup>CD21<sup>-/lo</sup> B cells from RA and SjS patients often express autoreactive and polyreactive antibodies, which reveals that they are the product of autoimmune responses<sup>85–87</sup>. The precursors of these B cells in some autoimmune diseases are currently unknown, but experiments in which the somatic hypermutations were reverted to germline counterparts in recombinant antibodies expressed by expanded CD19<sup>hi</sup>CD27<sup>hi</sup>CD21<sup>-/lo</sup> B cells in SjS suggest that their unmutated precursors



were already autoreactive<sup>87,92</sup>. Hence, the accumulation of CD19<sup>hi</sup>CD27<sup>-</sup>CD21<sup>-lo</sup> B cells in some autoimmune diseases may result from the activation of autoreactive naïve B cells that escaped the impaired early B cell tolerance in RA, SjS, and SLE. Of note, we did not observe an increase in CD19<sup>hi</sup>CD27<sup>-</sup>CD21<sup>-lo</sup> B cells in MS or T1D patients, suggesting that self-antigens targeted in these autoimmune diseases may not trigger the expansion of these B cells or that their expansion is not sufficient to be detected systemically in patient's blood<sup>45</sup> (E. Meffre, personal communication). CD19<sup>hi</sup>CD27<sup>-</sup>CD21<sup>-lo</sup> B cells are characterized by the expression of a specific set of molecules compared to other B cell subsets and which include CD11c and T-bet induced by IFN $\gamma$ <sup>85,86,93,94</sup>. Hence, the production of these B cells may occur in an inflammatory environment.

In agreement with this hypothesis, the mechanisms responsible for the generation of these B cells involve dysregulated IL-21/IL-4/ IFN $\gamma$  production during B cell responses in germinal centers<sup>93-96</sup>. A recent study from our group shows that CD19<sup>hi</sup>CD27<sup>-</sup>CD21<sup>-lo</sup> B cells are specifically enriched in RA patients with defective ATM activation and correlate with a high prevalence of erosive joint disease, likely through their increased expression of pro-osteoclastic RANKL and IL-6 cytokines upon activation<sup>68</sup>. Thus, elevated frequencies of circulating CD19<sup>hi</sup>CD27<sup>-</sup>CD21<sup>-lo</sup> B cells in newly diagnosed RA patients may represent a valuable biomarker to identify patients with a high risk for developing erosive joint damage. In line with this observation, increase in circulating CD19<sup>hi</sup>CD27<sup>-</sup>CD21<sup>-lo</sup> B cells in SLE patients is also associated with more severe autoimmune disease<sup>93</sup>. We conclude that the impaired selection of developing autoreactive B cells in patients with autoimmune diseases likely favors the production of circulating CD19<sup>hi</sup>CD27<sup>-</sup>CD21<sup>-lo</sup> B cells that express autoreactive antibodies, produce pro-inflammatory cytokines, and thereby foster severe disease manifestation.

### **B cell tolerance checkpoint defects promote autoantibody production**

While early B cell tolerance checkpoint defects in autoimmune diseases result in the accumulation of autoreactive naïve B cells with an altered BCR repertoire in patient's blood, it remained to be determined whether these naïve autoreactive clones may favor the production of autoantibodies in their sera. A direct method to test this hypothesis consists of measuring the affinity of recombinant monoclonal antibodies (mAbs) cloned from naïve B cells for self-antigens targeted by autoimmune responses. We recently evaluated by Surface Plasmon Resonance the affinity of mAbs expressed by mature naïve B cells from AIRE-deficient patients who display autoimmune manifestations including T1D and present a whole series of anti-cytokine autoantibodies in their serum, which target various IFNs and IL-17 family members<sup>19,97-99</sup>. We found that the impaired peripheral B cell tolerance checkpoint induced by AIRE deficiency results in the production of autoreactive mature naïve B cells that express antibodies devoid of somatic hypermutations that recognized IFNs, IL-17A, IL-17F and insulin with micromolar affinity and that were initially identified as polyreactive clones using our reference assay<sup>17,19</sup>. Thus, anti-cytokine and anti-insulin clones are already present in the naïve B cell compartments of AIRE-deficient patients and their affinity for self is further increased by somatic hypermutation<sup>100</sup>. It remains to be determined if patients with classical autoimmune diseases such as AIRE-deficient patients

harbor autoreactive clones in their naïve B cell compartments with measurable affinity for self-antigens recognized by serum autoantibodies.

A second indirect approach to assess if impaired early B cell tolerance checkpoints contribute to autoantibody production consisted of artificially removing somatic hypermutation from mutated recombinant autoreactive clones with known self-antigen specificity and then testing the specificity of the unmutated revertants that may correspond to the naïve germline-encoded precursors activated by the autoimmune response. This process involves the replacement of somatically mutated bases that result in an amino acid replacement back to the bases present in the corresponding germline sequence of Ig gene segment<sup>44,101</sup>. Because it is impossible to determine whether somatic mutations have been introduced in regions containing non-template N nucleotides that do not match germline Ig gene segments at V-D and D-J junctions, reversion accuracy is unclear. For instance, unmutated revertants from anti-cytokine autoantibodies in AIRE-deficient patients did not bind to their respective self-antigen, suggesting that these specificities emerged from unreactive clones through acquisition of somatic hypermutations, whereas we showed instead that anti-cytokine reactivity could be easily detected in the unmutated naïve B cell compartment of these patients as presented above<sup>19,100</sup>. In pemphigus vulgaris, somatically hypermutated pathogenic autoantibodies recognize desmoglein-3, whereas the vast majority of unmutated revertants did not bind this self-antigen<sup>102</sup>. Both of these studies did not include reversion of the IgH CDR3 region which can include identifiable mutations in the D and JH gene segments. In contrast, the germline-versions of human recombinant mAbs that recognize peptidylarginine deiminase (PAD) retained their anti-PAD binding although it was decreased compared to the mutated counterparts<sup>103,104</sup>. In addition, unmutated revertants of mAbs targeting infection-derived influenza antigens were also able to recognize the targeted antigen, suggesting that reactive clones from immune responses may emerge from the activation of clones with relative initial affinity for the antigen improved by somatic hypermutations<sup>105–107</sup>.

To establish a potential link between early B cell tolerance checkpoint defects and autoantibody production, we examined the reactivity of a set of unmutated revertants corresponding to pathogenic anti-AQP4 autoantibodies cloned from NMOSD patient cerebrospinal fluid (CSF) plasmablasts and plasma cells<sup>108,109</sup>. We increased reversion accuracy by only selecting autoantibody sequences that displayed short (less than ten) non template N-nucleotide additions in heavy chain CDR3s<sup>44</sup>. In addition we reverted any mutations that were identified in the D and JH gene segments. The affinity of the mature anti-AQP4 mAbs ranged from modest to strong ( $K_d$  15.2–559 nM), but none of the germline revertants bound to AQP4, suggesting that somatic hypermutation is required for the generation of NMOSD-specific anti-AQP4 autoantibodies<sup>44</sup>. However, several germline autoantibody revertants were found to be both polyreactive and autoreactive, suggesting that mutated anti-AQP4 autoantibodies may originate from the pool of autoreactive mature naïve B cells that escape deletion at B cell counterslection steps in these patients. Similarly, a fraction of mutated clones expressing autoantibodies directed towards the extractable nuclear antigens (ENA) Ro52 and La in SLE patients were found to be polyreactive or self-reactive when their sequence was reverted to germline<sup>110</sup>. Thus, impaired B cell tolerance checkpoints in patients with autoimmune diseases result in the production of autoreactive

clones that may be activated by T cells and increase their specificity for self-antigens by acquiring somatic mutations, which may lead to subsequent disease manifestation when pathogenic.

## Concluding remarks

We have presented data that support the important role of impaired central and peripheral B cell tolerance checkpoints in autoimmune diseases by producing autoreactive naïve B cells with altered BCR repertoire that may present self-antigens to T cells, become activated to produce autoreactive and potentially pathogenic autoantibodies, as well as pro-inflammatory cytokines favoring disease severity. While these autoreactive B cell selection defects pre-exist the onset of autoimmunity, environmental factors play an important role in triggering the events that lead to a break in tolerance and autoimmune diseases. For instance, viral infection by EBV has been associated with many autoimmune diseases including SLE, SjS, and RA and coxsackievirus B with T1D<sup>111–117</sup>. It is unknown if the altered naïve B cell repertoire in patients with autoimmune diseases may affect their anti-viral immune response. While some studies suggest that SLE patients may be more susceptible to infections, their anti-influenza responses appeared as good if not even better than those in healthy donors, suggesting that impaired early B cell tolerance checkpoints may actually favor anti-viral responses<sup>118</sup>. Similarly, anti-HIV responses may benefit from an increase in autoreactive naïve B cells since polyreactivity increases the affinity of anti-HIV antibodies by heteroligation<sup>119</sup>. However, anti-bacterial responses and especially the production of IgA targeting commensal bacteria may be altered in some patients with autoimmune diseases, resulting in a failure to maintain gut microbiota. For instance, monocytes from SLE patients shows a transcriptional signature characteristic of chronic endotoxin exposure that could indicate a breach in the gut barrier, allowing the escape of commensal bacteria or antigens in periphery<sup>120</sup>. In agreement with this hypothesis, SLE patients display autoreactive VH4–34-expressing IgG<sup>+</sup> memory B cells that may be produced by systemic anti-commensal bacteria responses and expand during flares<sup>79,121</sup>. In addition, Kriegel and colleagues recently reported that the translocation of commensal bacteria and especially *Enterococcus gallinarum* from the gut to the liver promotes the development of SLE, further suggesting that commensal bacteria fail to be restrained in the gut of these patients<sup>122,123</sup>. Finally, altered gut microbiota have been associated with the development of autoimmunity<sup>124–127</sup>. It remains to be determined whether the impaired early B cell tolerance checkpoints and the altered naïve B cell repertoire that they induce may favor intestinal dysbiosis in patients with autoimmune diseases.

Finally, anti-CTLA-4 and anti-PD-1/anti-PD-L1 “checkpoint inhibitors” (CPIs) that block immune inhibitory ligands have revolutionized the treatment of cancers<sup>128–132</sup>. However, CPI regimens also induce serious immune and autoimmune related adverse events (IrAEs), which may be life-threatening. Thyroiditis and hypophysitis with secondary or primary adrenal insufficiency, as well as gonadal deficiency, have been reported in 40% and 13% of patients treated with anti-CTLA-4 or anti-PD-1 mAbs but can involve nearly half of patients treated with the combination<sup>130,132–137</sup>. In addition, the development of insulin dependent diabetes may also occur in patients who were treated with anti-PD-1 or anti-PD-L1 mAbs with or without anti-CTLA-4<sup>138</sup>. Since classical, spontaneous T1D is characterized by early

B cell tolerance checkpoint defects, it is tempting to speculate that CPI may interfere with the establishment of B cell tolerance and potentially result in the accumulation of large numbers of autoreactive B cells in the blood of CPI-treated cancer patients, thereby rendering them susceptible to developing autoimmune manifestation. As a consequence, B cell depletion may represent a therapeutic strategy to prevent the development of IrAEs in CPI-treated cancer patients without interfering with CPI anti-tumor responses<sup>139</sup>.

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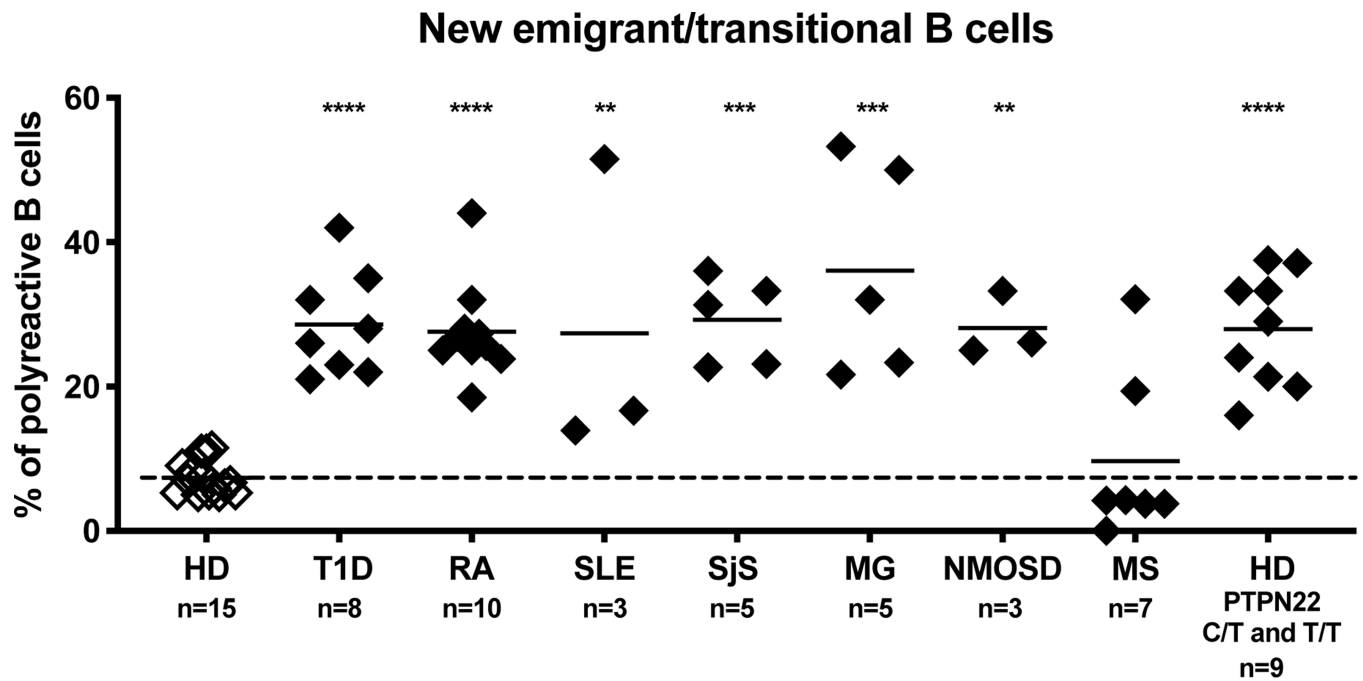
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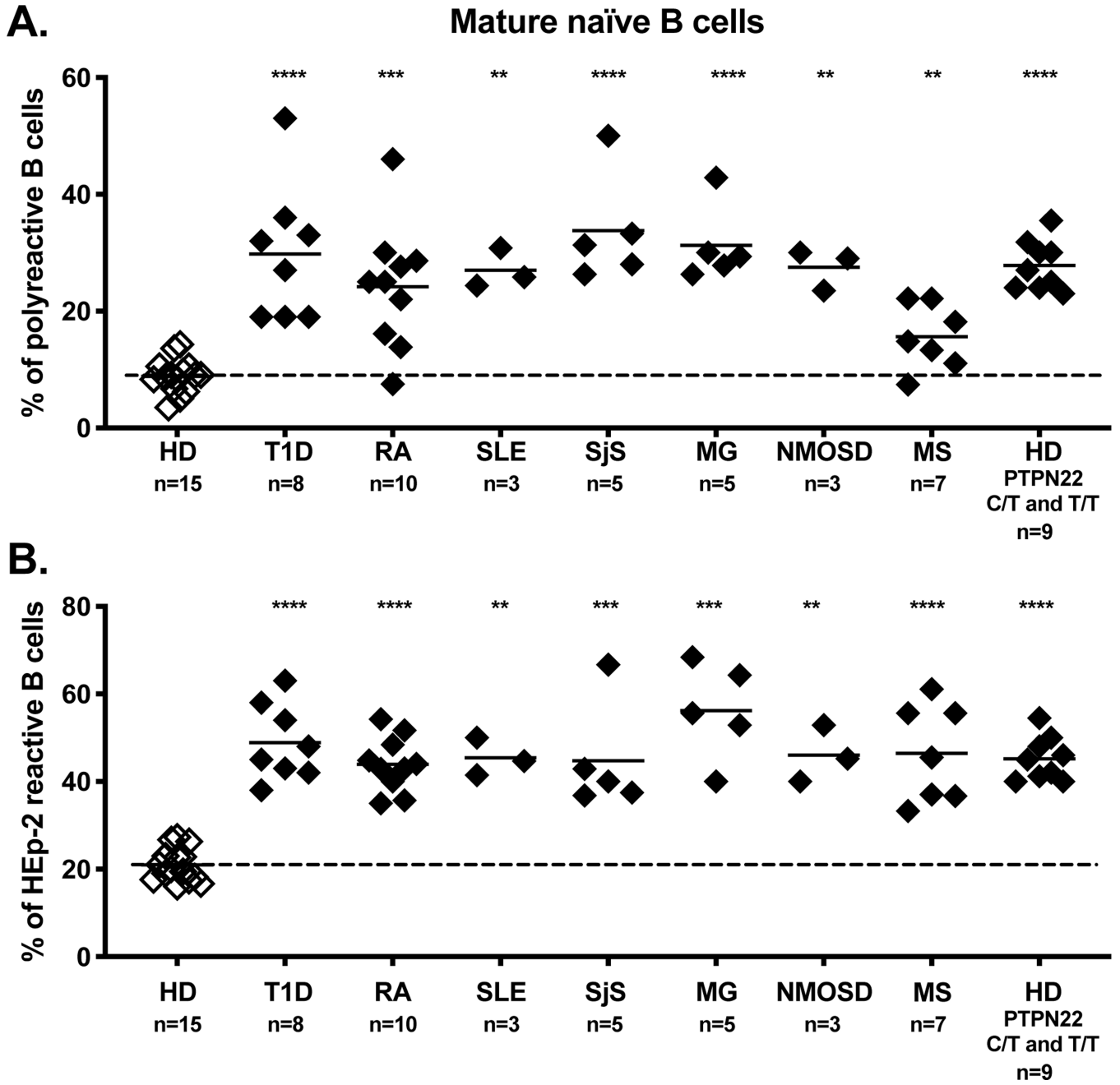
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**Figure 1. Central B cell tolerance is compromised in patients with autoimmune disease and healthy donors carrying the *1858T PTPN22* polymorphism.**

Frequencies of polyreactive new emigrant/transitional B cells in patients with type 1 diabetes (T1D), rheumatoid arthritis (RA), pediatric systemic lupus erythematosus (SLE), Sjögren's syndrome (SjS), myasthenia gravis (MG), neuromyelitis optica spectrum disease (NMOSD), multiple sclerosis (MS) and healthy donors (HD) with either heterozygous (C/T) or homozygous (T/T) *PTPN22* polymorphism were compared to the frequencies derived from a cohort of healthy donors who did not carry the *1858T PTPN22* risk allele. Proportions of polyreactive antibodies expressed by new emigrant/transitional B cells were plotted for each subject group along with the mean and standard deviation for each subject group. Statistical differences are shown when significant (\*\*\*\*,  $p < 0.0001$ ; \*\*\*,  $p < \text{or} = 0.001$ ; \*\*,  $p < \text{or} = 0.01$ ).



**Figure 2. The peripheral B cell tolerance checkpoint is compromised in patients with autoimmune disease and healthy donors carrying the 1858T PTPN22 polymorphism.** Frequencies of (A) polyreactive and (B) autoreactive (HEp-2 reactive) mature naïve B cells in seven distinct autoimmune diseases and healthy donors with either heterozygous (C/T) or homozygous (T/T) PTPN22 polymorphism were compared to the frequencies derived from a cohort of healthy donors who did not carry the 1858T PTPN22 risk allele. Proportions of (A) polyreactive antibodies or (B) autoreactive antibodies reactive toward a human epithelial type 2 (HEp-2) cell lysate expressed by mature naïve B cells were plotted for each subject group along with the mean and standard deviation for each subject group.

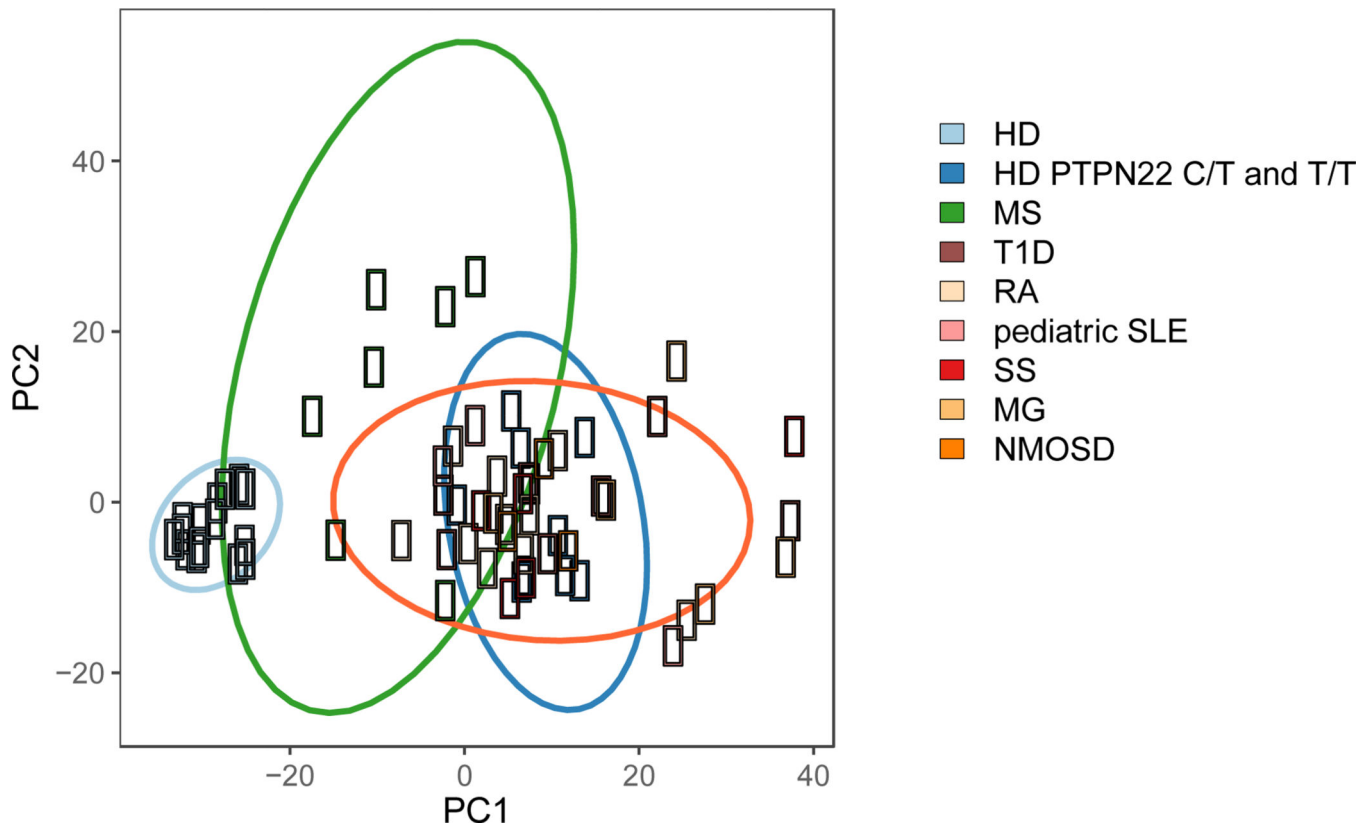
Statistical differences are shown when significant (\*\*\*\*,  $p < 0.0001$ ; \*\*\*,  $p < \text{or} = \text{to } 0.001$ ; \*\*,  $p < \text{or} = \text{to } 0.01$ ).

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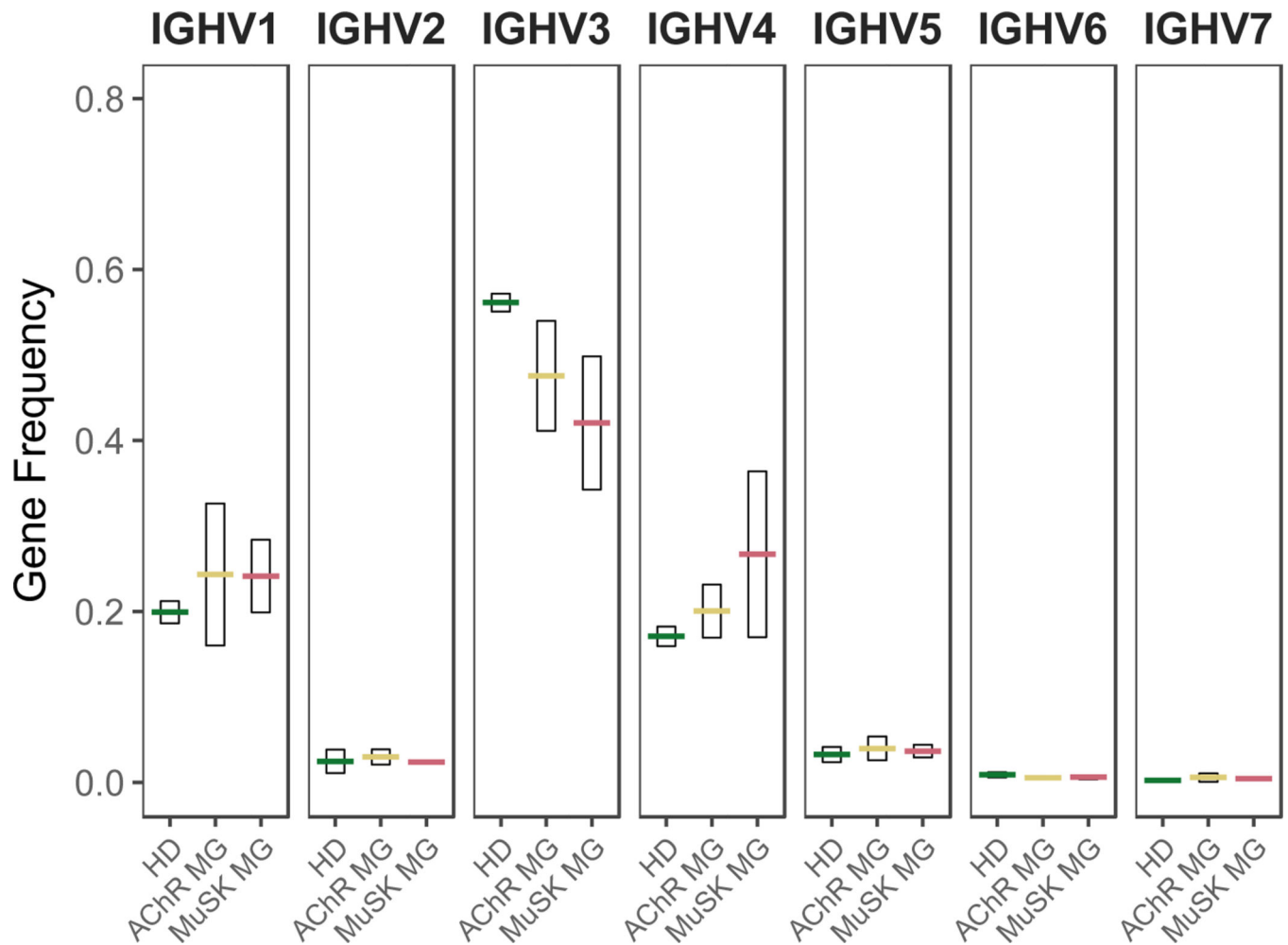
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**Figure 3. Principal component analysis of the frequency of polyreactive and autoreactive B cells in seven distinct autoimmune diseases, healthy donors carrying *1858T PTPN22* risk allele(s) and non-carrier healthy donors.**

Proportions of polyreactive antibodies expressed by new emigrant/transitional B cells and proportions of both polyreactive and autoreactive antibodies expressed by mature naïve B cells were plotted for each subject group. Healthy donor (HD)-derived B cells populations (light blue) cluster together, reflecting the low frequencies of polyreactive and autoreactive clones correlating with functional early B cell tolerance checkpoints. Type 1 diabetes (T1D), rheumatoid arthritis (RA), pediatric systemic lupus erythematosus (SLE), Sjögren's syndrome (SjS), myasthenia gravis (MG), and neuromyelitis optica spectrum disease (NMOSD) segregate away from healthy donors, illustrating the accumulation of polyreactive and autoreactive B cells due to impaired central and peripheral B cell tolerance checkpoints. Healthy donors with either a heterozygous (C/T) or homozygous (T/T) *PTPN22* polymorphism (dark blue), who also display defective early B cell tolerance checkpoints, cluster with the autoimmune disease cohort. B cells from MS patients (green) display a heterogeneous pattern. While two patients with MS cluster with the autoimmune cohort and displayed impaired central and peripheral B cell tolerance checkpoints, most MS patients cluster as an independent group characterized by specific defects of the peripheral B cell tolerance checkpoint.



**Figure 4. Variable region family usage is skewed in the naïve BCR repertoire of patients with myasthenia gravis who suffer from impaired early B cell tolerance checkpoints.**

Antibody heavy chain variable region family usage for the naïve (IgM) B cell compartment. The analysis was performed with 114,296 unique sequences collected from four HDs, three AChR autoantibody positive MG patients (AChR), and three MuSK autoantibody positive MG patients (MuSK). Usage is shown as a frequency of the total unique IGHV sequences (y-axis) for each subject (symbols). Horizontal bars indicate the mean abundance over all subjects of a given status and vertical shading indicates  $\pm 1$  SD about the mean. Data previously reported <sup>81</sup>.