Autoimmunity is the consequence of the combination of genetic predisposition and environmental effects, such as infection, injury, and constitution of the gut microbiome. In this edition of the JCI, Dai et al. describe the use of knockin technology to test the mechanism of action of a polymorphism in the protein tyrosine phosphatase nonreceptor 22 (PTPN22) (LYP) that is associated with susceptibility to multiple autoimmune diseases. The function of this allele, and that of a disproportionate number of autoimmune disease risk alleles, suggests that inhibitory signaling pathways that maintain B lymphocyte immune tolerance may represent an Achilles’ heel in the prevention of autoimmunity.
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Of immunologic tolerance, B cells, and autoimmunity
The immune system is charged with protecting us from the myriad pathogens in our environment and has the added chore of recognizing and eliminating rogue cells that threaten to cause cancer. Competence to generate immune responses is dependent in part on continued generation of new lymphocytes, T cells and B cells, each expressing receptors with unique specificity for antigen. Indeed, we each produce in excess of 10 billion lymphocytes each day. Just by chance, most of these newly produced lymphocytes recognize self antigens and must be silenced to prevent the generation of an immune response to self and resultant autoimmunity (1). Silencing of autoreactive lymphocytes leads to a state of unresponsiveness called immunological tolerance. SLE is an autoimmune disease that usually afflicts women and is caused by loss of immunological tolerance to nucleic acids and their associated proteins, resulting in the production of pathogenic autoantibodies that damage tissues and cause inflammation. A major thrust of contemporary biomedical science is to understand how and why immune tolerance fails in some individuals, thus leading to autoimmune diseases such as SLE.

It is clear that development of autoimmunity is determined by both nature and nurture. Susceptibility is affected by genetics as well as personal experience, such as history of infection and injury. As recently as 2008, only a handful of genetic polymorphisms that confer risk of SLE were recognized, and these had been identified based on candidate gene approaches. With the development of high-throughput genome-wide analysis of SNPs there has come a torrent of new information that has the potential to provide a much more comprehensive view of disease-associated variants. In circumstances in which the polymorphism is found in a structural gene or its regulatory regions, genome-wide association studies (GWAS) can implicate a specific protein and physiologic processes in disease. GWAS have expanded the list of genetic polymorphisms that confer risk of development of SLE to more than 25; most of these affect proteins involved in specific immune functions, particularly interferon signaling, antigen presentation, and lymphocyte antigen receptor signaling (2–6).

Studies of Dai et al. (7) in this issue of the *JCI* stand as testimony to the power of using complementary approaches: combining the identification of disease risk alleles with studies in mice that define the altered function of proteins encoded by risk alleles. Based on previous demonstrations of association of a specific allele of the phototyrosine phosphatase PTPN22 with risk of developing multiple autoimmune diseases, including SLE, RA, type 1 diabetes (T1D), and others (8–11), Dai et al. created and studied mice in which a mutation, R619W, analogous to the variance found in the human risk allele (R620W) (12) was knocked into the murine ortholog of the gene. The authors characterized the effect of the mutation on lymphocyte signaling and various immunological parameters. The results provide important new insight regarding the role of PTPN22 in regulation of signal transduction by antigen receptors and thus in maintenance of immune tolerance. Dai et al. found that the R619W variance did not affect protein half-life of PTPN22 as previously suggested (13), but rather altered receptor-mediated protein tyrosine phosphorylation and caused hypersensitivity to antigen receptor stimulation. Furthermore, B cell expression of the variant was sufficient to promote autoimmunity. Thus, PTPN22 is among the SLE risk alleles defined thus far that result in compromised control of intracellular BCR signaling, leading to loss of B cell tolerance and autoimmunity (2–7). It may be telling that genes encoding molecules that enforce B cell tolerance are disproportionately represented among risk alleles. These findings suggest that autoreactive B cells may be particularly important in the initiation of autoimmunity and that regulation of antigen receptor signaling pathways is fragile yet critical to preventing immune responses to autoantigens.

Anergic B cells, an Achilles’ heel of immune tolerance
Available evidence indicates that newly produced autoreactive B cells are silenced by three mechanisms (1, 14, 15). Those reactive with high-avidity antigens, such as cell-surface molecules, are induced by resultant strong B cell antigen receptor (BCR) signals to edit antigen receptor specificity, a mechanism called receptor editing. If editing fails to eliminate auto-reactivity, these cells are induced by auto-antigen to die, which is referred to as clonal deletion. Editing and clonal deletion are thought to occur primarily in the bone marrow where the cells are produced. B cells that recognize low-avidity self antigens, such as soluble proteins, proceed through development and can be found in peripheral lymphoid organs such as spleen and lymph nodes as well as...
Propagation of opposing signals by B cell antigen receptors

B cell antigen receptor signaling is induced by aggregation of membrane immunoglobulins and associated transducer chains CD79a and CD79b (Figure 1). The cytoplasmic tails of CD79 function as the nexus for recruitment of downstream signaling pathways. Phosphorylation of conserved CD79 tyrosine residues by SRC and Syk family tyrosine kinases facilitates SH2 domain–mediated binding and activation of effectors including these kinases themselves. Although the predominant SRC family kinase expressed by B cells is Lyn, these cells also express Blk and variable levels of Fyn. While Blk appears restricted in subcellular distribution primarily to cytoplasmic organelles (13) and thus may not participate in initial signaling events, both Lyn and Fyn are able to initiate BCR transduction of activating signals (16).
Lyn appears unique among SRC family kinases in its ability to engage not only activating signaling circuitry, but also the inhibitory circuitry that keeps anergic B cells in check (17). Lyn-knockout mice develop severe lupus-like disease consistent with lack of regulatory signaling. On the other hand, Blk- and Lyn-knockout mice do not develop autoimmunity (18, 19). However, BLK is implicated in negative regulation of BCR signaling (18, 19). Lyn mediates its inhibitory effects by phosphorylation of plasma membrane receptors such as CD22, CD72, and FcγRIIB, which act in turn by recruiting protein and inositol phosphatases (SHIP-1 and SHIP-1, respectively) (20). The activity of these enzymes can also be regulated by Lyn-mediated phosphorylation. While SHIP-1 mediates dephosphorylation of ITAMs and other proximal intermediaries in activating signaling pathways, SHIP-1-degrades PtdIns3,4,5P3 needed for activation of Akt, phospholipase C, and calcium signaling. Furthermore, PtdIns3,4P2 generated by SHIP-1 recruits the inhibitory adaptor proteins TAPPI and TAP2. Mice with B cell–targeted knockout of SHIP-1 (21) or SHIP-1 (22) as well as knockins of inactive TAPPs develop severe lupus-like disease (23). Lyn may also mediate inhibitory signaling via activation of cytosolic mediators such as casein kinase 2, which by phosphorylation of the tail of phosphatase and tensin homolog (PTEN) extends its half-life, promoting its inhibitory functions (24). PTEN expression appears important in maintenance of anergy (25). Finally, although less clear mechanistically, Lyn phosphorylates an ER-associated protein complex composed of BLK, BANK1, and the inositol triphosphate receptors (InsP3R), thereby regulating Ca2+ release from intracellular stores (13, 26).

Adding additional complexity, participation of Lyn (and other SRC family kinases) in antigen receptor signaling is regulated by phosphorylation of a tyrosine residue located near the C terminus of the molecule. When phosphorylated by CSK (c-SRC kinase), this phosphotyrosine mediates an intramolecular interaction with the SH2 domain, repressing enzymatic activity and preventing recruitment of the kinase to phosphorylated ITAMs.

SLE susceptibility alleles that affect regulatory signaling in B cells

Genetic polymorphisms affecting expression levels or function of the seven proteins annotated in Figure 1 are associated with SLE. A SNP in the promoter region of the CSK gene is associated with increased expression of CSK (5). Overexpression of CSK, a negative regulator of Lyn, would reduce the activity of inhibitory circuitry downstream from Lyn. PTPN22, a CSK-associated phosphatase, may somehow impinge on this phosphorylation, but based on the work of Dai et al., the risk allele also affects the spectrum of proteins phosphorylated upon antigen receptor stimulation (3). It has been reported that B cells in 66% of SLE patients exhibit reduced Lyn expression (4). While the genetic basis of this is unclear, reduced Lyn expression, like increased CSK expression, would be expected to reduce receptor activation of inhibitory signaling. An allele of CR2, the type 2 complement receptor, containing a 5′ UTR polymorphism that determines reduced expression, increases SLE risk (2). CR2 is a member of a B cell membrane protein complex containing CD19. CD19 is a substrate of Lyn and acts in the processive activation of Lyn (27). Decreased CD21 expression may therefore compromise regulatory Lyn signaling stimulated by opsonized antigens.

Polymorphisms in genes encoding three Lyn substrates also contribute to SLE risk. Risk alleles of the gene for the inhibitory receptor for IgG (FcγRIIB) encode receptors defective in signal transduction (7). As a consequence of this mutation, B cells are not subject to efficient regulation by IgG-containing immune complexes. Another risk allele promotes alternate splicing of BLK mRNA, resulting in reduced BLK expression and, presumably, regulation of its binding partners BANK1 and the InsP3 receptor. BLK haploinsufficiency in the mouse leads to autoimmunity and hypersensitivity to antigen receptor stimulation (18). Finally, a BANK1 risk allele may alter regulation of calcium mobilization following BCR stimulation. Thus, polymorphisms in CSK, PTPN22, LYC, FcγRIIB, BLK, and BANK1 may all compromise B cell tolerance by impairing regulation of antigen receptor signaling.

Conclusions

SLE is an autoimmunity mediated by autoantibodies produced by descendants of autoreactive B lymphocytes. While in healthy individuals, these B cells are silenced by regulatory signaling pathways, studies in mice demonstrate that failure of these mechanisms confers risk of disease development. Perhaps it should come as no surprise that some human SLE risk alleles, such as PTPN22R620W, have an impact on these signaling pathways. However, considering the myriad cells and processes that impinge on the immune response, it is surprising that such a large proportion of risk alleles defined to date are operative in regulation of B cell antigen receptor signaling. It will be interesting to see whether this trend continues as GWAS define new susceptibility alleles. These findings both underscore the importance of regulation of BCR signaling in preventing autoimmunity and indicate that operative mechanisms are finely tuned and fragile. Finally, they may reveal fruitful targets for disease prevention and therapy.

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10. Chung SA, Cruzwell LA. PTPN22: its role in SLE and...
Illuminating regeneration: noninvasive imaging of disease progression in muscular dystrophy

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Muscular dystrophies are characterized by progressive muscle weakness and wasting. Among the key obstacles to the development of therapies is the absence of an assay to monitor disease progression in live animals. In this issue of the JCI, Maguire and colleagues use noninvasive bioluminescence imaging to monitor luciferase activity in mice expressing an inducible luciferase reporter gene in satellite cells. These cells proliferate in response to degeneration, therefore increasing the level of luciferase expression in dystrophic muscle.

Introduction
Skeletal muscle has a robust regenerative capacity, with rapid reestablishment of full strength, even after severe damage to the tissue. Regeneration is mediated by muscle stem cells, called satellite cells. In response to muscle damage, satellite cells proliferate, differentiate into myoblasts, and fuse into myotubes, which act to repair damaged muscle. In muscular dystrophies, continuous muscle degeneration is accompanied by regeneration of muscle fibers mediated by satellite cell progeny (1).

Currently, the standard method for evaluating disease progression in muscular dystrophy animal models is muscle histopathology. This approach is labor intensive, as it involves the removal and processing of the tissue of interest, imaging of the slides, and analysis of the images. Furthermore, the invasiveness of this approach does not permit consecutive sampling, hindering the ability to evaluate the course of a disease or success of a therapeutic strategy. Other methods for evaluating muscle disease include behavior testing and force testing of the dissected muscle, although the specificity of the results obtained from these tests can often be difficult to assess. High levels of serum biomarkers, such as serum creatine kinase, can be indicative of muscle damage, but levels depend on muscle mass and can be widely variable over time in individual dystrophic mice (2).

Perhaps the best candidate technology for studying muscle disease in live animals is MRI, which can reveal the permeability of muscle fibers correlating with disease severity (3). While MRI is noninvasive, it is more expensive and less widely available than bioluminescence imaging systems in animal research laboratories.

A “regeneration reporter” mouse strain
The first group to use bioluminescence imaging to reveal satellite cell proliferation was Sacco et al., who transplanted a single luciferase-expressing satellite cell into the tibialis anterior (TA) muscle of NOD/SCID mice that were depleted of endogenous satellite cells by irradiation (4). They observed that a single luciferase-expressing satellite cell is capable of self renewal after transplantation. Further, they found a substantial increase in satellite cell proliferation, as indicated by increased bioluminescence values, in response to muscle tissue damage by notexin.

In this issue, Maguire et al. (5) utilized the Pax7CreER<sup>fl%</sup>/LuSEAP mouse first generated by Nishijio et al. (6) to develop a mouse model that could be used to monitor muscle regeneration in response to disease and injury. This mouse expresses a Cre-dependent firefly luciferase gene and an estrogen-responsive Cre-recombinase under the control of the Pax7 locus. Because satellite cells are the only muscle cells in the adult that express Pax7, these mice

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