

Minireview: Glucocorticoids in Autoimmunity: Unexpected Targets and Mechanisms

Jamie R. Flammer and Inez Rogatsky

Hospital for Special Surgery Research Division and Graduate Program in Immunology and Microbial Pathogenesis, Weill Cornell Graduate School of Medical Sciences, New York, New York 10021

For decades, natural and synthetic glucocorticoids (GC) have been among the most commonly prescribed classes of immunomodulatory drugs. Their unsurpassed immunosuppressive and antiinflammatory activity along with cost-effectiveness makes these compounds a treatment of choice for the majority of autoimmune and inflammatory diseases, despite serious side effects that frequently accompany GC therapy. The activated GC receptor (GR) that conveys the signaling information of these steroid ligands to the transcriptional machinery engages a number of pathways to ultimately suppress autoimmune responses. Of those, GR-mediated apoptosis of numerous cell types of hematopoietic origin and suppression of proinflammatory cytokine gene expression have been described as the primary mechanisms responsible for the antiinflammatory actions of GC. However, along with the ever-increasing appreciation of the complex functions of the immune system in health and disease, we are beginning to recognize new facets of GR actions in immune cells. Here, we give a brief overview of the extensive literature on the antiinflammatory activities of GC and discuss in greater detail the unexpected pathways, factors, and mechanisms that have recently begun to emerge as novel targets for GC-mediated immunosuppression. (*Molecular Endocrinology* 25: 1075–1086, 2011)

NURSA Molecule Pages: Nuclear Receptors: GR; **Coregulators:** SRC-1 | GRIP1 | AIB1 | CBP | p300; **Ligands:** Dexamethasone | Hydrocortisone.

In 1948, a patient at St. Mary's Hospital in Duluth, MN, received the first injection of synthetic cortisol to treat rheumatoid arthritis (RA). Two years later, Edward Kendall, Tadeus Reichstein, and Philip Hench received the Nobel Prize in Physiology and Medicine for their roles in isolating, synthesizing, and delivering cortisol (1, 2); more generally, for discovering the antiinflammatory properties of glucocorticoids (GC). Since then, GC have been used to treat a great variety of inflammatory disorders, and their therapeutic uses are ever widening. In 2008, over 44 million prescriptions for oral, topical, or inhaled GC were written in the United States alone, and GC are a standard in any situation where immunosuppression is desired: after transplant surgery, during severe allergic reactions or autoimmune flare-ups, and as a supplement to certain chemotherapies (3). Much like the diseases for which they are administered, the mechanisms

of action of these steroid molecules are extremely diverse. In fact, we now know that GC are immunomodulatory rather than indiscriminately immunosuppressive and that their molecular functions are far more complex than previously recognized. In this minireview, we discuss published examples of GC effects on cytokine-driven autoimmunity and highlight the emerging concepts of their therapeutic mechanisms in various disease states.

GC Receptor (GR) Signaling

GC are a class of cholesterol-derived steroid molecules that elicit an array of responses in virtually every tissue; indeed,

Abbreviations: AP, Activating protein; APC, antigen-presenting cell; CBP, cAMP response element-binding protein-binding protein; DC, dendritic cell; Dex, dexamethasone; dsRNA, double-stranded RNA; GC, glucocorticoid; GR, GC receptor; GRE, GC-response element; GRIP, glucocorticoid receptor-interacting protein; IFN, interferon; IRF, IFN regulatory factor; ISG, IFN-stimulated gene; ISRE, IFN-stimulated response element; Jak, Janus kinase; LPS, lipopolysaccharide; MΦ, macrophage; MS, multiple sclerosis; NCoA, nuclear receptor coactivator; NF, nuclear factor; NR, nuclear receptor; pDC, plasmacytoid DC; RA, rheumatoid arthritis; SLE, systemic lupus erythematosus; STAT, signal transducer and activator of transcription; TBK, TANK-binding kinase; TLR, Toll-like receptor.

ISSN Print 0888-8809 ISSN Online 1944-9917

Printed in U.S.A.

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doi: 10.1210/me.2011-0068 Received February 11, 2011. Accepted March 29, 2011.

First Published Online April 21, 2011

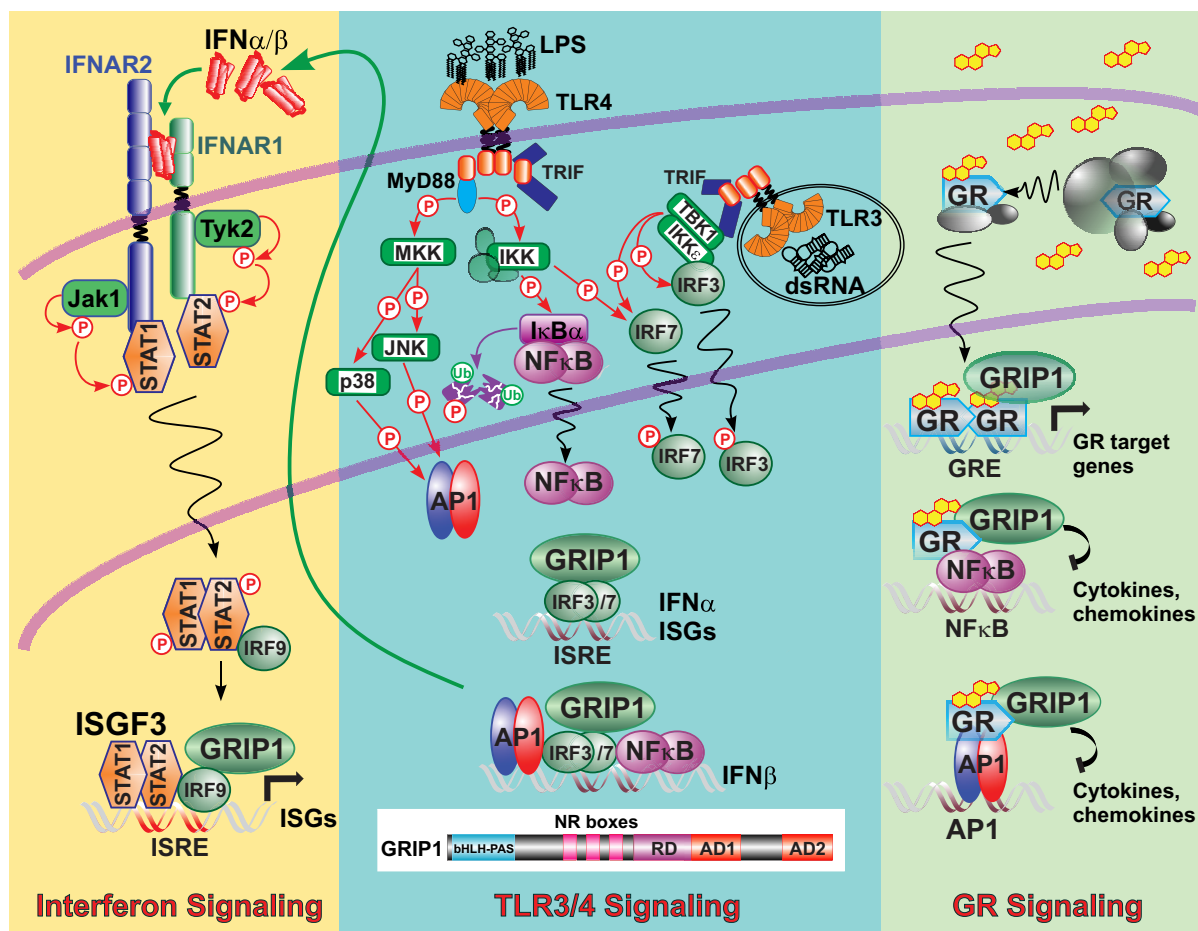


FIG. 1. A shared coregulator GRIP1 in the GR and type I IFN signaling networks. The three panels depict a GR signaling pathway (right) and the TLR3/4-induced type I IFN production (center) and signaling (left) cascades. The GRIP1 domain structure is diagrammed at the bottom center. Detailed description in the text. MKK, MAPK kinase; IKK, I κ B kinase; JNK, Jun kinase; Tyk2, tyrosine kinase-2; MyD88, myeloid differentiation primary response gene 88; TRIF, TIR-domain-containing adapter-inducing IFN- β .

GC are important for metabolism, circadian rhythm, reproduction, and immunity. An early indication of the effect of GC on the immune system was based on the observation that acute or chronic stress induced thymic atrophy, which was later shown to result from cortisol-induced T-cell apoptosis (4). GC signal through the GR, a steroid receptor within a larger nuclear receptor (NR) family of ligand-dependent transcription factors. In the absence of GC hormone, GR is a transcriptionally inactive cytoplasmic protein residing in an “aporeceptor” complex that includes heat shock proteins 70 and 90, immunophilins, and p23 (5). Upon GR association with hormonal ligand, this complex partially dissociates, enabling GR to translocate into the nucleus, where it binds genomic GC-response elements (GRE) and regulates transcription of associated genes (Fig. 1, right panel).

The GRE have been classified into three broad groups (6). “Simple” palindromic GRE are composed of two specific inverted hexamers (AGAACA) separated by a 3-bp linker to which GR binds, usually as a homodimer, and acts as the sole DNA-bound regulator. “Composite”

GRE sequences provide a binding surface for GR along with another regulator and may not resemble conventional binding sites for either partner. “Tethering” GRE are binding elements for other transcription factors, e.g. activating protein (AP)1 or nuclear factor (NF)- κ B, to which GR is recruited through protein-protein interactions. Although GR can either activate or repress transcription from GRE of all three types, GR binding to a palindromic GRE usually leads to transcriptional activation, whereas GR recruitment to tethering sites typically effects repression. Of note, repression of AP1 and NF- κ B activities via GR tethering (also known as “transrepression”) is viewed as a critical component of the inhibitory effects of GC on inflammatory and immune responses.

Similar to other mammalian transcription factors, including NR, GR relies on cofactors (coactivators and corepressors) to transduce hormonal signal to basal transcriptional machinery and/or chromatin. These coregulators, which are critical for transcriptional control in eukaryotes, encompass a variety of proteins, whose molecular actions range from stabilizing DNA-bound regulator complexes and recruiting compo-

nents of basal machinery to nucleosome remodeling and altering DNA topology. To date, nearly 250 coregulators have been described for NR alone (7). One extensively studied family of coregulators, the p160 proteins (steroid receptor coactivator-1/nuclear receptor coactivator (NCoA)1, TIF2/glucocorticoid receptor-interacting protein (GRIP)1/NCoA2, and NCoA3, were initially isolated in yeast two-hybrid screens with agonist-activated ligand-binding domains of several NR and shown to facilitate transcription by recruiting histone-modifying enzymes, including cAMP response element-binding protein-binding protein (CBP)/p300 acetyl transferases and coactivator-associated arginine methyl transferase-1 (reviewed in Refs. 8, 9). p160 proteins were later shown to function as coactivators for multiple transcription factors in addition to NR. Interestingly, different transcription factors preferentially interact with different p160, and these preferences are cell and target gene specific (reviewed in Ref. 9). Furthermore, although all three p160 family members can function as coactivators, TIF2/GRIP1 also serves as a GR agonist-dependent corepressor at tethering GRE (Fig. 1, *right panel*) (10, 11).

Multiple Pathways to Autoimmune Activation

GC have been regarded as potent wide-spectrum immunosuppressants for decades. However, the immune system is an intricate network of regulatory pathways and, as such, can be influenced by GC at multiple levels, sometimes with conflicting outputs. Interestingly, GC can modulate both arms of the immune system: innate, which functions as a first line of defense against invading pathogens; and adaptive, which is instructed by immune events that have already transpired and which responds by releasing high-affinity antibodies directed against foreign material. For example, by triggering apoptosis in both “innate” dendritic cells (DC) and “adaptive” T lymphocytes, GR simultaneously affects the activation and effector functions of immune cells through manipulation of their transcriptional pathways.

Innate immune cells, including granulocytes, macrophages (MΦ), and DC, recognize and are activated by molecules that are either nonhost-derived or associated with host cell injury or death. Upon activation, innate immune cells produce a battery of toxic chemicals, such as reactive oxygen and nitrogen species and complement proteins, which act as direct weapons against exogenous threats; chemokines, which attract leukocytes from the bloodstream to infiltrate infected tissues; and cytokines, which can activate or curb innate and/or adaptive responses. In addition, MΦ and DC act as antigen-present-

ing cells (APC), engulfing and degrading pathogens and then “presenting” molecular fragments (antigens) derived from the degradation process to T cells.

Under normal circumstances, in addition to clearing pathogens, APC and other phagocytes eliminate necrotic, apoptotic, and senescent host cells. However, a sustained failure of APC to properly clear these cells and their components can trigger or contribute to autoimmunity (for review, see Ref. 12). The exact causes of autoimmunity are unknown, although certain genetic risk factors, gender, environmental factors, and infections appear to play some role. Autoimmune responses can be driven by a specific antigen: for example, myelin (a protein that covers and protects neuronal axons) is an antigenic target in multiple sclerosis (MS). Other autoimmune diseases manifest systemically: in the case of systemic lupus erythematosus (SLE), B cells produce antinuclear antibodies directed against numerous nuclear components, including double-stranded DNA, histones, and ribonuclear proteins. Despite the great diversity in pathogenesis, both innate and adaptive responses are affected in most autoimmune diseases.

Under the guidance of innate immune cells, naïve T cells can differentiate into at least three T “helper” subsets: Th1, Th2, and Th17 (Fig. 2). The identity of each subtype is orchestrated by unique transcription factors [T-box expressed in T cells (T-bet), GATA3, and retinoic acid receptor-related orphan receptor (RORγt), respectively], which are instructed by the specific cytokine environment. Furthermore, each of the three Th subtypes produces a distinct milieu of cytokines that is inhibitory to the development of the other two. Although not fully understood (reviewed in Ref. 13), the cytokine combinations leading to Th cell specification are beginning to

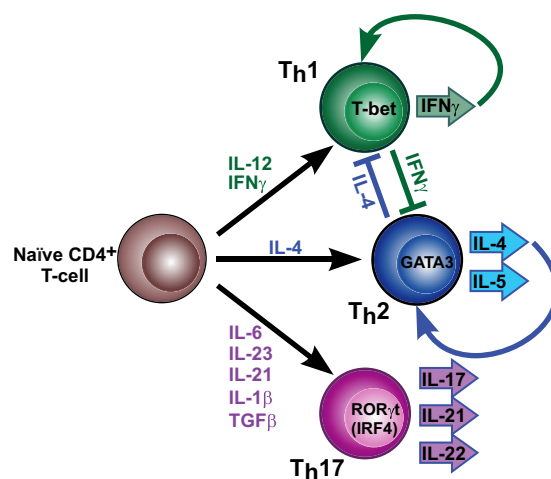


FIG. 2. Cytokine control of effector T-cell differentiation. The three effector T-cell subsets along with the cytokines driving their differentiation, key transcription factors identifying the lineage, and cytokines produced by each subset are shown.

emerge. For example, Th1 cell lineage commitment is driven by IL-12 (14) and, in human cells, type II interferon (IFN) (IFN γ) (15); these cells also produce large quantities of IFN γ , which inhibits Th2 differentiation. Conversely, Th2 cells are specified in part by IL-4, which along with IL-5, is also secreted by these cells and is inhibitory to Th1 differentiation. Recently described Th17 cells (Fig. 2), which characteristically produce IL-17, IL-21, and IL-22, arise from naïve CD4⁺ T cells in response to a unique cytokine combination that has not been completely elucidated but includes IL-6, IL-23, IL-21, IL-1 β , and TGF β (16, 17).

The specific roles of Th cell subsets in autoimmunity and inflammation have been reviewed elsewhere and remain the focus of intense investigation (18). In brief, Th2 cells are associated with allergic reactions, such as asthma. Th1 cells secrete IFN γ , which is a potent activator of inflammatory M Φ and granulocytes; IFN γ also stimulates B cells to produce IgG2, an antibody subclass associated with pathogenic autoantibodies (19). Th1 cells were originally described as the predominant subtype dysregulated in autoimmunity and are still regarded as a driving factor in autoimmune pathogenesis. However, excessive Th17 cell numbers have suggested a role for these cells in inflammation and tissue injury in MS, inflammatory bowel disease, psoriasis, and RA (20–22). Indeed, peripheral blood and tissue levels of IL-17, prominently produced by Th17 cells, were found to be elevated in patients with these disorders (23–28). In addition, studies in murine models of MS (experimental autoimmune encephalomyelitis) and RA (collagen-induced arthritis) have implicated IL-17 in the pathogenesis of inflammation (29–32). Interestingly, T cells producing high levels of both IFN γ and IL-17 were found in the kidneys of lupus patients with nephritis (33), and plasma levels of both IL-12 and IL-17 correlated positively with disease severity in SLE (34). Thus, it appears that either Th1 or Th17 can drive autoimmunity and that disease severity can correlate with either or both (35).

T Helper Cell Polarization Is Regulated by GC

The Th2-polarizing properties of GC have been extensively documented and are known to target T cells both indirectly, by affecting the immunomodulatory properties of APC (36–39), and by direct action on T cells themselves. Indeed, in naïve CD4⁺ T cells, treatment with the synthetic GC dexamethasone (Dex) induces IL-4 mRNA expression (37). Conversely, pretreatment with Dex for as little as 30 min renders naïve T cells incapable of re-

sponding to the Th1-polarizing cytokine IL-12, possibly by down-regulating the IL-12R β_1 - and β_2 -chain gene expression (40, 41). Studies from the Umetsu group in the late 1990s revealed that GC inhibit Th1 polarization indirectly in both mice and humans by specifying the cytokine repertoire produced by innate immune cells (38, 39). Human monocytes or murine splenic cells that were pre-exposed to GC and challenged with lipopolysaccharide (LPS) or heat-killed *Listeria monocytogenes* displayed a marked decrease in IL-12 production. Furthermore, naïve CD4⁺ T lymphocytes cocultured with the Dex-primed APC produced significantly more IL-4/IL-5 and less IFN γ relative to T cells cultured with unprimed APC, suggesting that the naïve T cells had been polarized by the APC to the Th2 phenotype.

The effects of GC on Th17 development are unknown, in part because the events leading to Th17 differentiation are not entirely understood. Overall, however, the indirect evidence available suggests that GC are likely to prohibit Th17 polarization: to wit, the expression of IL-23, which promotes the differentiation of Th17 cells, is inhibited by the GC prednisolone in DC (42, 43). Similarly, several groups, including ours, demonstrated that the induction of IL-6 by cytokines and pathogens in several cell types was GC-sensitive (44–47). Interestingly, GC administration has been shown to reduce IL-6 and TGF β expression in the joints of arthritic mice as well as IL-17 levels in their joints and lymph nodes (48), suggesting that both Th17 differentiation and function may be affected by GC. Furthermore, independent studies reported GC suppression of IL-17 production by purified T cells *in vitro* (49) and by peripheral blood mononuclear cells of patients suffering from Vogt-Koyanagi-Harada syndrome, an inflammatory autoimmune disorder (50). However, whether and to what extent Th17 differentiation and function are affected by GC, as well as the underlying molecular mechanisms and, ultimately, the possible impact on autoimmune disease, remain to be determined.

DC play a critical role in the activation of Th cells, and DC populations of distinct origins have been proposed to differentially regulate the Th subsets. For example, DC raised in an environment with IL-10, IL-6, and TNF α hinder Th1 cell activation (51). Interestingly, the authors later reported that exposure of DC to Dex induced the expression of the Toll-like receptor (TLR)2, a sensor of bacterial lipoprotein, on their surface and that a subsequent stimulation of these cells with a TLR2 ligand initiated the secretion of IL-10, IL-6, and TNF α (52). The provocative conclusion of this study is that GC may inhibit Th1 cell activation indirectly, through manipulation of DC subset identity. Mutual signaling between the TLR2 and GR pathways was further supported by the

unexpected observation that *TLR2* knockout mice display deficiencies in adrenal architecture and corticosteroid production (53).

GR Interferes with Inflammatory Cytokine Production

In addition to affecting differentiation of specific T-cell subsets, GC are widely known for their ability to suppress, directly or indirectly, the activation of proinflammatory cytokine genes. GC-mediated suppression of $\text{TNF}\alpha$ and $\text{IL-1}\beta$ production has long been considered the basis for their efficacy in relieving symptoms of RA, inflammatory bowel disease, and psoriasis. Furthermore, because chronic inflammation itself in certain autoimmune diseases (*e.g.* RA) is pathogenic, the ability of GC to attenuate inflammation speaks to the disease-modifying properties of these drugs (54, 55). The molecular basis for GC action has been reviewed in detail (56) and can be broadly classified into the following major mechanisms. First, liganded GR can interfere with the DNA binding of transcription factors, notably $\text{NF-}\kappa\text{B}$ and AP1, at proinflammatory gene promoters (57, 58). Second, GR engages in protein-protein interactions with transcriptional regulators on DNA (tethering GRE) and actively represses their activity by preventing the recruitment of key coactivators, chromatin modifiers, or components of basal transcriptional machinery (59–63). Third, activated GR was shown to antagonize cytokine gene transcription by sequestering common coregulators, such as CBP (64), although this observation was later debated, when GR was shown to repress the activity of $\text{NF-}\kappa\text{B}$ and AP1, irrespective of the amount of CBP in the cell (65, 66).

In addition to attenuating the activities of transcription factors driving proinflammatory cytokine gene expression, GR can activate certain genes encoding inhibitors of inflammation. For example, in thymocytes or HeLa cells, GC treatment increased the expression of $\text{I-}\kappa\text{B}\alpha$, an inhibitor of $\text{NF-}\kappa\text{B}$ signaling that sequesters $\text{NF-}\kappa\text{B}$ dimers in the cytoplasm and prevents their nuclear translocation (67, 68). This mechanism, however, was not operational in other cell types (69–71); thus, its physiological significance was later debated (reviewed in Ref. 72). GR was also shown to augment the levels of *dual-specificity phosphatase-1* (also known as MAPK phosphatase-1), which inactivates several MAPK, including p38, a critical kinase for AP1 and $\text{NF-}\kappa\text{B}$ activation (73, 74). The importance of this mechanism is exemplified in *dual-specificity phosphatase-1*-deficient MΦ, which are partially resistant to Dex-mediated down-regulation of a subset of proinflammatory cytokines, including $\text{TNF}\alpha$ and $\text{IL-1}\beta$

(75). Another GR target, GC-inducible leucine zipper, inhibits AP1 and $\text{NF-}\kappa\text{B}$ activity by direct protein-protein interactions, precluding their binding to DNA (76, 77). Collectively, these reports highlight the multifarious ability of GR to affect proinflammatory cytokine gene expression.

Type I IFN-Driven Autoimmunity

Although most autoimmune diseases involve an inflammatory component, not all are initiated by the classic proinflammatory cytokines such as $\text{TNF}\alpha$, IL-6, or $\text{IL-1}\beta$. Indeed, initiation and progression of a subset of immune disorders, including autoimmune thyroiditis and SLE, have been linked to dysregulated type I IFN. Unlike $\text{IFN}\gamma$, type I IFN ($\text{IFN}\alpha/\beta$) function primarily as antiviral cytokines in the innate arm of immunity. The recently identified type III IFN ($\text{IFN}\lambda$ also known as IL-28A/B and IL-29) is similar to $\text{IFN}\alpha/\beta$ in its antiviral function but signals through a different receptor complex whose expression is largely limited to cells of epithelial origin (78–80). A link between type I IFN and autoimmunity was suggested as early as 1971, when a high prevalence of the IFN-inducing Epstein-Barr virus was observed in SLE patient sera (81). Years later, Epstein-Barr virus was proposed to be an etiological cause for SLE in susceptible patients and, although a definitive link has not been established, a correlation between viral infections and incidence of SLE was noted (82). IFN therapy, common for the treatment of chronic myeloid leukemia, cutaneous T-cell lymphoma, and viral hepatitis, has also been causally linked to autoimmune side effects. Indeed, *de novo* appearance of autoantibodies against thyroid antigens, pancreatic islet cells, or the adrenal cortex have been reported in the serum of patients after IFN therapy (83–85). Similarly, autoimmune thrombocytopenia and anemia were observed in C57BL/6 mice injected repeatedly for 10 d with $\text{IFN}\beta$ (86).

A potentially fatal chronic disorder, SLE most commonly affects the skin (rash) and kidneys (nephritis) but can manifest anywhere in the body, including the heart (myocardial infarction), joints (arthritis), blood vessels (anemia, thrombocytopenia, and coronary artery disease), lungs (pulmonary hypertension), liver (serositis), and central nervous system (stroke, seizure, and psychosis). The course of the disease is variable, with periods of active disease (flares) alternating with remissions. SLE incidence is nine times higher in women (ages 15–50) than men, affecting approximately 1.5 million people in the United States alone (87). The underlying causes for this gender- and age-specific prevalence are unknown. Fur-

thermore, SLE still lacks a well-defined diagnostic signature. The early studies of disease pathogenesis date back to 1948, when a Mayo Clinic hematologist cultured bone marrow preparations from healthy subjects with serum from lupus patients and observed the formation of polymorphonuclear leukocyte clusters around amorphous masses of disrupted nuclei (88). This phenomenon was later attributed to γ -globulins in the lupus serum reacting with DNA-histone complexes in the nuclear material. These antinuclear antibodies (89), however, are not clearly pathological and fail to correlate with disease convincingly enough to establish them as a diagnostic tool.

Beginning in the late 1970s, multiple groups reported high serum IFN levels and IFN-stimulated gene (ISG) expression (“IFN signature”) in peripheral blood mononuclear cells of lupus patients (90–94), which was found to correlate with SLE severity (95–97). Remarkably, patients with active lupus displayed enhanced ISG expression even when serum IFN levels were normal, perhaps suggesting that aberrant IFN-dependent transcription could contribute to disease (94). This promising correlation, however, also fails to meet the criteria necessary to successfully diagnose SLE. Indeed, the IFN signature appears to be an early event in disease pathogenesis, and many patients display neither the IFN signature nor abnormal cytokine levels.

GC Regulation of Type I IFN Production

IFN gene expression is induced by viral components, such as double-stranded RNA (dsRNA), which bind pattern recognition receptors, specifically TLR (*e.g.* TLR3) on the cell surface or endosomal membranes (Fig. 1, *middle panel*). Receptor ligation initiates a signaling cascade that through a series of adapters ultimately leads to the activation of IFN regulatory factor (IRF)3, NF- κ B, and AP1, which cooperate to induce the transcription of IFN (98). IRF3 binding sites, IFN-stimulated response elements (ISRE), are tandem repeats of GAAA sequences (GAAANNGAAA), which also serve as binding sites for other IRF family members. Type I IFN β and α 1 (murine α 4) are considered to be “immediate-early” cytokines, their transcription being induced directly via the IRF3/NF- κ B pathways and not requiring prior synthesis of protein intermediates, such as IRF7 (98, 99). Transcriptional control of the *IFN β* gene involves a coordinate action of three families of factors, IRF3, NF- κ B, and AP1, which form an enhanceosome at the *IFN β* gene promoter (Fig. 1, *middle panel*); all three are required for the preinitiation complex assembly and efficient *IFN β* gene induction (100–102). Newly synthesized early IFN molecules signal

in an auto- or paracrine manner (reviewed in Refs. 98, 103) by binding their cognate receptor, IFN- α receptor, triggering the recruitment, phosphorylation, heterodimerization, and nuclear translocation of the signal transducer and activator of transcription (STAT) proteins 1 and 2 (Fig. 1, *left panel*). The association of a third transcription factor, IRF9 (p48/ISGF3 γ), with STAT2 completes the formation of a heterotrimeric complex, known as ISGF3, with the ISRE-binding specificity, which initiates a secondary wave of ISG transcription (104). Similar to IFN β , many ISGF3-driven genes contain binding elements for other transcription factors, including NF- κ B and AP1, whereas others are regulated exclusively via the ISRE. The majority of these ISGF3 target genes encode antiviral proteins, among them ISG56, ISG54, 2',5'-oligoadenylate synthetase-1 (OASL-1), and *myxovirus resistance-1* (Mx1), which are also part of the SLE IFN signature (95, 97).

Along with alleviating the symptoms of SLE, GC treatment suppresses ISG expression, thereby eradicating the IFN signature (96). Although the mechanistic basis of this suppression is not well understood, it could conceivably be attributed to the ability of GC to attenuate, directly or indirectly, the transcriptional activity of factors that regulate *IFN* gene expression. Notably, in addition to AP1 and NF- κ B, recent evidence points to the IRF family of transcriptional regulators as previously unrecognized targets for GR-mediated inhibition. Indeed, GC were shown to inhibit the activity of TANK-binding kinase (TBK)1 that activates IRF3 and IRF7, key components of the IFN β enhanceosome (101, 105). Specifically, Dex treatment of U373 astrocytoma cells abolished LPS- or dsRNA-induced phosphorylation of TBK1 at S172, required for TBK1 kinase activity (106). The exact contribution of this mechanism to GC inhibition of IFN gene transcription, however, remains to be determined, because residual IRF3 activity, ISG induction by dsRNA, and to a lesser extent, viral infection persisted in TBK1-deficient M Φ (107).

In 2005, studies from our laboratory and the Glass group described two distinct mechanisms targeting IRF3 transcriptional activity by the activated GR. Specifically, in an unbiased yeast two-hybrid screen, we isolated IRF3 as an interacting partner for GRIP1, a member of the p160 family of coregulators and a known cofactor for GR and other NR (Fig. 1, *center panel*) (108). The GRIP1-IRF3 interaction was also observed *in vitro* and in murine M Φ and was disrupted by Dex-activated GR. Furthermore, depletion of GRIP1 from IRF3 by small interfering RNA knockdown or liganded GR severely compromised the dsRNA-dependent induction of IFN β and other ISG, whereas GRIP1 overexpression relieved inhibition. These

studies implicated GRIP1 as a *bona fide* IRF3 coactivator, whose sequestration by hormone-activated GR attenuated the transcription of IRF3 target genes.

In parallel, Ogawa *et al.* (109) have shown that the induction of IRF3 target genes by bacterial LPS in MΦ can be inhibited by GC through a distinct mechanism. Specifically, they observed that LPS treatment induced corecruitment of IRF3 and the p65 subunit of NF-κB to both ISRE- or NF-κB-containing promoters and that p65 served as an IRF3 coactivator in this context. In response to GC, GR sequestered p65 from IRF3, thereby antagonizing the expression of ISRE-regulated ISG (109). Although *IFNβ* gene expression was not specifically examined, this report further corroborates the emergence of IRF as a previously unrecognized family of transcription factors under indirect GC control.

Recently, a link has been established between sustained TLR7/9 signaling and resistance to GC treatment in SLE (110). Specifically, it was shown that GC-induced apoptosis of plasmacytoid DC (pDC), critical IFN-producing cells contributing to the IFN signature, was attenuated by persistent TLR7/9 activation, whereas pharmacological blockade of TLR7/9 restored pDC sensitivity to GC and normalized ISG expression (110, 111). GC resistance of pDC was cell type specific and appeared to result from TLR7/9-induced escape of the NF-κB pathway from GC-mediated inhibition. Although the mechanistic basis of these latter observations remains unclear, they further suggest extensive cross talk between GR, NF-κB, and IRF-associated signaling pathways ultimately regulating IFN gene expression.

GC Regulation of the IFN Signaling Pathway Through a Shared Cofactor

Despite the wealth of evidence that points to GC-mediated inhibition of cytokine production, little is known about the effects of GC on Janus kinase (Jak)/STAT signaling pathways initiated by cytokines at the cell surface. GR has been shown to interfere with IL-2 signaling, although via an indirect mechanism whereby GR blocks the expression of the common receptor IL-2Rβ and the signaling intermediate Jak3 (112). In stark contrast, GR synergizes with prolactin-activated STAT5 and with IL-6-activated STAT3 (113–116), although the mechanisms of synergy remain unclear. In fact, most reports reveal little effect of GR on cytokine signaling via Jak/STAT. Unexpectedly, however, we found that the type I IFN-initiated Jak/STAT pathway is under GR control and that the target of GC inhibition is the effector complex, ISGF3 (45). Unlike other STAT complexes, the ISGF3 heterotrimer

contains a non-STAT subunit, IRF9, which is thought to dictate the ability of ISGF3 to recognize ISRE, rather than the TTCCNGGAA palindromic sequences targeted by STAT homo- or heterodimers. We found that GRIP1 physically interacted with IRF9, resembling its interactions with IRF3, and served as a coactivator for the IFN-inducible ISGF3 transcription complex. Furthermore, GR activation by coadministration of Dex in MΦ antagonized IFN-induced ISGF3 promoter occupancy, histone acetylation, and RNA polymerase II recruitment to IFN target genes and, similar to IRF3, effected an ISG expression profile identical to that observed upon GRIP1 knockdown or genetic disruption (45). Notably, this regulation was specific to MΦ, in which GRIP1 protein level is exceptionally low; IFN signaling was refractory to Dex in “GRIP1-high” fibroblasts. Supporting these observations, GRIP1 overexpression in MΦ-like RAW264.7 cells relieved GC control of ISG induction.

The fact that two fundamentally different transcriptional regulators (IRF3, responsible for IFN production; and ISGF3, controlling IFN signaling) both required GRIP1 for optimal target gene induction not only suggests a pivotal role of this coregulator in the innate immune response but also reveals a previously unrecognized ability of GC to target the IFN network at two distinct steps. Remarkably, *GRIP1* knockout mice display a hepatic expression profile with a disproportionately high number of down-regulated immune-related genes, a pattern not shared by mice deficient in other p160 family members (117, 118). Interestingly, the domain of GRIP1 responsible for binding IRF family members is not conserved among other p160, highlighting its unique role in mediating GC effects on the immune system. Conversely, the GRIP1-binding IRF association domain of IRF3 and IRF9 shares significant sequence homology with that of the other IRF proteins, and at least *in vitro*, GRIP1 interacts with IRF1, IRF5, and IRF7 (45, 108, 119), suggesting that a similar paradigm may hold true for other IRF family members. Unfortunately, due to their reproductive, metabolic, and endocrine phenotypes (120–123), *GRIP1*-null mice do not represent an appropriate model for studying autoimmunity. Conditional depletion of GRIP1 in specific immune cell compartments in the adult animal will further our understanding of the role of this protein, and its potential interactions with IRF, in autoimmune pathogenesis.

Conclusions

GC are a standard therapeutic approach in many diseases ranging from mild skin rashes to life-threatening syn-

dromes; autoimmune processes, in particular, have been managed with GC for decades. The common thread connecting all these disorders is an exaggerated proinflammatory cytokine response. Not surprisingly, the clinical efficacy of GC is often attributed to GR-mediated suppression of cytokine gene expression. However, our recent studies revealed that the Jak/STAT signaling pathway triggered by at least one cytokine, type I IFN, is directly controlled by GC. Although the presence of the IRF subunit in the IFN-inducible transcription complex, ISGF3, makes this signaling pathway, perhaps uniquely, susceptible to GC regulation, accumulating evidence suggests that the molecular mechanism of regulation is not specific to ISGF3. Indeed, with several IRF family members relying on GRIP1 coactivator properties, one envisions the implications of such interactions for other IRF-regulated pathways. For example, multiple association studies describing genetic polymorphisms in the *IRF5* gene and its regulatory region as risk alleles for SLE (124, 125) warrant an examination of the potential role of GRIP1 in this process. IRF4, a critical regulator of Th17 differentiation and pathogenesis of autoimmunity (126–129), is also of particular interest. It is tempting to speculate that by antagonizing IRF4-dependent transcription through a GRIP1-dependent mechanism, GC inhibit Th17 lineage commitment and autoimmune effects associated with Th cell dysregulation. As appealing as this model might be mechanistically, however, critical consideration needs to be given to the unique cell type-specific environment (developmental and epigenetic restrictions, relative expression levels of individual regulatory components and their posttranslational modifications, or the particular signaling inputs to which a given tissue is exposed *in vivo*) that would determine the balance between the individual signaling networks. Because cofactors such as GRIP1 are beginning to emerge as rheostats that determine the “current” through a given signaling pathway, understanding their physical and functional interfaces with specific regulators in the context of a disease-relevant cell type could reap therapeutic benefits.

Acknowledgments

We thank Dr. L. Ivashkiv for critical comments on the manuscript and Dr. Y. Chinenov for preparation of illustrations.

Address all correspondence and requests for reprints to: Inez Rogatsky, Hospital for Special Surgery Research Division and Graduate Program in Immunology and Microbial Pathogenesis, Weill Cornell Graduate School of Medical Sciences, 535 East 70th Street, New York, New York 10021. E-mail: rogatskyi@hss.edu; or inr2005@med.cornell.edu.

Disclosure Summary: The authors have nothing to disclose.

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