

MINIREVIEW

Molecular Actions of Prolactin in the Immune System (44111)

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Abstract. The immunoregulatory properties of prolactin, a pituitary peptide hormone, have received renewed attention. The prolactin receptor, a member of the hematopoietin/cytokine receptor superfamily, is ubiquitously expressed by cells in the immune system. Certain subpopulations of lymphocytes synthesize and secrete biologically active prolactin, which suggests that prolactin can act as an autocrine and/or paracrine factor to modulate the activities of cells of the immune system. This review focuses on the molecular actions of prolactin in the immune system. Emphasis is given to recent information about the molecular mechanisms of prolactin receptor signal transduction, and the signaling molecules and prolactin-inducible target genes that participate in these responses. In particular, the prolactin-inducible interferon regulatory factor-1 gene and its roles in mediating diverse immune responses are highlighted.

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Prolactin (PRL) is a peptide hormone that is synthesized and secreted primarily from the anterior pituitary. It belongs to a family of hormones that include growth hormone, placental lactogen, and proliferin (1, 2). In mammals, PRL regulates the growth and differentiation of several secretory glands such as the mammary gland (3), the ovary (4), and the male sex accessory organs (5). A role of PRL as a cytokine that modulates immune responses has received renewed and widespread attention, because of its synthesis and secretion from human and rodent lymphocytes (6–11), and the demonstration that its receptor (PRL-R), a member of the hematopoietin/cytokine receptor superfamily (12,

13), is expressed ubiquitously on hematopoietic cells. PRL may modulate the biology of immune function cells by regulating their potential for proliferation, differentiation, and/or apoptosis. These effects of PRL are accomplished in part by regulating the expression of a multifunctional transcription factor gene, interferon regulatory factor-1 (IRF-1). Understanding the various signals that regulate IRF-1 expression and potential IRF-1 functions in cells of the immune system should provide new insights into the immunoregulatory properties of PRL. Several excellent reviews have covered the potential role of PRL in immunity (14–21) and PRL regulation of gene expression in different target tissues (22–24). In this review, I will focus on the molecular aspects of PRL action in the immune system: (i) PRL and the immune response, including clinical, animal, and *in vitro* studies; (ii) lymphocyte PRL; (iii) lymphocyte PRL-R and signal transduction; and (iv) PRL-inducible IRF-1 gene and its potential functions.

PRL and Immune Response

Clinical Relevance. It is known that sex hormones such as estrogen contribute significantly to the patho-

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genesis of a number of autoimmune diseases, which are more common in women than in men (25). Estrogen is a prime regulator of both PRL and PRL-R expression (26). Recent clinical studies have focused on PRL and its possible involvement in immune dysfunction. PRL levels are higher in women than in men, and elevated PRL levels have been reported in patients with SLE (27, 28), multiple sclerosis (29), rheumatoid arthritis (30, 31), psoriatic arthritis (32), and AIDS (33), and in patients prior to transplant rejection (34). Furthermore, the bioactivity of serum PRL in some rheumatoid arthritis patients may be impaired (35). Bromocriptine (BRC), a dopamine agonist which inhibits PRL release from the pituitary, was shown to suppress autoimmune uveitis (36) and to correct T-cell and natural killer (NK)-cell abnormalities in patients with pathological hyperprolactinemia (37, 38). A reduction in the number CD8⁺ T cells was observed in hyperprolactinemic patients, which suggests a susceptibility of this T-cytotoxic/suppressor-cell subpopulation to PRL (39). Though a clear causal relationship is still lacking, these clinical data suggest that elevated PRL levels are often found in patients with immunological diseases.

Animal Studies. A better correlation between PRL and immune regulation is observed in animal studies, where circulating PRL levels have been increased by administering exogenous PRL or decreased by either removal of the pituitary gland or by BRC treatment. Hypoprolactinemic animals were shown to be deficient in mounting various B and T cell-mediated immune responses (40, 41). Injections of PRL and other lactogenic hormones restored immunocompetence to these animals. In aged rats, implantation of PRL- and growth hormone (GH)-secreting pituitary tumor cells reconstituted thymic structure, increased CD4⁺ thymocyte levels, and improved proliferative responses and interleukin-2 (IL-2) production in splenocytes (42, 43). A rise in PRL levels has been observed in rats with experimentally induced adjuvant arthritis (44) and encephalomyelitis (45), and lowering PRL with BRC treatment reduced disease symptoms. In the NZB/NZW mouse model of SLE, BRC was shown to delay mortality significantly, while PRL injection accelerated lupus-related death (46, 47). In DW/J dwarf mice, which lack PRL synthesis, PRL administration increased the number of circulating T cells and enhanced their antigen-specific proliferative responses (48). In Snell dwarf mice, PRL enhanced concanavalin (Con A)-stimulated IL-2 receptor expression on both the CD4⁺ and the CD8⁺ T-cell subsets in the popliteal lymph nodes (49). Finally, studies in athymic nude mice suggest that PRL influences thymic T cell development. Grafting of thymus (to provide thymocytes) and pituitary (to provide high levels of PRL) in nude mice decreased the number of CD4⁺CD8⁺ double-positive thymocytes, but increased CD4⁺ T lymphocytes in the periphery (50). This suggests that PRL

may enhance the development and exit of T lymphocytes from the thymus and influence functions of mature peripheral T cells. Whether PRL exerts immunostimulatory, inhibitory, or no effect on immune targets may be influenced by the dose of PRL employed (stimulatory at low but inhibitory at supraphysiological concentrations) (51–53) as well as by daily circadian rhythms in PRL secretion from the pituitary (54). Together, these animal studies support a role of PRL in promoting the growth and differentiation of immature lymphocytes as well as in stimulating mature lymphocyte functions.

In Vitro Studies. A third line of studies to support a role of PRL in modulating immune responses comes from analysis of hematopoietic cells, including T cells, B cells, hematopoietic precursors, macrophages, and NK cells. By lowering serum PRL levels with BRC treatment in rats and mice, several studies have shown a decrease in T lymphocyte responsiveness to mitogens *in vitro* (55), in mixed lymphocyte reactions (56), in graft-versus-host reactions *in vivo* (56), and in macrophage activation, presumably by suppressing γ -interferon (IFN- γ) production by T lymphocytes (55). However, BRC may exert direct effects on lymphocytes, suppressing T and B lymphocyte activities (57) but inducing CD8⁺ T suppressor cell functions (58). Another approach has been to add exogenous PRL to cells in culture, which demonstrated that PRL can act as a co-mitogen for Con A-stimulated splenocytes (59, 60), for thymocytes (6, 60), for peripheral blood lymphocytes (11, 49, 61), for IL-2-stimulated L2 T cells (62), and for antigen-specific proliferation of peripheral T cells (48), or as a direct mitogen for the rat Nb2 T cells (63, 64). These immunostimulatory effects of PRL may be due to its ability to directly induce the expression of growth-related genes (16, 63, 65) (see section entitled “PRL-Inducible Interferon Regulatory Factor–1 below) or indirectly by upregulating the expression of cytokine receptors, such as IL-2 receptor (IL-2R) on rat splenocytes (66), and mouse CD4⁺ and CD8⁺ T cells (67), erythropoietin receptor (EPO-R) expression on CD34⁺ hematopoietic precursor cells (53), and its own PRL-R receptors in T cells (68, 69) and peripheral blood mononuclear cells (PBMC) (70). Recent studies have also shown that PRL inhibits glucocorticoid-induced apoptosis in T cells (71, 72). Further, PRL has also been suggested to enhance mature B-cell functions by increasing IgG and IgM antibody production (46, 73). Hence, the biological effects of PRL are determined by cell lineage and their stage of differentiation, and involve various aspects of lymphocyte activation, proliferation, differentiation, effector functions, and apoptosis.

Lymphocyte PRL

Understanding PRL action in the immune response has been complicated by the demonstration that lymphocyte

phocytes themselves (6–11, 51, 74, 75) and other extrapituitary tissues (76) can synthesize and secrete biologically active PRL and PRL-like molecules. Blocking experiments that employed anti-PRL antibodies suggested that a PRL-like molecule is secreted by lymphocytes upon mitogenic stimulation and plays a critical role in T-cell proliferative responses (10). Endogenous PRL synthesis by lymphocytes may explain the inability of some studies to demonstrate any effect of exogenously added PRL on proliferation in lymphocyte cultures (10). Some controversy exists as to the exact molecular size (ranging from 22 to 60 kDa) and posttranslational modifications (glycosylation and phosphorylation) of lymphocyte PRL, and whether PRL from the serum of culture media can be “sequestered” and subsequently utilized by T cells (62, 77). A recent study also indicated that the PRL-like molecule secreted by mitogen-stimulated murine splenocytes may not be immunologically similar to pituitary PRL (78). Nevertheless, PRL has been cloned from human thymocytes (7) and PBL (8, 11). Interestingly, an alternative 5' exon situated 6 kb upstream of the pituitary PRL exon I is used to express PRL in lymphoid and other nonpituitary cells (79, 80). The signals that regulate expression of the nonpituitary PRL RNA transcripts are different from those regulating the pituitary counterpart (80, 81) and remain to be further defined. It is not known which lymphocyte subsets are expressing PRL, nor is it clear how pituitary, extrapituitary, and lymphocyte PRL act in concert to modulate immune cell biology.

Lymphocyte PRL-R: A Member of the Hematopoietin/Cytokine Receptor Superfamily

PRL-R on Lympho-Hematopoietic Cells. PRL action on hematopoietic cells is presumably mediated by PRL-Rs, which have been demonstrated at both the mRNA (69, 82–84) and the cell surface protein levels (67, 68, 70, 85) in human, rat, and mouse hematopoietic cells. With the use of monoclonal or polyclonal antibodies directed against the external domain of the PRL-R (86), high-intensity PRL-R staining (PRL-R^{hi}) was observed in the immature cells in the thymus and bone marrow (68, 70), whereas the more mature cells in the periphery (PBL) and the secondary lymphoid organs (spleen, lymph nodes) showed low to medium PRL-R (PRL-R^{med}) staining (67, 85). Unexpectedly, over 90% of bone marrow precursors were PRL-R^{hi} (67, 68, 70), which suggests a potential PRL action on hematopoietic precursor cells. Interestingly, the bone marrow stromal cells, which provide the necessary microenvironment (cytokines and adhesion molecules) for hematopoietic cell differentiation (87), also express the PRL-R during lineage-specific differentiation (88). Within thymocyte subtypes, PRL-R^{hi} to PRL-R^{med} staining is found in this order: double negative (recently arrived from the PRL-

R^{hi} bone marrow) > double positive > single positive, with CD8⁺ > CD4⁺ thymocytes in the mouse (68), and CD4⁺ > CD8⁺ thymocytes in humans (70). In the periphery, about 20% each of CD4⁺ and CD8⁺ T cells show PRL-R^{med} staining, while B220 B cells and macrophage are constitutively PRL-R^{hi}. In mature T cells, PRL-R levels can be induced by PRL (69), IL-2 (51, 89), and Con A (49, 68). Thus, lymphocyte PRL-R levels can be modulated by cytokines. These combined studies provide a broad basis for addressing the functional significance of PRL-R expression on various lineage as well as developmental stages of hematopoietic and stromal precursor cells.

PRL-R Structure/Function. PRL-R belongs to the hematopoietin/cytokine receptor superfamily, which now includes more than 20 members (12, 13, 16, 90). Other members include the receptors for IL-2 β , IL-2 γ , IL-3 to IL-7, IL-9, IL-12, IL-15, G-CSF, GM-CSF, EPO, GH, gp130, LIF, OSM, CNTF, MPL, and the more distantly related receptors for IFN- α/β and IFN- γ (13, 91). These receptors are broadly grouped by function, as they are all involved in the growth and differentiation of lympho-hematopoietic lineage cells, and by conserved extra- and intracellular structural motifs (13, 90–92). Three major PRL-R forms have been identified (93–95), which share identical extracellular ligand binding domain but differ in the length and sequence of the intracellular domains, suggesting potential differences in signaling capacities. The short (42-kDa) and long (80-kDa) PRL-Rs result from alternative splicing of 3' end exons from a single gene (94, 96, 97), whereas the Nb2 T cell PRL-R (65 kDa) contains an in-frame deletion of a 198-amino acid cytoplasmic domain relative to the long PRL-R (97). Interestingly, a PRL-R containing a truncation near the site of the rat Nb2 PRL-R deletion has been cloned from human breast carcinoma tissues (98), but the functional activity of this PRL-R form is unknown. Although the long PRL-R predominates in lymphoid tissues (83, 99), the Nb2 T cell PRL-R shows the highest affinity for PRL (K_d of 3 nM) (96), followed by the long and short PRL-R (93). Whether the deletion in the Nb2 PRL-R is a basis for its greater mitogenic potential is not known. Only the Nb2 and long PRL-Rs mediate mitogenic activities in hematopoietic cells, whereas the short PRL-R is inactive (95, 100, 101). Indeed, transfected short/Nb2 PRL-R heterodimers are incapable of signaling for proliferation (101), which has led to the suggestion that the short PRL-R may serve to modify the signaling capacities of the long PRL-R complex (95, 101).

PRL-R Signal Transduction. Until recently, how cytokine receptors transduce signals had been a puzzle because these receptors do not possess intrinsic kinase or catalytic domains in their intracellular domains, and classical second messengers do not mimic their actions (93). Cytokine receptors signal *via* a group of receptor-associated protein tyrosine kinases (PTK), including

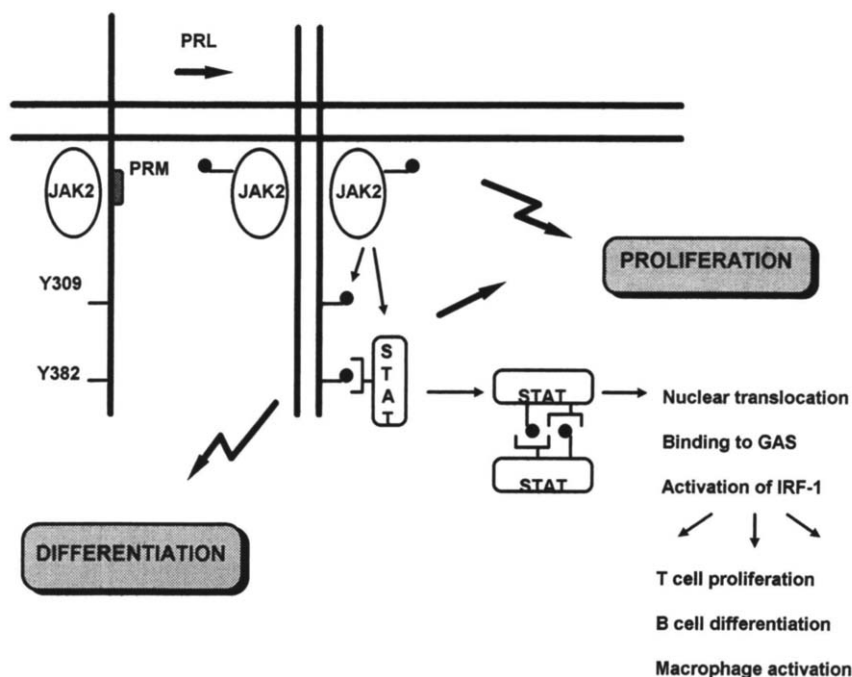


Figure 1. PRL-R signaling through the JAK/Stat pathway. See text for discussion.

Tyk2 (102), JAK1, JAK2 (103, 104), and JAK3 (105, 106), which are either bound to the unliganded receptor (107–110) or recruited (111) to the receptor upon ligand activation. Various combinations of activated JAK/Tyk2 then phosphorylate preexisting but latent cytoplasmic transcription factors, collectively called signal transducer and activator of transcription, or Stat (112) (see section of that name and Fig. 2 below). Tyrosine phosphorylated Stats translocate into the nucleus, bind to cognate DNA sequences, and activate different sets of target genes. This “JAK/Stat pathway” (112, 113) is the prototype signaling pathway used by all hematopoietin/cytokine receptors. In the case of the PRL-R, PRL binding to the PRL-R leads to receptor dimerization or oligomerization (114), which in turn leads to the activation of PRL-R-associated JAK2 kinases (109, 115, 116) (Fig. 1). Activated JAK2 then phosphorylates downstream targets, one of which is the PRL-R intracytoplasmic domain (ICD) itself (115–118) and another, the Stat proteins. Activated Stats form homo- or heterodimers, translocate into the nucleus, bind conserved DNA elements, and turn on target genes. Different parts of the PRL-R ICD regions are involved in signal transduction, including the proline-rich motif (PRM) or Box 1 (90, 117) and several tyrosine residues which become phosphorylated upon JAK2 activation of the PRL-R (118).

Proline rich motif or Box 1. An 8-amino acid (aa) proline-rich motif sequence, also called Box 1, is found close to the transmembrane domain not only in the PRL-R ICD (90) but also in the majority of the hematopoietic/cytokine receptors. The PRM sequence, aliphatic-aromatic-proline-X-aliphatic-proline-X-pro-

line, is critical for receptor signaling (92, 117, 119–124), as it mediates interactions between the receptors and the tyrosine kinase JAK2 (100, 111, 124–127). Although this relationship has been determined by mutagenesis and transfection analyses, it is still unclear how JAK2 physically interacts with the PRM region of the PRL-R (100). Interestingly, a peptide corresponding to the 8 aa PRM of the PRL-R was found to exist as a *cis-trans* conformer, leading to the speculation that isomerization of the proline residues within the PRM by a peptidyl prolyl *cis-trans* isomerase or immunophilin (127a, 127b) may play a role in PRL-R structure/function (127c). This hypothesis remains to be tested. However, the PRM, though critical, is not sufficient for signaling (100, 117, 118, 128). Other regions including Box 2 (100, 128) in the PRL-R, Box 3 (120) and other motifs (129) in other cytokine receptors, as well as tyrosine residues, are also important for receptor function and interactions with signaling molecules, as described below.

Tyrosines residues in the PRL-R. Mutational analyses have shown that multiple tyrosines in the carboxy terminus of the long PRL-R ICD are important for mediating differentiated functions (118). In the context of the Nb2 PRL-R, only the last tyrosine residue, Y382, appears to be critical for mediating differentiation-specific functions. However, studies from our laboratory with the Nb2 PRL-R suggest that both Y309 and Y382 are needed for mediating a proliferative response (Y-F Wang, KD O’Neal, L-Y Yu-Lee, unpublished observation). One function for phosphorylated receptor tyrosine residues is to act as “docking sites” for the recruitment of Stat factors (130–137), as an intermediary step in signal transduction (Fig. 1). Specific se-

quences around these tyrosine residues provide some specificity as to which Stat factors are recruited (134). Although several Stat factors are activated upon PRL stimulation of T cells (see section entitled “PRL-Inducible Stats” below), it is not clear whether they are recruited by “docking” at tyrosine residues on the PRL-R and/or on JAK2 (134, 138). Recent studies of the GH-R indicate that phosphorylated tyrosine residues in the GH-R ICD may not be needed for selected GH-mediated functions (139, 140). This suggests that tyrosine residues on the JAK kinase may be involved in recruiting and activating Stat factors in the GH-R signaling pathway (138). In general, membrane proximal regions of cytokine receptors are involved in mediating proliferative responses (100, 121, 129, 141–145), while the membrane distal regions are important for mediating differentiated functions (117, 118, 123, 126, 128). Interestingly, data from our laboratory indicate that the PRL-R utilizes the PRM as well as both Y309 and Y382 residues, that is, both membrane proximal and distal regions, for signaling to a growth-related gene promoter, interferon regulatory factor-1 (IRF-1) (Y-F Wang, KD O’Neal, L-Y Yu-Lee, unpublished observation) (see section entitled “PRL-Inducible Interferon Regulatory Factor-1” below).

JAK Tyrosine Kinases and PTP Tyrosine Phosphatases. *Kinases.* Cytokine receptor activation is mediated by the activation of JAK PTKs. Up to five tyrosine kinases have been identified (104), including Tyk2, JAK1, JAK2, and JAK3, which is primarily found in hematopoietic cells (106, 146), and a *Drosophila* homolog *hopscotch* (147). These PTKs are either pre-bound (EPO-R, PRL-R, gp130) or recruited (IFN- α / β -R, IFN- γ -R, GH-R) to the cytokine receptors upon ligand binding (104). The kinases are about 120–140 kDa in size and contain an inactive kinase-like domain followed by a carboxy kinase domain (103, 148–150). Mutagenesis and *in vitro* binding analyses have shown that the amino-terminal portion of JAK2 is involved in binding to cytokine receptors (127, 151), while the carboxy domain is critical for JAK kinase activity (148, 151, 152). However, since the JAK kinases do not possess *src* homology (SH) SH2 or SH3 domains, two protein/protein interaction motifs widely used in signaling molecules (153), it is not clear how these kinases physically associate with either cytokine receptors or downstream substrate proteins. In PRL-R signaling, JAK2 phosphorylation and activation are associated with cell proliferation in T cells (109, 115, 116), and dominant negative mutants of JAK2 inhibit PRL-R signal transduction (152).

Phosphatases. Rapid and transient activation of JAK kinases is followed by downregulation of kinase activity and receptor signaling. Receptor downregulation involves the activities of at least two types of protein tyrosine phosphatases, PTP1C, which is found primarily in hematopoietic cells (154), and PTP1D, which is ubiqu-

Signal Transducer and Activator of Transcription (Stat)

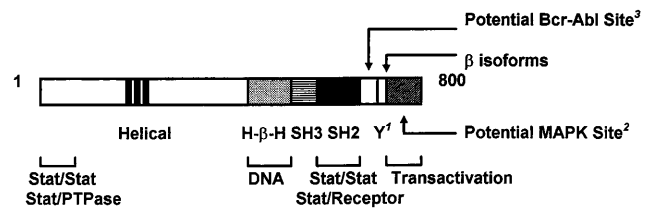


Figure 2. Structure conserved motifs in the Stats are shown, including helical region, a helix- β pleated sheet-helix region, an SH3-like domain that may not be functional, an SH2 domain, a critical tyrosine (Y) residue, and a carboxy-terminal transactivation domain. The β isoform of Stat, which lacks the carboxy-terminal transactivation domain, functions as a dominant negative mutant. See text for discussion. ¹Critical tyrosines in the Stat proteins are: Stat1, Y701; Stat2, Y690; Stat3, Y705; Stat4, Y694; Stat5a/b, Y699; and Stat6, Y641. ²Potential MAPK consensus site, XPXSP, is observed in Stat1 and Stat3 (173). ³Potential Bcr-Abl phosphorylation site, DEVYSKYYT, is observed in Stat5b (24).

itous (155). These PTPases contain two SH2 domains (156), which are involved in binding to the phosphorylated tyrosines on receptor ICDs. Interestingly, PTPases are themselves activated by tyrosine phosphorylation, and upon activation they can dephosphorylate JAKs and/or the receptor itself to downregulate the signaling process (134, 154, 157). Different PTPases appear to inactivate different JAK kinases (158, 159). However, not all receptor-associated PTPases are involved in downregulation of signal transduction. A complex of PRL-R/JAK2/PTP1D appears to be necessary for initiating PRL-R signaling (160). Studies employing genetic mutants that are defective in the expression of JAKs (102, 112) as well as PTPases (154, 158) will help to determine the roles that these enzymes play in cytokine receptor signaling.

Signal Transducer and Activator of Transcription. In addition to receptor ICDs, another target of JAK kinase action is the small family of latent, cytoplasmic transcription factors collectively called Stat (113, 161–163). Seven distinct mammalian Stats have been identified, including Stat1 α / β , Stat2, Stat3 α / β , Stat4, and Stat5a, Stat5b, and Stat6, and a *Drosophila* D-Stat, which is most like Stat5 (164, 165). Stat proteins are about 800 aa in size and range from 89 to 97 kDa. Several Stats also contain carboxy-terminal truncations as a result of alternative splicing of 3' sequences (166), which generates dominant negative β isoform variants (167–172) (Fig. 2). Stat proteins contain the following domains: (i) a helical domain in the amino terminus which appears to be involved in protein/protein interactions (174), (ii) a helix- β pleated sheet-helix domain important for DNA binding (136, 175), (iii) an SH2 domain which is critical for Stat/Stat and Stat/receptor interactions through phosphorylated tyrosines (168, 176), (iv) a critical tyrosine residue that is important for

Stat/Stat intermolecular interactions, nuclear translocation, and DNA binding (177, 178), and (v) a transactivation domain at the carboxy terminus (173, 178). The DNA binding, SH2, and carboxy transactivation domains function as modules, as demonstrated by studies with Stat1/Stat2 (176), Stat1/Stat3 (175), and Stat1/Stat6 (136) chimeric proteins. Additionally, Stat1 and Stat3 contain a potential MAPK phosphorylation site in the carboxy domain, and serine phosphorylation is thought to enhance Stat interaction with and transcriptional activation of target gene promoters (173, 179–181). Moreover, Stat5b contains a potential Bcr-Abl phosphorylation site (24) which may be targets of modification in certain leukemias (182, 183). Recent studies also showed that amino terminus of Stat proteins is also critical for dephosphorylation by PTPase (184). It is thought that the PTPases involved in dephosphorylating nuclear Stats are distinct from those dephosphorylating receptor and JAKs in the cytoplasm (158, 159, 185–187).

Stat binding sites. Two types of conserved DNA elements are targets for Stat factor binding. These sequences were determined initially from analyses of promoters of IFN- α/β -inducible genes (112, 113, 161, 163). The IFN-stimulated response element (ISRE) is comprised of TTTC NN TTTC (direct TTTC repeats) and binds Stat complexes containing Stat1, Stat2, and a non-Stat protein, p48, which stabilizes the Stat interactions at the ISRE (188, 189) (Fig. 2). Another conserved element determined from IFN- γ -inducible genes, called IFN-activation sequence (GAS), is comprised of TTTC NNN GAAA (inverted TTTC repeats or palindrome) and binds a host of Stat factors in response to numerous cytokines (162, 190). In addition, the spacing of the palindromic half sites within the GAS element affects which Stat complexes will preferentially interact at the GAS (163, 191). A GAS palindrome with 3-bp spacing has been shown to interact with Stat1, Stat3, Stat4, and Stat5, while that with 4 bp interacts preferentially with Stat6. Interestingly, in addition to Stat homodimers, Stat1/Stat2 (192) and Stat1/Stat3 (173, 179, 193, 194) heterodimers have been observed to bind at GAS elements and promote gene transcription (192). Further, non-Stat DNA binding factors, such as p48 (189), Sp1 (195), c-Jun (174), v-Src (196), and the glucocorticoid receptor (GR) (197), can interact with Stat complexes to modulate gene transcription. Recent studies of native tandem GAS-like sequences in the IFN- γ gene showed that Stats can interact cooperatively to form tetramers through amino-terminal domain interactions (198).

PRL-inducible Stats. Three PRL-inducible Stats have been described, and they differ in their relative abundance and functional importance depending on the target gene and cell type. The first PRL-inducible Stat was cloned by its ability to bind to a GAS-like

element in the promoter region of a mammary gland milk protein gene, β -casein, and hence it was initially called mammary gland factor (MGF) (199–201). MGF, now known as Stat5a, has been shown to interact with GAS and GAS-like sequences in the promoter regions of several other PRL-inducible genes, including IRF-1 (202–205), β -lactoglobulin (206, 207), whey acidic protein (208), and α_2 -macroglobulin (209). Indeed, Stat5a and Stat5b are two of the most widely used Stats in cytokine receptor signaling. A second and equally prominent Stat, Stat1, has also been shown to bind to the IRF-1 GAS in a PRL-inducible manner in hematopoietic cells (202, 203, 205, 210, 211) (see section entitled “Stats at the IRF-1 GAS” below). A third Stat, Stat3, has been shown by immunoblotting to become tyrosine phosphorylated upon PRL stimulation of premyeloid (212) and T cells (data not shown), but the molecular targets of PRL-inducible Stat3 activation have yet to be identified. Our transfection studies addressing the functional significance of Stat1 and Stat5 interactions at the IRF-1 promoter have shown that Stat1 is a positive regulator of IRF-1 gene expression, whereas, surprisingly, Stat5a and Stat5b both inhibit PRL-inducible IRF-1 promoter activity (G Luo, L-Y Yu-Lee, unpublished observations). The specific effects of PRL-inducible Stat complexes at either the IRF-1 or the β -casein gene promoters are influenced by the presence of other factors interacting at nearby sites (213–215), which provides another level of specificity of JAK/Stat signal transduction. Although Stat1, Stat3, and Stat5 are all activated by PRL stimulation, no Stat1/Stat5 (135, 216, 217) or Stat3/Stat5 (217) heterodimers have been convincingly observed in the same complex. PRL-inducible Stat5a/Stat5b heterodimer formation has been described (218).

Other Potential Signaling Molecules. In addition to the JAK/Stat signaling pathway, other PTKs such as Fyn (219), Raf (220), and Src (221), as well as serine/threonine kinases MAPK (222) and protein kinase C (77), have all been suggested to play a role in PRL-R signaling. How these parallel kinase cascades elicit coordinated gene transcription in PRL-stimulated target cells is currently still unclear (223). Since some of these molecules are pre-associated with the inactive monomeric PRL-R (219, 220), the possibility exists that other PRL-R signaling proteins may be interacting at the PRL-R and can therefore be cloned by genetic means. Using the PRL-R ICD as a bait, our laboratory has cloned 40 potential PRL-R interacting proteins by the yeast two-hybrid interacting cloning strategy (224). The significance of these proteins in PRL-R signal transduction is under investigation. The pleiotropic actions of PRL on cellular proliferation, differentiation, or apoptosis will be determined by the activation and interactions of these potential signaling proteins and parallel kinase cascades.

INTERFERON REGULATORY FACTOR-1

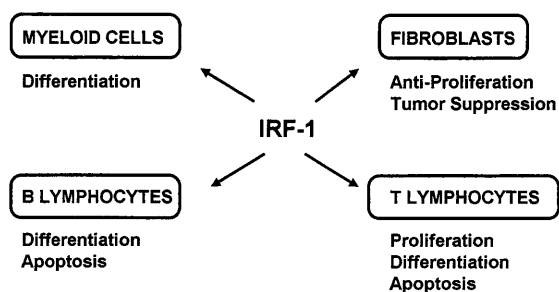


Figure 3. Potential IRF-1 functions. See text for discussion.

PRL-Inducible Interferon Regulatory Factor-1

Several years ago, our laboratory cloned a panel of novel PRL-inducible genes in activated T cells as one way of studying PRL-inducible proliferative responses in T lymphocytes. A PRL-sensitive T lymphoma cell line, Nb2, which was derived from the lymph node of an estrogen-treated male rat (64), was employed. The Nb2 T cells express a high number of high-affinity PRL-R (225), and can be synchronized in lactogen-deficient culture medium and restimulated to grow with 1–10 ng/ml PRL. A cDNA library from PRL-stimulated Nb2 T cells was generated and 26 PRL-responsive gene sequences were isolated by differential screening (65). The most PRL-inducible gene encoded a transcription factor called IRF-1. IRF-1 is currently used not only as a target gene for understanding PRL regulation of gene transcription, but also as a multifunctional factor for understanding how PRL modulates various immune responses.

A Multifunctional Transcription Factor. IRF-1 belongs to a small family of transcription factors, which includes IRF-2 (226), IFN consensus sequence binding protein (ICSBP) (227), IFN- α stimulated gene factor 3 γ (ISGF3 γ) (228), PU.1 interacting protein (PIP) (229), and IRF-3 (230). These factors act as either transcriptional activators or repressors. IRF-1 actions are antagonized by IRF-2 (226) and ICSBP (231), which have similar DNA binding but different transactivation domains. IRF-1 is inducible by PRL and IL-2 in rat Nb2 (65, 232) and murine L2 T cells (233), and by Con A in murine splenocytes (232), which suggests a role in T-cell activation. Originally cloned as a factor involved in IFN- β gene expression (234), IRF-1 turns out to be a more versatile factor which can be induced in a wide variety of tissues (65) in response to cytokine stimulation and host defense against viral infection (234–240). Thus, IRF-1 mediates diverse functions including tumor suppression (241, 242), myeloid differentiation (239), macrophage activation (243, 244), antigen presentation (245, 246), T- and B-cell differentiation (247, 248), and apoptosis (249–251) (Fig. 3) (see Table I below). A role

for IRF-1 in hematopoietic cell differentiation, maturation, and function has been demonstrated by transgenic studies. Animals carrying a disrupted IRF-1 gene (IRF-1^{-/-}) show a 90% reduction in CD8⁺ single-positive T lymphocytes within the thymus (248, 252), severely impaired macrophage functions (243, 252), and an inability to clear certain viruses (237, 248, 253). Further, overexpressing IRF-1 under a heavy chain μ enhancer resulted in a block in bone marrow precursor B-cell differentiation and an absence of mature B cells in the periphery (247). Thus, the transgenic studies showed that IRF-1, or an appropriate level of this transcription factor, is critical for T- and B-cell differentiation and maturation processes as well as macrophage functions. Recent studies have also revealed that IRF family members are expressed in activated T cells and in B cells of all developmental stages (254). Together, these studies agree with our cell culture studies, which show that IRF-1 modulates the activation (65) and proliferation of T cells (65, 255).

Signals That Regulate IRF-1. IRF-1 gene expression is regulated by many signals which are dependent on the particular cell type examined. In fibroblasts, IRF-1 expression is stimulated by virus, IFN, TNF, IL-1, and activators of the protein kinase C pathway such as phorbol esters and calcium ionophore (236, 238). In embryo carcinoma cells, IRF-1 is regulated by developmental cues (256). In myeloid lineage cells, LIF and IL-6 inhibit IRF-1 expression as part of the differentiation pathway (239, 240). In myeloid leukemia cells, IRF-1 is induced by all-*trans* retinoic acid, as part of the growth inhibition pathway (257). Studies from our laboratory show that IRF-1 mRNA is found in various normal proliferating and post-proliferating tissues (65). These combined data support the view that IRF-1 is a multifunctional transcription factor which can respond to a variety of external signals in different tissues and cell types (Fig. 3). In T cells, IRF-1 expression is exquisitely sensitive to PRL (65), IL-2, and Con A (232) stimulation, and is correlated with T-cell activation (G1 phase), cell cycle progression (S phase), and cell proliferation (233, 254, 255, 258).

Biphasic IRF-1 Gene Transcription. In most cell types, IRF-1 induction by cytokine stimulation is rapid and transient. In contrast, IRF-1 is induced twice in a single cell cycle in PRL-stimulated Nb2 T cells. In quiescent and synchronized Nb2 T cells, PRL stimulates IRF-1 gene transcription first at about 30–60 min during early G1, then again at 10–12 hr in early S phase (255, 258). This biphasic transcriptional response is mediated by multiple PRL responsive regions in the IRF-1 promoter and upstream 5'-flanking DNA (211, 258). By transfection analyses, a 1.7-kb IRF-1 5'-flanking DNA was shown to contain elements that promote not only G1- but also S-phase induction of IRF-1 gene transcription, while a 0.2-kb IRF-1 promoter mediates primarily

G1 induction (211). Within this minimal 0.2-kb promoter is a single copy of a GAS element (−123/−113), which can act as a PRL responsive enhancer element (211). Nearby 5′ to the GAS element are additional sites that interact with DNA binding proteins such as Sp1, a constitutive transcription factor (259), and other complexes containing cell cycle regulated proteins, such as Rb, cyclins, and CDKs (260, 261) (data not shown). The integration of cell cycle-regulated proteins and cytokine-regulated Stat factors at the IRF-1 promoter is likely to coordinate the biphasic expression of the IRF-1 gene over the cell cycle in PRL-stimulated Nb2 T cells.

Stats at the IRF-1 GAS. Gel shift analysis has been extensively used to examine which Stat proteins interact at the IRF-1 GAS in a PRL-inducible manner. Thus, Stat1 (202, 205, 210, 211) and Stat5 (203–205) have been detected at the IRF-1 GAS in a PRL-inducible manner in Nb2 T cells (see also section entitled “PRL-Inducible Stats” above). However, this approach is limited, as it does not address the functional significance of Stat interaction at the IRF-1 GAS. Transfection studies employing a PRL-R reconstituted COS cell system showed that Stat1 is a positive regulator of IRF-1 promoter activity, but both Stat5a and Stat5b inhibit PRL-inducible IRF-1 gene expression (G Luo, L-Y Yu-Lee, unpublished observations). Studies are underway to determine whether the different Stat proteins are competing for binding to the IRF-1 GAS element, or whether Stat5 may be “squenching” (262) or competing for factors interacting with Stat1 which are needed for transcriptional activation of the IRF-1 promoter. In this regard, it is possible that how Stat1, versus Stat5, interacts with nearby factors, such as Sp1 (195, 259), Sp1-associated TAF proteins (263), p300/CBP co-activators (263a, 263b, 263c), and cell cycle-regulated proteins (264), may explain their functional antagonism at the IRF-1 promoter. Understanding the kinetics of Stat1 and Stat5 translocation into the nucleus, their relative binding affinities, and their on/off rates at the IRF-1 GAS will elucidate how these different Stats are involved in the rapid up- and downregulation of IRF-1 gene transcription in response to PRL stimulation over the cell cycle. Other molecules, such as PTPases, may be involved in dephosphorylating Stats, JAKs, and the PRL-R to reset the system and to shut down IRF-1 transcription during G1 and early S phase of the cell cycle. Such tight regulation of the expression of a potent transcription factor is consistent with IRF-1’s playing an important role in hematopoietic cell biology.

IRF-1 Target Genes. Understanding how IRF-1 modulates T-cell, B-cell, and macrophage biology is aided by studies of IRF-1 target genes in these cell types. Functional IRF-1 binding sites (IRE) with the consensus sequence GAAAGT (234, 265, 266) have been found in the promoter of numerous genes (Table I). These

Table I. Potential IRF-1 Functions and Target Genes

Functions	Target Genes	References
Immune responses	IFN β	234
	IL-7R α	267
	MHC Class I	245, 268, 269
	TAP1	270
	LMP2	270
	iNOS	243, 244
	OAS	244, 271
	PKR	272–274
Cytokines	IL-4 ^a	265
	IL-5 ^a	265
	IL-6	275
Cell growth	ODC	276
	Angiotensin Type II receptor	277
	GTPase guanylate BP	278, 279
Cell cycle	CKI or P21 ^a	251
Cell differentiation	MyD88	280
Oncogenesis/tumor suppression	IRF-2	281
Apoptosis	p53 ^a	282
Cell adhesion	ICE ^a	250
	V-CAM	283
	E-cadherin ^a	265

Note. Functional IRF-1 binding site or IRF responsive element (IRE) has been demonstrated in these genes, whose expression contribute to diverse functions attributed to IRF-1.

^a IRE not defined yet.

include the oncogene IRF-2 (281); genes involved in immune responses such as IFN- β (234), IL-6 (275), IL-7R α (267), MHC class I (245, 246, 268, 284), transporter associated with peptide processing (TAP1) (270), LMP2 (270), inducible nitric oxide synthase (iNOS) (243, 244), 2′,5′-oligoadenylate synthetase (OAS) (244, 271), and double-stranded RNA-dependent protein kinase (PKR) (272–274); genes involved in cell growth such as ornithine decarboxylase (ODC) (276), angiotensin II Type 2 receptor (277), and GTPase guanylate binding protein (GBP) (278, 279); cell adhesion molecules V-CAM (283) and E-cadherin (265); and an IL-6-inducible, differentiation-specific gene MyD88 (280). In addition, IRF-1 has also been suggested to regulate the expression of cell cycle genes, such as the cyclin-dependent kinase inhibitor CKI or p21 (251) and the tumor suppressor gene p53 (282), cytokine genes IL-4, IL-5 (265), and IL-6 (275), and the apoptosis-related gene IL-1-converting enzyme (ICE) (250). Judging from the complex array and nature of these target genes, IRF-1 is indeed a multifunctional transcription factor which is involved in mediating diverse functions, ranging from immune responses, cell growth, and differentiation to apoptosis. With its potent transcriptional capabilities, it is not surprising that the IRF-1 protein has a short half-life, from 25 min during G1 phase to slightly over 60 min during S phase in T cells (255). Often, IRF-1 works in concert with Stats (270, 279, 280), other IRF members (231), and other DNA binding proteins (275, 285) in mediating

PROLACTIN IN IMMUNE REGULATION

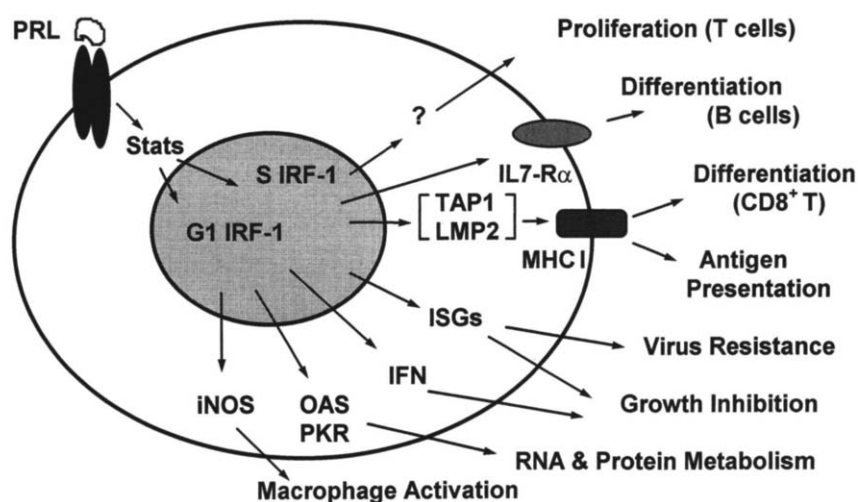


Figure 4. PRL and immune regulation through the transcription factor IRF-1. This cartoon represents a composite look at potential PRL actions in the immune system, through its regulation of the multifunctional IRF-1 gene. IRF-1 functions and IRF-1 target genes (see Table I) are determined in virus-infected fibroblasts (237, 248, 252, 253), cytokine-stimulated T cells (65, 232), B cells (267), and macrophages (243, 244), using cell lines as well as wild-type or IRF-1^{-/-} animals.

rapid as well as sustained or delayed responses at these promoters. The recent demonstration that IRF-1 can interact directly with members of the Rel transcription factor family (246, 268, 283), a process known as cross-coupling (286, 287), broadens the transcriptional potentials of IRF-1 and vastly increases its pool of target genes.

Potential IRF-1 Functions. In fibroblasts, IRF-1 has been shown to be a tumor suppressor gene, involved in antioncogenic activities, suppression of oncogene-induced transformation (249, 288) and apoptosis (249, 250). However, IRF-1's functions in hematopoietic lineage cells are quite different (Fig. 4), as illustrated by studies with IRF-1 knock-out animals. In the IRF-1^{-/-} mice, the three most remarkable phenotypes (i.e., reduction in CD8⁺ thymocytes, impaired macrophage function, and weakened antiviral responses) may be explained in part by the loss of IRF-1 target gene expression in the affected tissues and by a general dampening of the IFN γ response pathway (253). The lack of CD8⁺ thymocytes may be related to a loss of IRF-1-inducible IL-7R α expression in the developing thymocytes (289, 290), resulting in an inability of CD4⁺CD8⁺ double-positive cells to switch to the IL-7R α ⁺CD8⁺ single-positive cells. Although no gross alterations in MHC class I were detected (248), MHC I complex stability and/or function may nevertheless be compromised, a problem compounded by the lack of TAPI expression, resulting in a block in MHC I-dependent CD8⁺ T-cell differentiation in the thymus (291). These combined defects in IRF-1-regulated MHC class I, TAPI, and IL-7R α expression may result in the drastic reduction in CD8⁺ T-cell numbers and CD8⁺ T-cell functions, such as the inability to clear certain viral infections in the IRF-1^{-/-} mice. The loss of

IFN- γ -inducible macrophage activation may be due to the lack expression of iNOS, OAS, PKR, and ODC, which are regulated by IRF-1. The lack of NO production underlies the inability of the IRF-1^{-/-} macrophages to fight infections after challenge by bacteria, fungi, and viruses (237, 248, 253). In view of the central regulatory role played by IRF-1 and the ubiquitous expression of the PRL-R on various immune function cells, it is pertinent to reevaluate a potential role of PRL, through the JAK/Stat/IRF-1 pathway, in modulating some of these immune responses.

PRL and IRF-1 in Immune Regulation. It is becoming clear that an abnormal level of PRL is often associated with altered immune responses in animal models and autoimmune patients. In general, high PRL levels are immunostimulatory, and low PRL levels are immunoinhibitory. It is hypothesized that some of PRL's actions will be exerted through its activation of the IRF-1 gene. However, the functional outcome of IRF-1 expression is different, depending on the cell type and its stage of differentiation and development in the lymphoid tissues. This is best illustrated by IRF-1 functions in fibroblasts (antiproliferation, apoptosis, tumor suppression) versus T lymphocytes (proliferation, antiapoptosis) versus B lymphocytes (differentiation, apoptosis). The PRL/IRF-1 pathway may be involved in B-cell differentiation and apoptosis in the bone marrow, as overexpressed IRF-1 led to a depletion of B cells in the bone marrow (247). The PRL/IRF-1 pathway in developing thymocytes may promote TAPI/LMP2/MHC I expression and play a role in CD8⁺ T-cell differentiation in the thymus, as IRF-1^{-/-} animals have a 10-fold decrease in CD8⁺ T cells (248). In T lymphocytes, PRL has been shown to protect against glucocorticoid-induced apoptosis (71, 72). One way in which PRL ex-

erts its antiapoptotic effects may be through the induction of Bcl-2 and Bax (292) gene expression. Another way in which PRL antagonizes glucocorticoid actions in lymphoid cells may be through modulating GR action *via* the formation of Stat/GR complexes (197). In this way, PRL-inducible Stat factors may antagonize the activities of GR and other members of the steroid receptor family at the promoters of either growth-related or apoptotic-related genes in immune function cells. A closer examination of PRL actions, through the JAK/Stat/IRF-1 pathway, in various cells of the immune system, will provide new insights into the role of PRL in immune regulation.

Summary

Several lines of research have pointed to a role for PRL and IRF-1 in modulating the immune response. The molecular analyses of PRL-R, its ligand PRL, and a PRL-inducible transcription factor, IRF-1, provide insights and generate tools with which to reexamine PRL's role in modulating immune function cell biology in both normal lymphocytes as well as in clinical diseases involving hyperprolactinemia. In the next few years, detailed analysis of the functional domains of the Stat and JAK proteins, cytokine receptors, and other signaling proteins will undoubtedly elucidate how these molecules regulate distinct patterns of gene transcription in various lymphoid cell types. As knock-out animals of PRL, PRL-R, JAKs, and Stats develop and become available for analysis along with IRF-1 knock-out mice, a better understanding of which immune targets and responses are affected or regulated by PRL will emerge. These transgenic animal studies, combined with comprehensive ongoing molecular, genetic, biochemical, and immunological studies in tissue culture, will help to elucidate the immunoregulatory properties of PRL and define its role as a cytokine.

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