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Biology and significance of the JAK/STAT signalling pathways

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Abstract

Since its discovery two decades ago, the activation of the JAK/STAT pathway by numerous cytokines and growth factors has resulted in it becoming one of the most well studied intracellular signalling networks. The field has progressed from the identification of the individual components, to high-resolution crystal structures of both JAK and STAT, and an understanding of the complexities of the molecular activation and deactivation cycle which results in a diverse, yet highly specific and regulated pattern of transcriptional responses. While there is still more to learn, we now appreciate how disruption and de-regulation of this pathway can result in clinical disease and look forward to adoption of the next generation of JAK inhibitors in routine clinical treatment.

Keywords

JAK; STAT; signalling; cytokine; receptor; SOCS

The canonical JAK/STAT pathway

No longer “Just another kinase”, the Janus Kinase (JAK) protein tyrosine kinases are now recognised as an integral component of the cytokine receptor subunits, and enzyme activation, as the initiating step in a signalling cascade required for embryonic development, tissue growth, haemopoietic development and differentiation, innate and adaptive immunity and the inflammatory response.

Upon ligand binding to the cognate transmembrane receptors, two or more receptor-associated JAKs are brought into close proximity through receptor oligomerization to allow auto-phosphorylation and/or trans-phosphorylation by the opposing JAK kinase. Once activated, JAKs then phosphorylate signature tyrosine residues in the cytoplasmic region of the receptors to create docking sites for members of the signal transducers and activators of transcription (STAT) family, so named for their dual ability to function as cytoplasmic signalling modules and transcription factors (1). Upon binding to the receptor through their Src homology 2 (SH2) domain, the STATs themselves become a JAK substrate.

Phosphorylation of the conserved tyrosine residue located between the SH2 domain and the C-terminal transactivation domain results in the formation of parallel STAT dimers, which are stabilized by reciprocal phosphotyrosine and SH2 domain interactions (2,3). Dimer formation is followed by translocation to the nucleus (4–9) where the STAT dimers bind to

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specific palindromic sequences within the promoter regions of target genes to initiate the appropriate transcriptional response (10,11).

Just another kinase: an historical perspective

The JAK/STAT pathway has become one of the most well studied signalling cascades of the past two decades. There are four members of the mammalian JAK family, JAK1-3 and tyrosine kinase 2 (TYK2). JAK1 and JAK2 were discovered using a degenerate PCR screen based on conserved residues in the catalytic units of known protein tyrosine kinases (12–14). Tyk2 was identified by homology screening to the c-fms kinase domain (15) and JAK3 was discovered shortly thereafter (16–18). As their significance became apparent, the acronym transitioned from being “just another kinase” to “Janus” kinase, after the two-faced Roman god Janus (19), and in reflection of the characteristic tandem kinase domains.

The intimate connection between JAK and the cytokine receptors was first revealed by an elegant series of experiments by Ian Kerr, George Stark, Sandra Pellegrini and colleagues. The somatic cell genetic screen resulted in six different complementation groups (U1–U6), which were unresponsive to IFN α (1,20–22). U2–U6 were also unresponsive to IFN β and U2–U4 were unresponsive to IFN γ , strongly suggesting that the complementation groups were deficient in components both unique to and shared between the different ligand responses. Indeed, genetic studies revealed that U1A cells were deficient in Tyk2, whereas the U4–U6 cells were eventually found to be deficient in other components of the IFN β and IFN γ JAK-STAT signaling cascades (1,23–25). An analogous screen selecting for cells that were only unresponsive to IFN- γ identified a mutant cell line (γ 1A) that could be complemented by JAK2 (26). These experiments also defined the pathway hierarchy, as expression of JAK1 in U4A cells restored phosphorylation of STAT1 (24), and conceptually suggested that the JAKs may be utilised by other cytokine receptors. Subsequently, JAK3 was shown to interact with the IL-2 receptor (IL-2R) common gamma chain (γ_c) in a region commonly mutated in patients suffering from severe combined immunodeficiency disease (SCID) (27).

The STATs were originally characterised as components of the IFN α/β and IFN γ transcriptional response (28,29) and this early data preceded the genetic complementation studies. STAT1 and STAT2 (together with IRF9) were found to form a three-protein transcription complex (ISGF3; interferon-stimulated gene factor-3), which bound to common promoter elements within IFN α -responsive genes (ISRE; interferon-stimulated response element) (5,30–33). Similarly, STAT1 complexes were found to bind promoter elements within IFN γ -responsive genes (GAS; IFN γ activation site) (34,35).

Numerous papers followed, identifying a bewildering array of JAKs and STATs that were activated in response to different cytokines/growth factors. The definitive papers utilised gene targeting to demonstrate a layer of specificity, which until that point, had not been fully appreciated.

Studies in non-mammalian species have also made important contributions to our understanding of JAK-STAT biology and its significance, for instance see (36–38). Due to space constraints, this review is limited to mammalian studies.

Non-redundant biological roles of JAK

JAK1 knockout mice die shortly after birth and analysis of JAK1-deficient cells revealed a requirement for JAK1 in signalling via the class II receptors (IFN α/β , IFN γ , IL-10), those cytokines which signal through the γ_c receptor (IL-2, IL-4, IL-7, IL-9, IL-15, IL-21), and those that utilise gp130 (39). JAK2-deficient mice were embryonic lethal due to a lack of

definitive erythropoiesis and analysis of JAK2-deficient cells revealed non-redundant roles for JAK2 in regulating TPO, IL-3, GM-CSF and IFN γ (40,41). While the majority of JAKs are ubiquitously expressed (42–44), JAK3 expression is restricted to the haemopoietic lineages and vascular muscle cells (43,45,46). Gene targeting in the mouse confirmed a critical role for JAK3 in lymphocyte development and function, mediated through cytokines that share the IL-2R γ_c chain (47,48), and this was paralleled by human studies, which identified a JAK3 mutation in a patient with SCID (49). In contrast, deletion of the Tyk2 gene revealed a slightly different picture to that suggested by the genetic complementation experiments, with Tyk2-deficient mice displaying only a modest reduction in signalling capacity in response to IFN α . Responses to IL-12 however, were severely impaired (50).

Non-redundant biological roles of STAT

There are seven STATs in mammalian cells, STAT1-4, 5a, 5b, and 6 (31,33,51–55). STAT5a and STAT5b are closely related and result from a gene duplication event (56), while splice variants of STAT1, 3, 4 and 5 have been reported, which result in a truncated C-terminus (1,57–59). STAT1 is widely expressed, with high levels in heart, thymus and spleen, STAT4 is found mainly in testis, thymus and spleen (60,61), while STAT5a and 5b exhibit differential expression in muscle, brain, mammary gland and secretory organs (seminal vesicles and salivary gland) (56). STAT2, STAT3 and STAT6 are expressed in the majority of tissues (55,60,62).

Stat1-deficient mice display deficiencies in immune responses mediated by IFN α and IFN γ and are highly susceptible to infection with *L. monocytogenes* and vesicular stomatitis virus (VSV) (63,64). The complete lack of responsiveness to interferon confirmed the earlier studies, which had predicted a critical role for Stat1 in interferon signalling. Similarly, *Stat2*-knockout mice are also sensitive to viral infection (65), with analysis of *Stat2*-deficient mice and cells confirming a critical role in regulating signalling by the type I interferons (65).

In contrast, *Stat3*-deficient mice were embryonic lethal (E6.5–7.5), most likely due to a failure to form visceral endoderm (66). Conditional deletion of Stat3 in adult mouse tissues has demonstrated the importance of Stat3 for a wide range of physiological processes, with defects found in lung (67), bone (68), colon (69), heart (70), the nervous system (71) and skin (72), and are consistent with Stat3 inducing biological responses for a large variety of cytokines, including the IL-6/gp130 family (73–77), IL-10 (78,79), G-CSF (80), leptin (81) and IL-21 (82,83). *Stat4*-deficient mice fail to respond to IL-12 and to IL-23 (which shares the IL-12R β 1) resulting in reduced Th1 differentiation and NK cell function (84,85).

Stat5a and Stat5b are required to elicit biological responses to IL-3, GM-CSF (86–88), γ_c cytokines (89–91), growth hormone and prolactin (86,87,92,93). *Stat5a/Stat5b* double deficient mice have impaired mammary gland development and growth retardation, consistent with the roles of STAT5a and STAT5b in mediating prolactin and growth hormone responses, respectively (86,93–95). Mice lacking both Stat5a and b are severely anaemic and the majority die perinatally (95), with an earlier study suggesting reduced erythropoiesis and increased cell death due to reduced EPO-STAT5 driven Bcl-X_L expression (96). Most recently, STAT5 has been found to play additional roles in haemopoietic cell development, differentiation and survival (97–99). *Stat6*-deficient mice are refractory to IL-4 and IL-13 and as a consequence have defective Th2 polarisation, IgG1 and IgE class switching, and greater susceptibility to parasite infection (100–103).

The requirement for individual JAK and Stat molecules is summarised in figure 1.

Domain architecture and mechanism of action

JAK protein tyrosine kinases

Sequence alignment identified seven JAK homology (JH) regions (14) starting with a tyrosine kinase domain (JH1) at the carboxyl (C)-terminus, a pseudokinase domain (104–106) (JH2), an SH2-like domain (JH3-4) (107,108), and finally a divergent four-point-one, ezrin, radixin, moesin (FERM) homology domain (JH4-7) at the amino (N)-terminus (109), with JH4 crossing into both the SH2-like and FERM domains (Figure 2). The high-resolution crystal structures of all four active JAK JH1 domains have now been solved and reveal a highly conserved and typical bi-lobed kinase domain (110–112).

Until recently, the pseudokinase domain was believed to be catalytically inactive as it lacked the key amino acids required for enzyme function, and instead had an autoinhibitory role, with deletion or mutation of the domain resulting in enhanced JAK2 and JAK3 kinase activity (104,105,113). While it was known for some time that phosphorylation within the pseudokinase domain was required for inhibition (114–116), it now appears that the domain is a dual specificity kinase and that autophosphorylation of Ser523 and Tyr570 is required to maintain the inactive kinase in its basal state (117). This result implies that a key step in activation of the JAKs might be de-phosphorylation of Ser523, and the identification of the phosphatase/s responsible will be an intriguing piece of the puzzle. Understanding exactly how the pseudokinase domain mediates its inhibitory function will require the three dimensional structure of the JH2:JH1 complex. The biological significance of this domain is underscored by the acquired mutations found in human myeloproliferative neoplasms (discussed in more detail below), which are predicted to mitigate its autoinhibitory function and which include point mutation of valine 617.

The SH2-like domain has many of the structural and sequence-related hallmarks of a classic SH2 module, yet lacks some of the key residues normally conserved within the SH2 domain family, with experimental mutation of the critical arginine further suggesting that an ability to bind phosphotyrosine is not required for its function (118). Instead, the SH2-like domain is likely to have a structural role and is for instance, required for JAK1 binding to the OSM-R (119) and for TYK2 to maintain surface expression of IFNAR1 (120,121).

FERM domains classically form a three-lobed structure; encompassing a ubiquitin-like fold (F1), an acyl-coenzyme A binding-like fold (F2) and a pleckstrin homology domain fold (F3) (122). The JAK FERM domain mediates binding to the receptor cytoplasmic domains (123–125) and with the suggestion that the FERM domain also contributes to kinase integrity, may be involved in a more complex structural interplay with other JH domains (126,127). The FERM F1 and F2 subdomains (JH6-7) are the minimum requirement for interaction with the membrane-proximal, proline-rich Box 1 region of the receptor cytoplasmic domains (120,124,128–130), although in some instances, other receptor residues such as those within the hydrophobic Box 2 region of the G-CSF-R and EPO-R, are required for both interaction and full JAK activation (131,132).

Careful biochemical studies by Claude Haan and colleagues (133,134) would suggest that the JAKs are an integral component of the receptor subunit with very little release or exchange into the cytoplasm and as such are located primarily at the plasma membrane. This relationship may be functionally required even before the receptors reach the cell surface, with data showing that an interaction with the JAK2 FERM domain is required for proper processing of the immature EPO-R in the endoplasmic reticulum and its subsequent surface expression (135).

STATs

Each STAT has seven conserved features: an N-terminal domain (NT), a coiled-coil domain (CC), a central DNA-binding domain (DBD), a linker region, an SH2 domain followed by a single conserved tyrosine residue, and a C-terminal transactivation domain (TAD). Prior to cytokine stimulation, non-phosphorylated STATs exist as anti-parallel dimers, formed through reciprocal interactions between the N-terminal domains (136–140), which continuously shuttle between the cytoplasm and nucleus. Upon cytokine stimulation, the STATs are localised to the receptor complex by interaction of the SH2 domain with the receptor phosphotyrosine residues (Table 1). JAK phosphorylation of the STAT proteins then results in a spatial reorganisation of the dimer complex, to form an active, parallel dimer stabilised by reciprocal SH2 and phosphotyrosine interactions, which disengages from the receptor and translocates to the nucleus. STAT1, 3, 4, 5 and 6 form homodimeric complexes, while STAT1 and STAT3, at least in vitro, can also form a heterodimeric complex. STAT2 primarily functions as a heterodimer with STAT1 (together with IRF9), but can also act independently of STAT1 (141,142).

To enter into the nucleus, STAT dimers need to traverse the nuclear pore complex (NPC); a bi-directional transport channel embedded in the nuclear envelope and composed of nucleoporins (143,144). Importin α 5 binds to the nuclear localising signal (NLS) of phosphorylated and dimerized STAT1 and 2, and acts as a chaperone to actively traffic the STATs into the nucleus (6,7,145). In the non-phosphorylated state, the NLS is masked and nuclear translocation of STAT1 and 2 is thought to be facilitated by direct binding to nucleoporins; alternatively the STAT protein may be transported by binding to heterologous NLS-containing proteins (146,147). Interestingly, another mechanism has been described for STAT1 during monocyte differentiation, whereby STAT1 binds to nucleolin and it is the NLS of nucleolin that facilitates STAT1 nuclear translocation (148).

In contrast to STAT1 and 2, STAT3 contains a constitutive form of the NLS that allows nuclear accumulation of both phosphorylated and non-phosphorylated STAT3 through association with importin α 3 and in a tissue-dependent manner, with importin α 6 (149,150). Less is known about nuclear trafficking of other STATs although the importin system has been implicated for both STAT5A and STAT6 (9,151). Rac1 and Rac GTPase-activating protein (MgcRacGAP) have been reported to enhance the nuclear accumulation of STAT3 and STAT5A and subsequent transcriptional activity (8,9).

Once in the nucleus, STAT dimers or higher order complexes, are stabilised by NT:NT interactions and bind cooperatively to tandem sequence elements within promoter regions, (often referred to as gamma-activated sequence (GAS) elements) (152,153), to activate the transcription of specific gene subsets. All STATs bind to similar palindromic elements represented by a core TTCN₂₋₄GAA consensus sequence (154). STAT1, 3 and 4 prefer a sequence separated by 3 nucleotides, whilst STAT6 prefers a sequence separated by 4 nucleotides (155). The crystal structure of the phosphodimer core (coiled:coil, DBD and SH2 domain) bound to DNA revealed a clamp-like configuration stabilised by the reciprocal SH2-phosphotyrosine interactions and the interface of the DNA-binding domains with DNA, with the four alpha-helices of the coiled-coil domain projecting outward (156,157).

Serine phosphorylation of a conserved MAPK consensus sequence within the transactivation domain (PMSP within STAT1, 3 and 4 and PLSP within STAT5), (158–161) by various serine kinases (e.g. MAPK, p38, JNK, PKC δ , mTOR, PI3K) (162–166) greatly increases STAT-mediated gene transcription (159,160,162,167,168) and the truncated STAT isoforms, which lack the TAD are largely thought to act as dominant negatives (4,169,170). To add another layer of complexity, it has been suggested that unphosphorylated STAT3b

dimers are also transcriptionally active, and initiate a distinct set of genes from that of the phosphorylated STAT (171,172).

Once released from DNA, the STAT dimer is thought to undergo a conformational change (parallel back to antiparallel, stabilised by NT:NT and CC:DBD interfaces), which exposes the C-terminal phosphotyrosines to phosphatase activity. Dephosphorylation and detachment of DNA are required for STATs to exit the nucleus (173,174) via a process that is dependent on the nuclear export signal (NES) of the STAT molecules and the nuclear export factor, chromosome region maintenance 1 (CRM1) (146,147,175–181); thus completing the activation and deactivation cycle.

In addition to tyrosine and serine phosphorylation, a number of post-translational modifications have been reported to regulate STAT activity. Acetylation of STAT3 on Lys685 by p300/CBP contributes to stable dimer formation and to transcriptional activation (182–186); controversially, acetylation has also been suggested to facilitate dephosphorylation and latency of STAT1 (187). While STAT1 may be acetylated in some circumstances, others cannot reproduce the link between acetylation and dephosphorylation (188). The role of PIAS1 in regulating STAT1 activity by small ubiquitin-like modifier (SUMO) conjugation of Lys703 has also been controversial (189–192). PIAS1 and the impact of SUMO-conjugation are discussed in more detail in the following section.

Negative regulation of JAK-STAT signalling

Given that JAK-STAT signalling is the universal and essential intracellular pathway for cytokine action, a number of regulatory mechanisms have evolved to control the magnitude and duration of signalling. This allows fine-tuning of cytokine-mediated cellular effects and prevents the inappropriate activity often associated with disease development. There are three major mechanisms for negative regulation: receptor internalization, dephosphorylation by phosphotyrosine phosphatases (PTPs), and direct inhibition by protein inhibitors of STATs (PIAS) and suppressor of cytokine signalling (SOCS) proteins. The importance of receptor internalization by endocytic vesicles and subsequent receptor degradation by proteasomal and/or lysosomal pathways (193–200) is classically illustrated by the mutations acquired in the cytoplasmic domain of the G-CSF receptor and found in patients with severe congenital neutropenia. These mutations result in truncation of the cytoplasmic tail of the G-CSFR, simultaneously blocking maturation signalling by G-CSF and leading to defective ligand-induced internalization, as a consequence, the strong proliferative signal predisposes these patients to acute myeloid leukemia (AML) (201–203).

Since tyrosine phosphorylation is integral to JAK-STAT signal transduction, various tyrosine phosphatases such as SH2 domain-containing phosphatase (SHP) 1, SHP2, protein tyrosine phosphatase (PTP) 1B, T cell PTP (TC-PTP) and CD45 are involved in attenuation of signalling, acting either at the membrane to target the receptor-kinase complex, or in the nucleus to target STAT. SHP1 can directly interact with a number of receptors (including the EPOR and IFN α -receptor complex) and can inhibit JAK1 and JAK2 phosphorylation (204) (205). SHP2 has been shown to prevent JAK1 (206), STAT5 α (207), and STAT1 phosphorylation (the latter at both tyrosine and serine residues) (208). PTP1B dephosphorylates JAK1 and TYK2 (209), while TC-PTP targets JAK1 and JAK3 (210). TC45, a nuclear isoform of TC-PTP, dephosphorylates STAT1 and STAT3 (211). Unlike other PTPs, expression of CD45 is restricted to haemopoietic cells and has been demonstrated to indiscriminately dephosphorylate the various JAKs (212).

The PIAS family of E3 SUMO ligases consists of four members, PIAS1, PIASx, PIAS3 and PIASy, and various alternatively spliced isoforms. They were originally named as protein inhibitors of activated STAT because of the observation that PIAS1 and PIAS3 could block

STAT1 and STAT3 DNA binding activity when over-expressed (213,214). PIASx and PIASy were also shown to inhibit STAT4 and STAT1-mediated transcription, respectively, but without affecting DNA binding, presumably by recruiting co-repressors such as histone deacetylases (215,216). The role of PIAS1-mediated SUMO-conjugation of STAT1 has been controversial; SUMOylation of Lys703 has been suggested to selectively inhibit a subset of STAT1-responsive genes (189), while contradictory results suggesting that it is unlikely to have an effect on STAT1 transcription (191). Apart from PIAS1, which is indeed a partial physiological regulator of STAT1 (217), knockouts of other PIAS members revealed relatively little role in STAT-dependent pathways (218–220). It is now clear that the primary E3 activity of PIAS regulates proteins other than the STATs, and may in fact, regulate a general cellular process that impacts on many proteins (221–223).

A new twist on the SUMOylation story has recently emerged from the Vinkemeier group with evidence that SUMO-conjugation obstructs tyrosine phosphorylation of STAT1, resulting in “semi-phosphorylated” dimers and preventing the polymerization and assembly of STAT1 into paracrystalline arrays in the nucleus, enhancing STAT1 de-phosphorylation (224). The physiological consequences of SUMO-conjugation were explored with a “knock-in” mutation (Glu705-Gln), which abolished SUMO-conjugation of Lys730 and resulted in enhanced IFN- γ signalling, suggesting that SUMOylation of STAT1 may be a unique mechanism that has evolved to negatively regulate this pathway. The identity of the E3 SUMO ligase responsible remains unclear (225).

The suppressors of cytokine signalling (SOCS)

Perhaps the most studied inhibitors of JAK-STAT signalling are the SOCS proteins (226). This family of small, cytokine-inducible proteins inhibits signal transduction by blocking JAK and STAT activation and phosphorylation, creating a negative feedback loop. Their induction by cytokines or other stimuli can also cross-regulate signals downstream of other cytokines (227,228). There are eight family members, SOCS1-7 and CIS (cytokine-inducible SH2-containing protein) (226,229); each containing an N-terminal region of variable length with little sequence conservation, a central SH2 domain and a conserved C-terminal SOCS box motif, which interacts with elongins B and C, recruiting Cullin5, and RING-box2 (Rbx2) to form an E3 ubiquitin ligase complex (230). The SOCS proteins therefore function as adaptors to bring the E3 ligase into close proximity with its substrate, promoting the ubiquitination and subsequent proteasomal degradation of SOCS binding partners (231–233).

In addition to their role as E3 ligases, SOCS1 and SOCS3 are able to directly inhibit JAK enzymatic activity. SOCS1 and SOCS3 have a 12 amino acid region adjacent to the SH2 domain, known as the kinase inhibitory region (KIR), which was originally thought to act as a pseudo-substrate blocking the enzymatic activity of JAK by binding to its catalytic cleft (234–236). We now know that the SOCS3 KIR binds directly to a conserved “GQM” motif located within the atypical insertion loop of the JAK1, JAK2 and TYK2, but not JAK3 kinase domains, with the KIR binding in a manner that doesn't compete with either substrate or ATP binding (237).

SOCS1 and SOCS3 can be recruited to the receptor complex through the SH2 domain binding directly to JAK or to the receptor, although the former probably only occurs with SOCS over-expression (238–244). It is most likely that SH2 binding to phosphorylated receptor tyrosine residues brings the KIR into close proximity with the JAK kinase domain, and indeed SOCS3 can bind simultaneously to a gp30 phosphopeptide via its SH2 domain and to JAK via the KIR (237). SOCS1 and SOCS3 can also attenuate signal transduction by targeting the receptor and/or JAK for ubiquitination and proteasomal degradation, although

gene-targeting studies in which only the SOCS box was deleted, suggest that regulation by the SOCS box is the lesser component of SOCS1 and SOCS3 activity (233,245). Other SOCS proteins such as SOCS2 and CIS also appear to have a dual inhibitory function, blocking signalling by competitive binding to STAT docking sites on the receptor (246–249) and via SOCS box-dependent mechanisms (246,250–252).

SOCS1, SOCS2, SOCS3 and CIS are the best characterised of the SOCS family proteins. As revealed by gene-targeting experiments, loss of SOCS1, SOCS2 or SOCS3, results in excessive STAT activity in response to IFN γ , IL-4 (SOCS1), growth hormone (SOCS2), G-CSF and those cytokines which signal through gp130 (SOCS3) (253–255). SOCS1-deficient mice die shortly after birth, due to widespread inflammation and SOCS3-deficient mice are embryonic lethal, due to inappropriate LIF signaling (256–258), while SOCS2-deficiency leads to abnormal postnatal somatic growth (259). In contrast, CIS-deficient mice reportedly have no overt phenotype (256), despite overexpression of CIS implicating it in regulation of growth hormone, prolactin and IL-2 signalling (260,261). The pathways regulated by SOCS4-7 are not as well characterized, with these SOCS proteins functioning largely outside of the JAK-STAT paradigm.

Methylation of the SOCS genes provides another layer of regulation within the JAK-STAT pathway, with hypermethylation of CpG islands within the SOCS1 and SOCS3 promoters correlating with transcriptional silencing in various tumors (262–265).

While much of the JAK/STAT signalling cascade is well understood, surprisingly, some important aspects remain unknown, resulting no doubt from the difficulties in producing recombinant full-length JAK protein, the low levels of endogenous proteins and a lack of quality, high-affinity antibodies. Some questions remain, such as: how the signal is initiated, which JAK initiates the signal, and what is the sequence of phosphorylation events required for activation (and deactivation)? Complete structural information will no doubt clarify how JAK interacts with the receptor and the interplay between the different JAK domains. Similarly, the structure of JAK bound to its negative regulators, the SOCS proteins, is likely to reveal how this family of small molecules controls the extent and magnitude of signalling.

Specificity and diversity of action

Specificity and diversity is introduced into the JAK-STAT signalling pathway by a number of mechanisms. It is initiated by ligand binding to specific receptors, with the differential expression of various receptor subunits determining the cell types that will respond and the magnitude of the response. The receptor-JAK complex is determined by the sequence of the receptor cytoplasmic domains and although this results in different combinations of JAKs (Figure 1), it is not yet clear whether the JAKs display selectivity for phosphorylation of individual STAT or receptor tyrosine motifs and indeed, a comparison of the JAK2 and JAK3 JH1 domains suggests a significant overlap in substrate specificity (266). Rather, it is the STAT-SH2 domain, which drives specificity of signalling, with the sequences surrounding the phosphorylated receptor tyrosine residues determining STAT recruitment to the receptor (Table 1). Similarly, the combination of STATs and the pairing of SH2 domain with phosphotyrosine ligand, determines formation of the homo or heterodimeric complexes (267,268). The relative stabilities of STAT homodimers and heterodimers and their association with other transcription factors (e.g. IRF, Sp1, Jun, Fos, NF-kB, glucocorticoid receptor) and/or coactivators (e.g. p300/CBP, PCAF, GCN5, BRG1, HDAC) further broadens the range of STAT/DNA-binding complexes and transcriptional activities, contributing to the biological diversity (183–186).

In addition to tyrosine and serine phosphorylation, various post-translational modifications (as discussed earlier) provide another level of regulation to modulate STAT transcriptional

responses. The negative regulators of JAK-STAT signalling are also important determinants of specificity. A typical example of this is SOCS3 regulation of IL-6 signalling, where expression of SOCS3 prevents IFN γ -like STAT1 transcriptional responses (254). In fact, the differential expression of downstream components such as the JAKS, STATS or SOCS can also contribute to the specificity of the cytokine response. Limited proteolytic processing of the C-terminus has been described for a number of the STAT proteins and is generally thought to generate a dominant-negative protein, reviewed in (269). However, a recent study suggests that estrogen-induced proteolytic cleavage of STAT1 may enhance, rather than inhibit, inflammatory responses (270).

Role of the JAK/STAT pathway in clinical disease

There have been many papers examining the role of STATs in malignancy and transformation, reviewed in (271–274). In this context, studies expressing mutant JAK (275) and STAT proteins (either dominant-negative or constitutively active) have been particularly informative (276–280). Here we have chosen to focus on the role of the JAK kinases in clinical disease.

Loss of function mutations

Inactivating JAK3 mutations have been documented in humans with severe combined immunodeficiency disease (SCID), characterized by loss of T and NK cells, abnormal B cell function and hypoplasia of lymphoid tissues (49,281). The clinical phenotypes induced by JAK3 mutations are indistinguishable from those resulting from loss-of-function mutations in the γ_c (282), indicating that JAK3 is indispensable for signal transduction from these receptors and hence indispensable for lymphoid development. Similarly, a homozygous mutation in TYK2 that resulted in the generation of a premature stop codon and subsequent loss of protein expression has been reported in a patient with hyper-IgE syndrome. This patient was highly susceptible to infections by multiple microorganisms and the patient's cells showed defective responses to IL-12, type I IFNs, IL-6, IL-23 and IL-10, demonstrating the importance of TYK2 for both innate and acquired immunity in humans (283). This study also highlights some of the species differences that exist between mouse and humans as for instance the *Tyk2*^{-/-} mice do not appear to have defective IL-6 signalling (283,284).

Gain-of-function mutations

While loss-of-function mutations in JAK3 and TYK2 are associated with immunodeficiency, the majority of naturally occurring mutations in JAK2, including chromosomal translocation, point mutations, insertions and deletions, are gain-of-function mutations and are associated with acute leukemia or myeloproliferative disorders (MPDs). The chromosomal translocations of JAK2 loci (e.g. TEL-JAK2, PCM1-JAK2, BCR-JAK2 and PAX-JAK2) lead to the development of both myeloid and lymphoid hematological malignancies (285). These translocations result in fusion of the JAK2 catalytic kinase (JH1) domain with multimerization subunits of partner proteins leading to constitutive tyrosine kinase activity and transformation.

Interestingly, point mutations, deletions and insertions in JAK2 are localized to the pseudokinase (JH2) domain and are associated with patients with MPDs. Since its discovery in 2005, most of the research has focused on the JAK2 V617F mutation (286–289). It is a somatic, gain-of-function mutation that has been frequently found in classic Philadelphia chromosome-negative myeloproliferative neoplasms (MPNs), in more than 90% of patients with polycythemia vera (PV), and in over 50% of patients with essential thrombocythemia (ET) and primary myelofibrosis (PMF) (290). Valine 617 lies within the pseudokinase (JH2) domain, and substitution of the valine with phenylalanine reduces the ability of JH2 to

repress kinase activity, leading to constitutive tyrosine phosphorylation of JAK2. As a result, it confers cytokine independence and/or hypersensitivity to the mutated cells giving them a survival advantage.

It is believed that STAT5 is required to mediate altered gene expression and subsequent transformation by mutant JAK2 (291). However, recent findings suggest that JAK2 can also bypass STAT transcriptional activity by acting as an epigenetic modulator. Dawson et al., observed nuclear localization of JAK2 in haemopoietic cells, where it phosphorylated histone 3 at tyrosine 41 (H3Y41) to inhibit binding of the transcriptional repressor heterochromatin protein-1 α (HP1 α), enhancing the expression of genes that are not necessarily under direct STAT-mediated control (292). Similarly, in ES cells JAK2V617F was able to bypass Stat3 activation to maintain pluripotency, again correlating with an increase in H3Y41 phosphorylation (293). Liu et al., found that JAK2 interaction with and phosphorylation of a type II arginine methyltransferase, PRMT5, inhibited its methyltransferase activity and consequently, histone methylation (294). While some controversy still surrounds JAK localization in the nucleus (295), these studies demonstrate the ability of JAK2 to disrupt chromatin stability and potentiate the oncogenic properties of the V617F mutation.

Given the involvement of the V617F mutation in MPNs, most of the therapeutic development has focused on identifying low molecular mass ATP-competitive JAK2 inhibitors, reviewed in (296,297). TG101348 and Ruxolitinib (or INCB018424) (298,299) are two of many selective and potent JAK inhibitors currently in use in phase II and III MPN clinical trials, respectively. Ruxolitinib has a strong inhibitory effect on both JAK1 and JAK2, while TG101348 has greater selectivity for JAK2. Both of these inhibitors effectively attenuate downstream signalling, including phosphorylation of STAT and ERK1/2, and induce apoptosis *in vitro*. MPN patients treated with these inhibitors demonstrated a dramatic improvement in constitutional symptoms and a reduction in spleen size. Although unpleasant side-effects and a less satisfactory improvement in cytopenia, marrow fibrosis and JAKV617F burden were also observed, inhibition of JAK2 has already proven to be an excellent target for therapeutic intervention in MPNs.

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What the future holds

The past 20 years have seen the JAK/STAT field progress from the discovery of the individual components and delineation of the pathway, to an understanding of the role of the JAKs and STATs in human disease, which coupled with resolution of the molecular structures should result in JAK inhibitors becoming a routine part of clinical treatment.

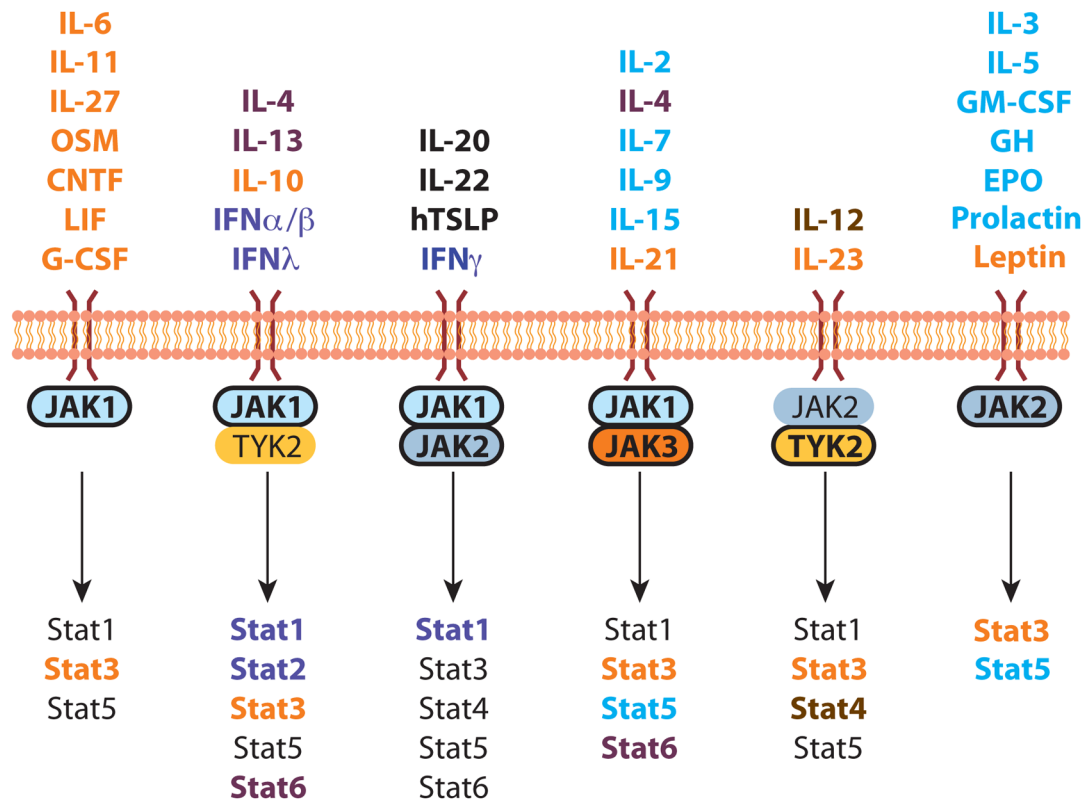


Figure 1. Non-redundant JAK/STAT signalling in mice

Schematic showing the preferential cytokine/growth factor usage of different JAKs and STATs, as based on gene-targeting studies in mice. Emphasis in bold indicates the dominant JAK of the pair and colour coding links the individual cytokine/growth factors with their requisite STAT/s. See text for references.

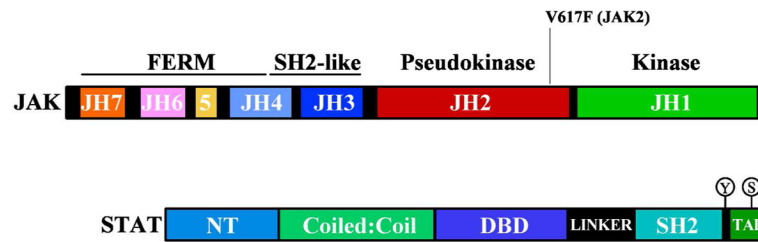


Figure 2. JAK and STAT domain organisation

Schematic showing the domain organisation of JAK and STAT proteins. The valine 617 commonly mutated in JAK2 in myeloproliferative neoplasms is shown. NT: N-terminal region, DBD: DNA binding domain, TAD: transcriptional activation domain.

Table 1

Phosphotyrosyl sites shown to bind STAT-SH2 domains

	SH2 Binding¹	Receptor	References	Dimerization motif²
STAT1	pYXPQ, pYDXXH	IFN γ R α	(300,301)	TG _p YIKT
STAT2	pYVXXXS	IFN α R1	(302,303)	RK _p YLKH
STAT3	pYXXQ	GP130, LIFR, G-CSFR	(268,304)	AP _p YLKT
STAT4	TXXG _p YLXX	IL-12R β 2	(305,306)	KG _p YVPS
STAT5	DX _p YXXL/F	EPO, IL-2R β , IL-7R	(307–309)	DG _p YVKP
STAT6	pYKXF	IL-4R	(55)	RG _p YVPA

¹Known consensus sites for STAT-SH2 domain binding together with the relevant receptor subunit, where pY indicates phosphorylated tyrosine and X is any amino acid.

²Sequences surrounding the C-terminal STAT phosphotyrosine that mediates STAT dimerization. Sequences are identical in mouse and human STATs, with the exception of STAT6 (RGpYVST in mouse)