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SPOTLIGHT REVIEW

Aberrant signal transduction pathways in myeloproliferative neoplasms

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The BCR-ABL-negative myeloproliferative neoplasms (MPNs), polycythemia vera (PV), essential thrombocythemia (ET) and primary myelofibrosis (PMF), entered the spotlight in 2005 when the unique somatic acquired *JAK2* V617F mutation was described in >95% of PV and in 50% of ET and PMF patients. For the very rare PV patients who do not harbor the *JAK2* V617F mutation, exon 12 *JAK2* mutants were discovered also to result in activated forms of JAK2. A minority of ET and PMF patients harbor mutations that constitutively activate the thrombopoietin receptor (TpoR). In bone marrow reconstitution models based on retroviral transduction, the phenotype induced by *JAK2* V617F is less severe and different from the rapid fatal myelofibrosis induced by TpoR W515L. The reasons for these differences are unknown. Exactly by which mechanism(s) one acquired somatic mutation, *JAK2* V617F, can promote three different diseases remains a mystery, although gene dosage and host genetic variation might have important functions. We review the recent progress made in deciphering signaling anomalies in PV, ET and PMF, with an emphasis on the relationship between *JAK2* V617F and cytokine receptor signaling and on cross-talk with several other signaling pathways.
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Introduction

Functional hallmarks of myeloid progenitors in myeloproliferative neoplasms

The BCR-ABL-negative myeloproliferative diseases, which include polycythemia vera (PV), essential thrombocythemia (ET) and primary myelofibrosis (PMF), were recently renamed myeloproliferative neoplasms (MPNs).[1] PV, ET and PMF are disorders of hematopoietic stem cells (HSCs) and early myeloid progenitors,[2,3] where myeloid progenitors are hypersensitive and/or independent of cytokines for survival, proliferation and differentiation. For instance, the majority of PV patients harbor erythropoietin (Epo)-independent erythroid colonies.[4] Several intracellular anti-apoptotic pathways and molecules, such as STAT3, Akt or BclXL, are activated/induced constitutively in such MPN myeloid progenitors,[5–7] along with hypersensitivity to insulin-like growth factor 1 (IGF-1), granulocyte macrophage colony-stimulating factor, interleukin 3 (IL-3), granulocyte colony-stimulating factor (G-CSF) or thrombopoietin (Tpo).[8–11] Unlike many malignancies, where the INK4a locus is inactivated, erythroid progenitors from PV patients exhibit increased expression of the INK4a/ARF locus.[12]

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Mutations involved in PV, ET and PMF

The acquired somatic *JAK2* V617F mutation is harbored by the majority of PV patients and by more than 50% of ET and PMF patients.[13–17] Subsequent identification of exon 12 mutants of *JAK2* in a minority of PV patients gave a molecular lesion to virtually all PV cases.[18] Sequencing of the gene coding for the Tpo receptor (TpoR/c-Mpl) identified mutations in the juxtamembrane tryptophan residue W515 (W515L and W515K) in a low percentage of PMF and ET patients, the majority of which are *JAK2* V617F-negative.[19,20] The W515 residue of TpoR is required to maintain the receptor inactive in the absence of ligand.[21] All these mutations lead to constitutively active JAK–STAT pathway, especially JAK2, STAT5, STAT3, MAP kinase ERK1,2 and Akt.[13,16,21]

Major questions

Advancement over the past 3 years in the MPN research field has raised several major questions, such as: (i) What are the molecular bases for the significant differences in the *in vivo* phenotypes induced by *JAK2* V617F and TpoR W515L? (ii) How can a unique somatic mutation, *JAK2* V617F, be involved in the induction of three different diseases ET, PV or PMF? (iii) What mechanisms are responsible for the evolution of MPNs toward acute myeloid leukemia? (iv) What are the effects of *JAK2* V617F and of the other JAK2 and TpoR mutants at the level of HSC? and (v) What preceding and subsequent (to *JAK2* V617F) genetic events contribute to myeloproliferative diseases?

Answers to these questions have begun to emerge. Gene dosage, as initially suggested by genotype/phenotype studies in patient cells,[22] by retroviral bone marrow reconstitution studies[23] and most recently probed in transgenic mice,[24] could be critically involved in inducing one or the other of the MPN phenotypes. It is fascinating that progenitors homozygous for the *JAK2* V617F mutation occur in almost all PV patients, but very rarely in ET patients.[25,26] Although this can be seen as an argument in favor of the gene dosage hypothesis, other preceding or subsequent genetic changes might have an important function. Interestingly, host-modifying influences might have a major part in establishing the disease phenotype.[27] A screen for genetic variation within the genes coding for EpoR, TpoR, G-CSF receptor (G-CSFR) and JAK2 led to the discovery of three JAK2 single nucleotide polymorphisms that were significantly but reciprocally associated with PV and ET, but not with PMF. Three additional JAK2 single nucleotide polymorphisms were uniquely associated with PV. Such single nucleotide

polymorphisms, although not in the coding region of the genes, might affect the levels of gene transcription, regulation by other factors or possibly expression of other genes.

Unknown effects of JAK2 V617F signaling in HSCs

JAK2 V617F mutation was detected at the HSC and the common myeloid/lymphoid progenitor levels, it skews the HSC differential potential toward the erythroid lineage and gives a selective proliferative advantage to myeloid lineages.[28,29] The HSC compartment of PV and PMF patients was found to contain *JAK2* V617F-positive long-term, multipotent and self-renewing cells, with a much higher proportion of mutated HSCs in PMF than in PV.[30] It is not clear at this moment whether *JAK2* V617F profoundly affects the biology of HSCs[30] or whether it only gives a strong selection advantage past the HSC stage. A certain degree of heterogeneity exists between HSC subsets.[31] HSCs exist in niches, some near osteoblasts and others near endothelial cells. Exactly where and in which HSC subset the *JAK2* V617F mutation initially occurs might have a major impact on the subsequent disease phenotype.

The *JAK2* V617F mutation was present in 30–40% of splanchnic venous thrombosis patients (Budd–Chiari syndrome and portal vein thrombosis).[32–35] A 'special' stem cell with hematopoietic/endothelial potential was suggested to be at the origin of splanchnic venous thrombosis, and it might harbor *JAK2* V617F.[36] A recent case report described a human allogeneic transplantation with *JAK2* V617F-positive cells from such a splanchnic venous thrombosis donor (with one episode of *JAK2* V617F-positive splanchnic venous thrombosis), but no MPN, to her HLA-matched sister with high-risk myelodysplastic syndrome (RAEB2).[37] The recipient exhibited a *JAK2* V617F burden similar to the donor immediately after transplant, but this burden decreased over time, and 7 years later, the recipient continues to be in remission and to exhibit low levels of *JAK2* V617F positivity.[37] These data suggest that, indeed, the *JAK2* V617F mutation can occur in an HSC, but at least in the transplantation setting, this HSC has no proliferative advantage.

A considerable amount of data suggests that in addition to the presence of the *JAK2* V617F mutation, preceding or subsequent genetic events might be necessary for developing the MPN disease.

First, in certain MPN patients, the clonality of expanded myeloid progenitors is found to be larger than the *JAK2* V617F clone, with the acquisition of *JAK2* V617F being a late genetic event.[38] Second, acute myeloid leukemia cases developed in *JAK2* V617F-positive patients can occur with leukemic blasts not harboring *JAK2* V617F.[39] Third, Epo-independent colonies might not always harbor the *JAK2* mutation in patients with the *JAK2* V617F mutation.[40] Such preceding or subsequent events could be associated differently with the three diseases, namely ET, PV and PMF.

The signaling space

Molecular cell biology textbooks list eight major signaling pathways that control gene expression that are linked to eight classes of cell surface receptors: cytokine receptors, receptor tyrosine kinases, receptors for transforming growth factor (TGF)-β, Wnt, Hedgehog, tumor necrosis factor (TNF)-α, Notch (Delta) and G-protein-coupled receptors.[41] Nuclear and corticoid receptor pathways, as well as integrin signaling, complete the picture of intracellular cell signaling. In this review, we describe that aberrant signaling occurs in MPNs through some of the listed pathways, such as cytokine receptors, receptor tyrosine kinases, TGF-β and TNF-α. It is not clear whether aberrant signaling in MPNs is simply due to the constitutive nature of signaling induced by mutated JAK2 or TpoR, or whether specific cross-talk events occur to other pathways that might confer specificity to JAK2 V617F versus JAK2 signaling.

It is important to recognize from the outset that the experimental systems used by signal transduction research, such as phosphorylation studies, co-immunoprecipitation, gene expression and determination of protein localization, may not be able to identify subtle relative changes, such as kinetics and amplitude differences, between signals engaging generic pathways that are redundantly triggered by many stimuli. Such subtle quantitative differences might, however, be crucial for the disease phenotypes *in vivo*. That is the reason why genetics, *in vivo* models, results obtained with inhibitors and data derived from primary cells, must be taken into account to draw a picture describing aberrant signaling in MPNs.

Constitutive signaling and kinase activity of JAK2 V617F

The Janus kinase family

The mammalian genome codes for four Janus kinases (JAKs), JAK1, JAK2, JAK3 and Tyk2. On the basis of homology, JAKs share seven JAK homology domains (JH), denoted as JH1–JH7. From the C to the N terminus, JH1 represents the kinase domain, JH2 the pseudokinase domain, JH3 and JH4 contain an SH2-like domain and linker regions, whereas JH5–JH7 contain a FERM (band 4.1, ezrin, radixin, moesin) domain[42,43] (Figure 1). JAKs have been proposed to have a bipartite structure and the N terminus is required for binding to receptors, chaperoning and stabilizing them at the surface,[44–47] whereas the kinase domain is absolutely crucial for signaling. The pseudokinase domain precedes the kinase domain, and because of sequence differences at key residues required for catalysis, it cannot transfer phosphate and thus is catalytically inactive.[42] Nevertheless, the pseudokinase domain is structurally required for the response of JAKs to cytokine receptor activation and for inhibiting the basal activity of the kinase domain.[48,49] The

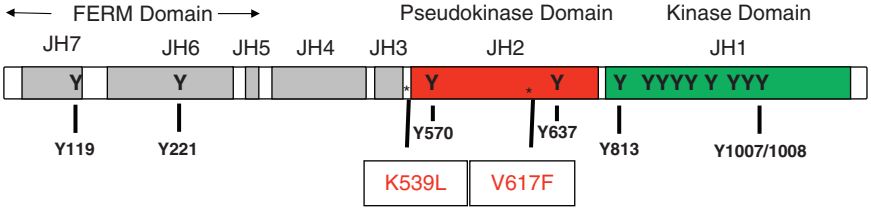

Figure 1 Schematic illustration of Janus kinase (JAK)2 and the different JAK homology (JH) domains. The V617F mutation occurs in the pseudokinase domain rendering the kinase domain constitutively active. Exon 12 mutations, such as K539L, occur in the linker region between the JH3 and JH2 domains. Tyrosine residues that can be phosphorylated are depicted by their single letter. See text for details.

V617F mutation occurs in the pseudokinase domain, leading to constitutive activation of the kinase domain (Figure 1).

Although no X-ray crystal structure of full-length JAK2 exists, modeling has suggested that the pseudokinase domain of JAK2 maintains the kinase domain inactive in the basal state.[50] Thus, the V617F mutation is expected to relieve the inhibitory effect of JH2 on JH1 and to lead to basal kinase activity. The homologous V617F mutations in JAK1 and Tyk2 also lead to constitutive activation,[51] which strongly supports this model. Activating mutations in the pseudokinase domain of JAK1 at the homologous V658 position or at neighboring residues have been reported in 20% of patients with T-acute lymphoblastic leukemia.[52,53]

Constitutive kinase activity

In transiently transfected JAK2-deficient cells, such as the γ-2A human fibrosarcoma cell line,[54] JAK2 V617F expression leads to constitutive activation of STAT5 and STAT3 signaling. In such transient transfection experiments, JAK2 V617F is constitutively tyrosine phosphorylated at the activation loop Y1007. Co-transfection of wild-type JAK2 reduces signaling by JAK2 V617F, presumably due to competition for an interaction partner, such as a cytokine receptor,[13] but does not prevent constitutive phosphorylation of JAK2 V617F.[16]

To investigate the catalytic activity of JAK2 V617F mutation, kinase assays have been performed on GST fusion proteins. In COS7 overexpression conditions, when compared with wild-type JAK2, the JAK2 V617F mutated protein exhibits enhanced basal kinase activity on a reporter GST fusion protein containing the sequence of the activation loop of JAK2 containing tyrosine (Y) 1007.[17,55] The kinase activity was clearly increased, but it appeared to be weak. In stably transfected Ba/F3 cells, JAK2 V617F also exhibits enhanced kinase activity on the same Y1007-containing GST fusion protein, but the levels of activation were also small (C Pecquet *et al*., unpublished results). This is very different from BCR-ABL or other fusion proteins such as TEL-JAK2, where the kinase domain alone is oligomerized and activated by a fused exogenous oligomeric domain. In contrast, the kinase domain of JAK2 V617F is expected to maintain most of the negative regulatory intramolecular interactions that normally limit kinase domain activation.

JAK2 V617F and cytokine receptors

An intact FERM domain is required for constitutive signaling by JAK2 V617F

The FERM domain of JAKs is responsible for appending JAKs to cytokine receptors. Cytokine receptors contain in the cytosolic juxtamembrane region a proline-rich sequence, usually PxxPxP, denoted as Box 1, located 10–15 amino acid residues downstream of the TM domain, and further down 50–60 amino acid residues downstream of the TM domain, a sequence composed of hydrophobic and charged residues denoted as Box 2.[56]

JAK2 binds to the region of EpoR that encompasses cytosolic residues of Box 1, Box 2 and also most of the residues between these boxes.[44,56]

Interaction between JAK2 and EpoR or TpoR is disrupted by a point mutation (Y114A) in the FERM domain.[47] Expression of the double-mutant JAK2 V617F Y114A in Ba/F3-EpoR cells did not lead to constitutive signaling through STAT5 or to autonomous growth,[57] suggesting that the V617F mutation does not suffice for activation in the absence of the assembly between the JAK2 V617F and a cytokine receptor. It can be noted that members of the JAK family are localized to membranes through recruitment by cytokine receptors, whereas mutations such as Y114A lead to cytosolic localization.[58] Furthermore, a mutation in the pseudokinase domain of JAK2 was identified (Y613 to glutamic acid, Y613E), which promotes constitutive activation only when JAK2 is in complex with the EpoR.[59] This result suggests that in the absence of an association with a cytokine receptor, JAK2 is locked into an inactive state and that receptor binding through the FERM domain is important for activation.[59]

Another argument supporting the notion that binding to a cytokine receptor is important for the activity of the V617F mutant arises from the lack of activation of JH2–JH1 fusion proteins where the V617F mutation was introduced in the JH2 sequence.[60] The low basal activity of JH1 was shown to be suppressed by fusion with JH2.[49,61] However, the presence of the FERM–SH2 domains is required for the activation effect exerted by the V617F mutation.

JAK2 is crucial for signaling by EpoR[62] and TpoR,[63,64] participates in signaling by G-CSFR[65,66] (Figure 2) and also mediates signaling by the IL-3/IL-5/granulocyte macrophage colony-stimulating factor family of cytokines, as well as by several type-II cytokine receptors, such as interferon-γ receptor 2.[67] Given that MPNs mainly affect the erythroid, the megakaryocytic and the granulocyte lineages, as stated before, complexes between JAK2 V617F and EpoR, TpoR and G-CSFR may explain cytokine hypersensitivity and independence in these diseases (Figure 2).

EpoR and MPNs

EpoR and JAK2 V617. EpoR functions as a preformed dimer on the cell surface, which upon cytokine binding undergoes a conformational change that triggers the activation of the receptor pre-bound JAK2.[68,69] This involves a rotation of the receptor monomers within the dimer,[70] which is transmitted to JAK2 by switch residues, that is W258 in the juxtamembrane domain of EpoR.[69] Current data suggest that JAK2 V617F can scaffold on the cytosolic domain of EpoR and induce Epo-independent signaling, possibly by phosphorylating key cytosolic tyrosine residues on EpoR, which leads to strong STAT5 activation.[71]

Early on after the identification of *JAK2* V617F, the need for a co-expressed type I dimeric cytokine receptor for constitutive signaling by JAK2 V617F provoked a controversy, which in the end led to a model of how dimeric receptors might actually promote JAK2 V617F activation. One study by Levine *et al*.[16] reported that JAK2 V617F readily induced autonomous growth in Ba/F3 cells engineered to express the EpoR (Ba/F3 EpoR cells), but not in parental Ba/F3 cells. In contrast, the study by James *et al*.[13] had shown that JAK2 V617F could induce autonomous growth in both Ba/F3 EpoR and parental Ba/F3 cells. This controversy (also described in Ihle and Gilliland[72]) was solved by carefully assaying the levels of JAK2 V617F transduction: at low levels, co-expression of a type I cytokine receptor was necessary for autonomous growth, whereas at higher levels JAK2 V617F alone induced autonomous growth, most likely by binding to an endogenous cytokine receptor, such as the IL-3-receptor β-subunit.[60] It is not clear whether other receptors—besides dimeric type I—could also promote signaling by low levels of transduced JAK2 V617F (Figure 2b). Nevertheless, given that EpoR is a dimer in the absence of ligand, an insightful model was proposed by Harvey Lodish. In it, dimerization of JAK2 V617F by such a receptor is considered necessary for the activation of JAK2 V617F signaling, and the subtle V617F mutation promotes kinase activation when JAK2 is scaffolded on

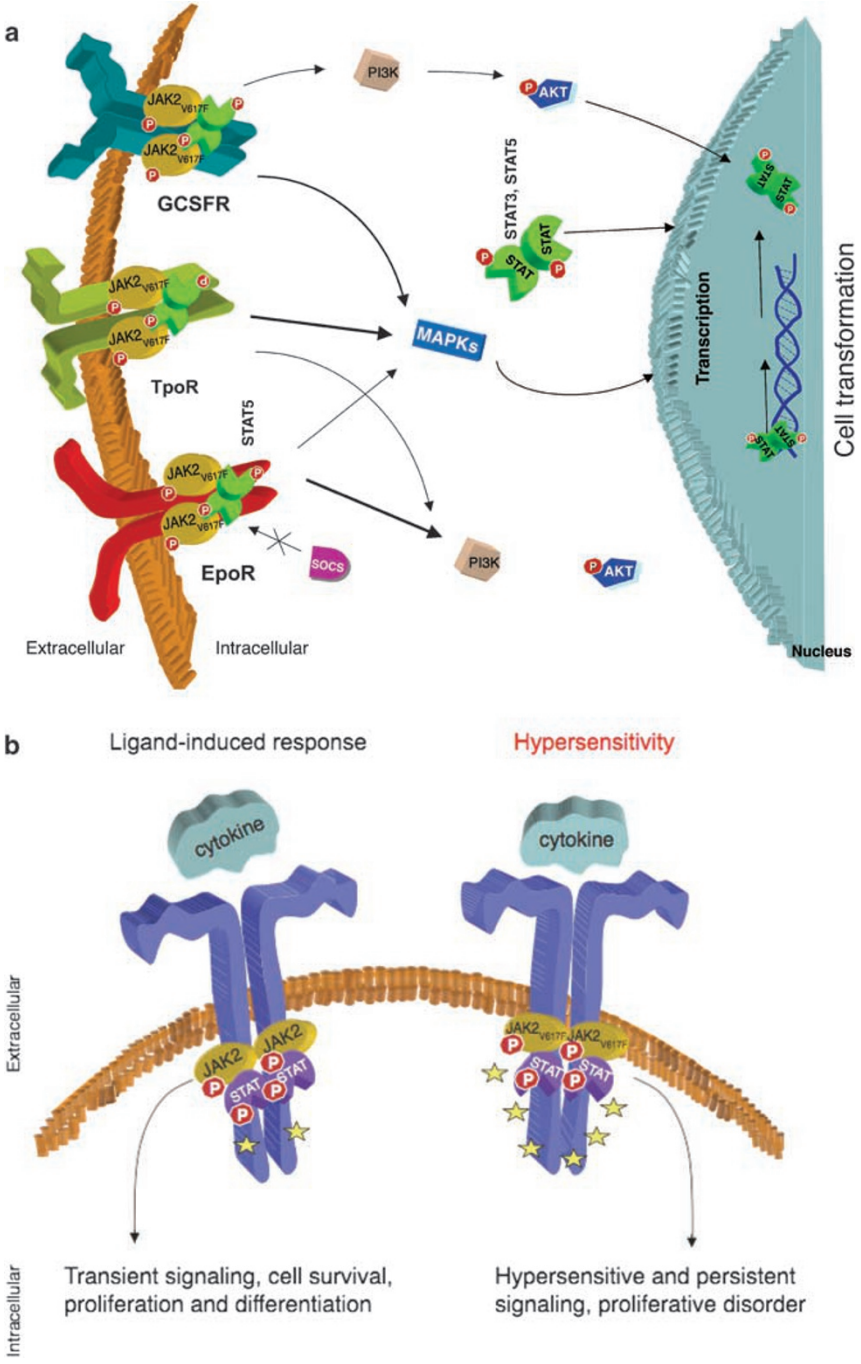

Figure 2 Model of constitutive (ligand-independent) signaling induced by JAK2 V617F through erythropoietin receptor (EpoR), thrombopoietin receptor (TpoR) and granulocyte colony-stimulating factor receptor (G-CSFR). (**a**) Janus kinase 2 (JAK2) is the main JAK used by EpoR and TpoR, but JAK1 is also used physiologically by G-CSFR. Primarily, EpoR and TpoR are expected to be bound by JAK2 V617F, whereas G-CSFR is expected to be in complex with JAK2 V617F at high JAK2 V617F levels, i.e., in homozygous *JAK2* V617F situations. Scaffolding of JAK2 V617F on the cytosolic tails of cytokine receptors leads to the enhanced activation of JAK2 V617F and downstream signaling through STATs, MAP kinase, PI-3-kinase (PI3K) and Akt. SOCS proteins are expected to engage both EpoR and activated wild-type JAK2, leading and down-modulation of JAK2 activity; the EpoR–JAK2 V617F complex appears to escape the down-modulation activity of SOCS3. (**b**) Cytokine receptors that are in complex with JAK2 V617F are hypersensitive to their ligands for signaling. Cytokine binding to receptors coupled to wild-type JAK2 induce transient physiologic signals, leading to survival, proliferation and differentiation of myeloid progenitors. In contrast, receptors coupled to JAK2 V617F respond to lower levels of ligand, and are constitutively signaling after ligand withdrawal. It is not known whether dimeric receptor complexes, where one monomer is coupled to JAK2 V617F and the other to wild-type JAK2, are also hypersensitive to ligand or constitutively active.

an inactive receptor dimer (Figure 2a).[71] Given that in MPNs the three lineages affected are controlled by the three type I dimeric cytokine receptors, EpoR, TpoR and G-CSFR, the model that JAK2 V617F mainly functions as a transforming kinase in association with these receptors is very plausible.

EpoR signals mainly by JAK2–STAT5 and PI-3–kinase/Akt (Figure 2a) pathways. It is a weak activator of MAP kinase and of

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STAT3,[73] as it does not contain a consensus site for STAT3 binding, whereas several phosphorylated tyrosine residues (Y343, Y401, Y429 and Y431) can bind STAT5 and are required for maximal STAT5 activation.[74,75] A consequence of STAT5 activation is induction of the anti-apoptotic BclXL protein expression,[76] which is constitutively expressed in PV erythroid progenitors.[7] The connection of EpoR with the PI-3–kinase pathway is accomplished by specific tyrosine residues, that is Y479, which appears to bind the regulatory subunit p85.[77,78] PI-3–kinase and Akt activations are critically involved in erythroid differentiation,[79] possibly by the involvement of the transcription factor Forkhead family, FKHRL1.[80] Another mechanism appears to be the phosphorylation of S310 of GATA1.[81] Thus, scaffolding of an activated JAK2 to EpoR is predicted to activate the JAK2–STAT5 and PI-3–kinase/Akt pathways and stimulate proliferation and differentiation of erythroid progenitors.

EpoR and exon 12 JAK2 mutations. Patients with exon 12 *JAK2* mutations, such as JAK2 K539L, exhibit an erythrocytosis phenotype, without pathology changes to megakaryocytes typical for MPNs.[18] Unlike the uniqueness of the point mutation that generates JAK2 V617F, several deletions and insertions were noted in the case of exon 12 mutations.[18,82] An attractive hypothesis is that exon 12 mutants of JAK2 favor interaction with EpoR over TpoR or G-CSFR, although a mechanistic basis for such a preference has yet to be found. Modeling of JAK2 suggests that the K539L falls in a loop in the linker region between the SH2 and the JH2 domain (Figure 1), which would be placed in space quite close to the loop represented by β4–β5 where V617 is located.

TpoR and MPNs

TpoR is coupled to and activates both JAK2 and Tyk2,[64,83,84] which appear to have comparable affinities for the receptor juxtamembrane domain and to promote cell surface traffic of the receptor to a similar extent.[47] However, JAK2 is much more effective than Tyk2 in transmitting the signals of the receptor.[47,64] TpoR activates JAK2, STAT5 and PI-3–kinase/Akt,[85] but in contrast to EpoR, it is a very strong activator of Shc, of the MAP kinase pathway and of STAT3 (Figure 2a).[83,86–90] It is interesting that the first consequence of expressing the JAK2 V617F (at lower than physiologic levels in the transgenic model) mutation is to promote platelet formation.[24] Bipotential megakaryocyte–erythroid progenitors appear to be stimulated to engage on the platelet formation by STAT3 activation, whereas STAT5 activation favors erythroid differentiation programs.[91] STAT5 emerged as a critical factor for lineage commitment between erythroid and megakaryocytic cell fates. Depletion of STAT5 from CD34(+) cells in the presence of Tpo and stem cell factor favors megakaryocytic differentiation at the expense of erythroid differentiation.[91] Overexpression of an activated form of STAT5 impaired megakaryocyte development favoring erythroid differentiation at the expense of megakaryocyte differentiation.[91] Thus, at low levels of expression, JAK2 V617F might only activate STAT3, which might suffice for platelet formation. At higher expression levels, coupling to both TpoR and EpoR will lead to STAT5 activation, and this would favor the erythroid program. It is not clear at this point whether the PV phenotype is exclusively the result of EpoR activation or whether the pathologic activation of TpoR might also contribute to the PV phenotype. It is interesting to note that overexpression of TpoR in certain animal models led to an expansion of the erythroid compartment.[92]

The SH2 and PH (pleckstrin homology domain) adapter protein Lnk was shown to not only bind to phosphorylated tyrosine residues of both TpoR and EpoR but also to exert a negative role on signaling by these receptors.[93,94] It is not known whether the defects in this negative regulatory mechanism are operating in MPNs.

Co-expression of JAK2 V617F and TpoR in Ba/F3 cells leads to down-modulation of TpoR, most likely due to internalization and down-modulation seen after excessive activation of cytokine receptors (J Staerk, C Pecquet, C Diaconu and SN Constantinescu, unpublished observations). This is consistent with early studies that have identified a maturation defect and down-modulation of cell surface TpoR in platelets and megakaryocytes from MPN patients.[95] More recently, an inverse correlation was reported between the burden of *JAK2* V617F and the levels of cell surface TpoR on platelets.[96] Although these results suggest that JAK2 V617F may contribute to the down-modulation of TpoR, several patients with MPNs in the absence of JAK2 V617F also exhibited down-modulated TpoR. Such down-modulation is not seen for EpoR. TpoR is a long-lived receptor at the cell surface[47] and recycles,[97] which is not the case for EpoR. Further experiments are necessary to follow up on the original observation of TpoR down-modulation in MPNs, which may be due to traffic alterations, excessive internalization and degradation or decreased protein synthesis.

Several mutations in Mpl induce myeloid malignancies. A mutation in the transmembrane domain of Mpl, S505N, constitutively activates the receptor[98] and has been discovered in familial ET.[99] The S505N mutation in the transmembrane domain is expected to promote constitutive activation due to polar interactions between the asparagines that replace the natural serine. As stated earlier, mutations in Mpl at W515 induce severe MPNs with myeloprofibrosis.[19,20] W515 mutations activate constitutive signaling by the receptor because W515 belongs to an amphipathic juxtamembrane helix (RWQFP in the human receptor), which is required for maintaining the un-liganded receptor in the inactive state. Another activating mutation was recently described for TpoR, where a threonine residue in the extracellular juxtamembrane region (located symmetrically from the W515 mutation on the N-terminal side of the transmembrane domain) is mutated to alanine (T487A) in a non-Down's syndrome childhood acute megakaryocytic leukemia.[100] In bone marrow transplantation assays, this Mpl T487A also induces a severe myeloproliferative disease, close to the phenotype induced by TpoR W515L.[100] Juxtamembrane mutations such as W515L/K or T487A may not only promote active dimeric conformations, but they could also induce receptor conformational changes by changing crossing angles between receptor monomers, whereas the S505N highly polar mutation in the transmembrane domain is predicted to stabilize an active dimeric conformation of the receptor. It will be interesting to test side by side in bone marrow transplantation experiments the effects of S505N, W515L and T487A mutations and to assess whether indeed the phenotype of the TpoR S505N mutation would be milder.

G-CSFR and MPNs

Bone marrow transplanted mice with HSCs expressing JAK2 V617F present not only an MPN phenotype, with low Epo, as predicted, but also with low G-CSF serum levels, suggesting that constitutive activation of G-CSFR occurs in these mice.[101]

G-CSFR uses both JAK1 and JAK2 for signaling.[65,66] JAK2 V617F may affect G-CSFR signaling with less efficiency than for EpoR and TpoR, as JAK1 may be the key JAK for G-CSFR. This is

perhaps the reason why the granulocytic lineage is affected to a lower extent in MPNs, when compared with the erythroid and megakaryocytic lineages, especially at low levels of JAK2 V617F.

Activation of the G-CSFR JAK2 V617F complexes may lead to enhanced numbers of granulocytes, constitutive activation of granulocytes (with release of enzymes) as well as interactions with platelets, which would contribute to thrombotic complications.

It is not clear whether leukocytosis, which is seen in certain MPN patients and which appears to be associated with certain complications or evolution toward leukemia,[102] may be due to the pathologic activation of G-CSFR by JAK2 V617F. Granulocytes from patients with MPNs presented altered gene expression promoted by JAK2 V617F expression and confirmed a recapitulation of cytokine receptor signaling, resembling profiles of granulocytes activated by G-CSF.[103]

Similar to TpoR, G-CSFR activates STAT3 and MAP kinase pathways, in addition to the JAK2–STAT5 and PI-3–kinase/Akt pathways. It can be noted that for this receptor, a very delicate balance has been identified between the activation of STAT3, required for differentiation and inducing a stop in cell growth (necessary for differentiation), and STAT5, which promotes proliferation.[102] Binding of SOCS3 through its SH2 domain to a phosphorylated tyrosine residue in the receptor's cytosolic end specifically downregulates STAT5 signaling. Deletion of the cytosolic region, which contains the binding site for SOCS3, leads to enhanced STAT5-to-STAT3 signaling ratio,[102] and this is associated with evolution toward acute myeloid leukemia of patients with severe congenital neutropenia.

G-CSFR activation might synergize with other mechanisms and promote the mobilization of CD34(+) stem cells and progenitors from the bone marrow to the periphery.

Interestingly, an increased number of circulating CD34(+) cells in MPN patients has been observed, and they exhibit granulocyte activation patterns similar to those induced by the administration of G-CSF.[104] The release of CD34(+) cells is generally due to a combination of increased levels of proteases[105] and especially due to the downregulation of the CXCR4 receptor on CD34(+) cells.[106] An altered SDF-1/CXCR4 axis was demonstrated in PMF patients with CD34(+) cells in the periphery.[107] These findings are supported by the rapid mobilization of CD34(+) cells with AMD3100, a CXCR4 antagonist.[108]

Tyrosine phosphorylation pattern of JAK2 V617F

JAK2 V617F is constitutively tyrosine phosphorylated. However, besides Y1007 in the activation loop, which is crucial for activation,[109] it is not known whether other phosphorylated tyrosines overlap with those phosphorylated in the wild-type JAK2. It can be noted that, JAK2 contains multiple tyrosine residues, of which at least 14 can be phosphorylated[110] (Figure 1). Some of these tyrosine residues exert positive (Y221) and other negative (Y119, Y570) effects on signaling by JAK2.[111–113] Y813 is a recruitment site for SH2-containing proteins,[114] such as SH2B, which can promote homodimerization of JAK2.[115] In theory, the constitutive activation of JAK2 V617F might promote a different pattern of phosphorylated tyrosines from that of wild-type JAK2.

STAT activation and MPNs

A hallmark of MPNs is constitutive or hypersensitive activation of the STAT family of transcription factors in myeloid precursors. As mentioned, the expressions of JAK2 V617F, TpoR mutants or exon 12 JAK2 mutants lead to constitutive STAT5 and STAT3 activation in various systems.[18,116] As a function of the MPN disease type, one or the other of the STATs was suggested to be predominantly activated by JAK2 V617F. For example, in myelofibrosis, JAK2 V617F expression in neutrophils is associated with the activation of STAT3 but apparently not with that of STAT5.[117] In another study, in bone marrow biopsies and irrespective of JAK2 V617F, PV patients exhibited high STAT5 and STAT3 phosphorylation and ET patients exhibited high STAT3, but low STAT5 phosphorylation, whereas myelofibrosis patients exhibited low STAT5 and STAT3 phosphorylation.[118] Thus, constitutive activation of the STAT5/STAT3 signaling appears to be a major determinant of MPNs, irrespective of the particular JAK2 or receptor mutation.

Furthermore, STAT3 activation by IL-6 has been shown in a murine model system to hold the potential to experimentally induce MPN. Mice homozygous for a knockin mutation in the IL-6 receptor gp130 (gp130(Y757F/Y757F)), which leads to gp130-dependent hyperactivation of STAT1 and STAT3 develop myeloproliferative diseases with splenomegaly, lymphadenopathy and thrombocytosis. gp130(Y757F/Y757F) is hyperactive owing to impaired recruitment of negative regulators such as SOCS3 and the SHP2 phosphatase.[119,120] The hematological phenotype disappeared when the knockin mice were crossed with heterozygous Stat3(+/−) mice.[121] Thus, the threshold of STAT3 signaling elicited by IL-6 family cytokines may have an important function in the myeloid lineage and may contribute to the development of MPN.

SOCS3 and JAK2 V617F

Suppressors of cytokine signaling (SOCS) proteins negatively regulate cytokine receptors and JAK–STAT signaling. There are eight members of the SOCS/CIS (cytokine-inducible SH2-domain-containing protein) family, namely SOCS1–SOCS7 and CIS. Each SOCS molecule contains a divergent N-terminal domain, a central SH2 domain, and a C-terminal 40 amino acid domain known as the SOCS box.[122] CIS/SOCS proteins are supposed to function as E3 ubiquitin ligases and target proteins bound to the SOCS N terminus, such as active JAKs, as well as themselves for proteasome-mediated degradation.[122] SOCS1 and SOCS3 can also inhibit the catalytic activity of JAK proteins directly, as they contain a kinase inhibitory region (KIR) that targets the activation loop of JAK proteins. SOCS proteins bind receptors and then target the activation loop of JAKs for inhibition by KIR and SH2 interactions.[122]

SOCS3 is known to strongly down-modulate EpoR signaling.[123] JAK2 V617F appears not to be downregulated by SOCS3, possibly due to continuous phosphorylation of SOCS3, which can impair its E3 ligase activity.[124] Constitutive tyrosine phosphorylation of SOCS3 was also reported in peripheral blood mononuclear cells derived from patients homozygous for the JAK2 V617F mutant.[124] Taken together, a model was proposed in which JAK2 V617F may escape physiologic SOCS regulation by hyperphosphorylating SOCS3. It would be important to also determine whether exon 12 mutants of JAK2 are able to overcome down-modulation by SOCS3.

Furthermore, one of the two tyrosine residues in the C terminus of SOCS3 that become phosphorylated upon ligand-activated cytokine receptors interacts with the Ras inhibitor p120 RasGAP.[125] This leads, in the case of IL-2 signaling, to sustained ERK activation, whereas the JAK–STAT pathway is down-modulated.[125] Whether part of the sustained ERK activation detected in cells transformed by JAK2 V617F may involve

complexes of degradation-resistant SOCS3 and p120 RasGAP is yet to be determined.

Other JAK2 V617 mutations activate JAK2

Substitution of pseudokinase domain residue V617 by large non-polar amino acids causes activation of JAK2.[126] Saturation mutagenesis at position 617 of JAK2 showed that, in addition to V617F, four other JAK2 mutants, V617W, V617M, V617I and V617L, were able to induce cytokine independence and constitutive downstream signaling. However, only V617W induced a level of constitutive activation comparable with V617F, and like V617F it was able to stabilize tyrosine-phosphorylated SOCS3.[126] Also, the V617W mutant induced a myeloproliferative disease in bone-marrow-reconstituted mice, mainly characterized by erythrocytosis and megakaryocytic proliferation. Although JAK2 V617W would predictably be pathogenic in humans, the substitution of the Val codon, GTC, by TTG, the codon for Trp, would require three base pair changes, which makes it unlikely to occur. Therefore, codon usage and resistance to SOCS3-induced down-modulation are two mechanisms that might explain the uniqueness of JAK2 V617F in MPNs.

Animal models of MPNs

JAK2 mutants

Mouse bone marrow reconstitution experiments with HSCs retrovirally transduced with JAK2 V617F resulted in strain-dependent myeloproliferative disease phenotypes. In these models, JAK2 V617F is expressed at ~10-fold higher than endogenous levels. In C57Bl6 mice, JAK2 V617F induces erythrocytosis, and in some animals myelofibrosis, although most reconstituted mice remain alive several months, and in some the erythrocytosis regresses; in Balb/c mice, the phenotype is more severe with erythrocytosis being followed by myelofibrosis.[13,23,127] Only very rarely, at low transduction levels, was a thrombocytosis phenotype observed, which, together with initial studies on primary patient cells,[22] led to the suggestion that gene dosage may be important for a particular phenotype to develop.[23] This hypothesis has been supported by studies in transgenic mice in which the expression of the JAK2 V617F was carefully regulated.[24] When JAK2 V617F levels were lower than endogenous JAK2 levels, an ET phenotype was obtained. When levels of JAK2 V617F were similar to those of endogenous wild-type JAK2, a PV-like phenotype was developed. Interestingly, upon development of the PV phenotype, a selection for higher levels of JAK2 V617F occurs, up to 5- to 6-fold higher than the endogenous JAK2 levels, which is not the case for the ET phenotype.[24] This indicates positive selection for JAK2 V617F expression in PV progenitors, a phenomenon that can be detected in stably transfected Ba/F3 cells.[51] In addition overexpression of several non-mutated JAK proteins, including JAK2, was shown to promote hematopoietic transformation to cytokine independence.[128]

The phenotype induced by exon 12 mutants of JAK2 is more restricted to erythrocytosis, without the abnormal megakaryocyte clusters seen in the classical MPNs.[18] These *in vivo* data indicate that a difference must exist between signaling by JAK2 V617F and exon 12 JAK2 mutants.

Mpl (TpoR) mutants

The phenotype induced by TpoR W515L is different than that induced by JAK2 mutants, in that it is much more severe, with initial myeloproliferation, marked thrombocytosis, splenomegaly and myelofibrosis, and is established within 20–30 days after reconstitution.[19] At least one other mutation at W515 was identified in patients with PMF and ET, that is W515K.[20] W515 is located in an amphipathic motif (RWQFP) at the junction between the transmembrane and cytosolic domains. This motif is required to maintain the un-liganded TpoR in an inactive state. Given that a W515A mutation is also active,[21] it is not surprising that such different residues (Leu and Lys) are found in active TpoR mutants. We predict that other W515 mutations will be found in patients, as the loss of a Trp (W) residue is responsible for activation.

The striking difference in severity and histopathology between the phenotypes induced by JAK2 V617F and Mpl 515 mutants is hard to understand when standard phosphorylation studies are performed on cell lines, such as Ba/F3 cells, where the same redundant pathways are activated by both JAK2 V617F and Mpl 515 mutants. Interestingly, deletion of the amphipathic motif (Δ5TpoR) that contains W515 or the mutation of either the lysine K514 (R514 in the human receptor) or the W515 in this motif to alanine leads to constitutive JAK2 and STAT activation and colony formation in primary cells and hypersensitivity to Tpo.[21] In hematopoietic cells transformed by Δ5TpoR (amphipathic motif deleted) or TpoR W515A, we noted enhanced STAT5 and MAP kinase activation in the absence of Tpo, and high levels of activation of STAT5, STAT3 and MAP kinase pathways on Tpo treatment.[21] Such TpoR mutants do not down-modulate cell surface levels of TpoR,[21] unlike TpoR in complex with JAK2 V617F, which is down-modulated (J Staerk *et al*., unpublished observations). It is therefore tempting to speculate that prolonged activation of MAP kinase and STAT3 might be a distinct feature of TpoR W515 mutants, whereas JAK2 V617F, which couples not only to TpoR but also to other cytokine receptors expressed in myeloid progenitors, would generate a weaker or different signal. Taken together, these data suggest that some level of signaling specificity must exist, which would make the excessive activation of TpoR through JAK2 V617F qualitatively different from that induced by W515 mutations. Understanding this difference at the signaling level will be of utmost importance.

Lessons from JAK2 inhibitors

An impetus driving the search for mutations in *JAK2* was given by the finding that a JAK2 inhibitor, AG490, as well as inhibitors of the PI-3-kinase, was able to inhibit the Epo-independent colony formation from myeloid progenitors of PV patients.[13,129] After the discovery of *JAK2* V617F, several selective JAK2 inhibitors have been developed. These inhibitors do not discriminate between the wild-type and the mutant JAK2, but show specificity for JAK2 when compared with JAK1, JAK3, Tyk2 and other tyrosine kinases. As the expression of JAK2 V617F leads to constitutive activation and hypersensitivity to cytokines (Figure 2b), such inhibitors might inhibit pathologic hematopoiesis at lower doses than those that would suppress normal hematopoiesis. One such molecule, TG101209, was able to inhibit proliferation of both *JAK2* V617F- and *TpoR* W515L/K-expressing hematopoietic cells.[130] It may be recalled that TpoR W515-mutated proteins are expected to constitutively activate the wild-type JAK2.

Another selective JAK2 inhibitor, TG101348, was effective in a murine model of MPN induced by *JAK2* V617F[131] and inhibited the engraftment of *JAK2* V617F-positive HSCs and myeloid progenitors in a bioluminescent xenogeneic

transplantation assay.[132] Importantly, the inhibitor decreased GATA1 expression and phosphorylation of GATA1 at S310 and, as expected, STAT5 activation. These signaling events might be associated with erythroid-skewing of *JAK2* V617F-positive progenitor differentiation, as phosphorylation at GATA1 S310 was shown to be important for erythroid differentiation.[81] GATA1 is absolutely required for erythroid and megakaryocyte formation.[133,134] Although both EpoR and GATA1 are crucial for erythroid differentiation, this phosphorylation event, which depends on PI-3-kinase and Akt,[81] appears to be the only one described where a direct EpoR downstream signal affects GATA1.

Cross-talk: JAK2 V617F and other pathways

JAK2 V617F and other tyrosine kinases

Tyrosine kinase receptors have been suggested to contribute to the pathogenesis of PV. In patients with PV, circulating erythroid progenitor cells are hypersensitive to IGF-1 and this effect requires the IGF-1 receptor.[10,135] Expression of JAK2 V617F in Ba/F3 cells renders the cells responsive to IGF-1 at doses where parental Ba/F3 cells are unresponsive.[51] After selection for autonomous growth, these Ba/F3 JAK2 V617F cells acquire the ability to respond to IGF-1 by further tyrosine phosphorylation of the mutant JAK2 and of STAT5 and STAT3. Which adaptor/signaling protein mediates this cross-talk is not clear, but it might be relevant for the hypersensitivity of PV erythroid progenitors to IGF-1.

Treatment with imatinib, an inhibitor of the Abl, c-KIT and PDGF receptor kinase, leads to minimal responses in PV, but nevertheless some rare patients achieve remission and a decrease in the *JAK2* V617F allele burden.[136] Imatinib exerts a dose-dependent growth inhibitory effect on factor dependent cell paterson (FDCP) cells expressing JAK2 V617F, most likely by interrupting the cross-talk between JAK2 V617F and c-KIT.[137] Thus, this study predicts that in PV patients where imatinib exerts benefic effects, pathologic signaling occurs through c-KIT.

Src tyrosine kinases have also been suggested to contribute to signaling by EpoR.[138] However, Src kinases were dispensable for the polycythemia phenotype induced by JAK2 V617F, as shown by bone marrow reconstitution studies in mice deficient for Lyn, Fyn or Fgr kinases.[139]

JAK2 V617F and TNF-α

In BALB/c mice reconstituted with HSCs transduced for the expression of JAK2 V617F, the PV-like phenotype is associated with increased serum levels of TNF-α.[101] TNF-α might be required for suppressing normal hematopoiesis, and in this manner it might favor the mutated clone. Reconstitution experiments in TNF-α knockout mice supported the notion that TNF-α might be required for the establishment of the MPN phenotype and for clonal dominance (Bumm TGP, VanDyke J, Loriaux M, Gendron C, Wood LG, Druker BJ, Deininger MW. TNF-α plays a crucial role in the JAK2-V617F-induced myeloproliferative disorder. *Blood* 2007; **110**. American Society of Hematology 2007 Abstract 675). Further studies will be required to firmly establish whether TNF signaling may contribute to clonal dominance.

Erythroblasts from JAK2 V617F-positive PV patients show increased death receptor resistance, which may give them a proliferative advantage over the non-mutated erythroblasts.[101,140] This effect was mediated by incomplete caspase-mediated cleavage of the erythroid transcription factor GATA-1, which in normal erythroblasts is completely degraded on CD95 stimulation.

MPNs and TGF-β

An increase of TGF-β expression in circulating megakaryocytic cells and platelets was demonstrated in PMF.[141] Fibroblasts participating in myelofibrosis were shown to be polyclonal, as opposed to the hematopoietic progenitors, thus suggesting that myelofibrosis is a reactive process.[141]

In myelofibrosis induced by excessive levels of Tpo,[142] severe spleen fibrosis was seen only in wild-type mice but not in homozygous TGF-β1 null (TGF-β1 (−/−)) mice.[143] Studies using peripheral CD34(+) cells cultured in medium with Tpo and stem cell factor concluded that PMF is a consequence of an increased ability of PMF CD34(+) progenitor cells to generate megakaryocytes and a decreased rate of megakaryocyte apoptosis, which lead to high levels of megakaryocyte-produced TGF-β.[144] In other models with hyperactive JAK–STAT signaling, such as knock-in with a mutant hyperactive gp130 receptor, the activation of the JAK–STAT pathway led to the expression of the inhibitory Smad7, which prevents the anti-proliferative effect of TGF-β.[145] A pathway linking Tpo, GATA-1 and TGF-β in the development of myelofibrosis was invoked, given that mice expressing low levels of the transcription factor GATA-1 also develop myelofibrosis.[146]

JAK2 V617F and chromatin

Studies in *Drosophila melanogaster* show that persistent activation of D-STAT by mutated D-JAK leads to chromatin effects and gene induction other than the normal targets of D-STAT, with counteracting heterochromatic gene silencing.[147] A genome-wide survey of genes required for JAK/STAT activity identified a WD40/ bromodomain protein *Drosophila* homolog of BRWD3,[148] a gene that is disrupted in human B-cell leukemia patients. Whether any histone acetylase, deacetylase, methyltransferase or other proteins containing bromo-, chromo- or chromoshadow domains are direct targets of JAK2 V617F is not clear. Recently, encouraging results were obtained with an HDAC (histone deacetylase) inhibitor, which seems to target only *JAK2* V617F-positive cells among primary myeloid progenitors from PV patients.[149] Thus, like other cancers,[150] MPNs might also show restriction of fate options through hypermethylation. This notion is supported by the different effects of sequential treatment with the DNA methyltransferase inhibitor, decitabine, followed by the histone deacetylase inhibitor, trichostatin A (TSA), on normal CD34(+) versus PMF CD34(+) cells. In the former, the treatment led to the expansion of cells, whereas in the latter the total number of CD34(+) cells and hematopoietic cells was reduced.[151]

Furthermore, promoter de-methylation appears to be at least partially at the basis of the dysregulated expression of the polycythemia rubra vera-1 (PRV-1) protein,[152] which is a key marker of PV.[153] Finally, hypermethylation of the SOCS1 promoter was reported approximately in 15% of MPN patients irrespective of *JAK2* V617F positivity.[154] SOCS1 promoter methylation may contribute to growth factor hypersensitivity, as SOCS1 appears to maintain the ability to down-modulate JAK2 V617F signaling.[124]

Concluding remarks

In committed progenitors, it is very likely that JAK2 V617F forms complexes with EpoR, TpoR and possibly with G-CSFR,

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and that these complexes are responsible for cytokine hypersensitivity or cytokine independence described in MPNs. The choice for one or the other receptor could depend on levels of expression of JAK2 V617F and possibly on host genetic factors. Through cross-talk with other signaling pathways, JAK2 V617F may exert a more profound effect on myeloid progenitors, going beyond simply recapitulating the effects of Epo, Tpo and G-CSF. The three oncogenic proteins, JAK2 V617F, JAK2 exon 12 mutants and TpoR W515L, induce in biochemical assays a similar picture of pathway activation. However, the *in vivo* phenotypes induced by these mutants are very different, suggesting a level of signaling specificity that must be deciphered. A major question remains whether JAK2 and cytokine receptor mutations suffice in humans to initiate MPNs or whether other events must precede or succeed them, before an HSC harboring the JAK2 mutation can take over blood formation and generate clonal MPN. It is thrilling that JAK2 inhibitors are already being tested in clinical trials for PMF associated with the *JAK2* V617F mutation. Results from such trials will teach us important lessons on whether JAK2 inhibitors will specifically reduce pathological hematopoiesis.

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