Mutation of JAK2 in the myeloproliferative disorders: timing, clonality studies, cytogenetic associations, and role in leukemic transformation

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The identification of an acquired mutation of JAK2 in patients with myeloproliferative disorders has raised questions about the relationship between mutation-positive and mutation-negative subtypes, timing of the JAK2 mutation, and molecular mechanisms of disease progression. Here we demonstrate that patients with V617F-essential thrombocythemia do not commonly progress to become V617F+. Consistent with the concept of distinct pathogenetic mechanisms, we show that patients with and without the JAK2 mutation have different patterns of cytogenetic abnormality, with virtually all patients carrying the 20q deletion or trisomy 9 being V617F+. We also investigated the existence of a “pre-JAK2” phase by comparing the proportion of clonally derived granulocytes, estimated from X-chromosome inactivation patterns (XCIPs), with the proportion of V617F+ granulocytes. Our results demonstrate that inherent XCIP variability between granulocytes and T cells produces a systematically biased pattern of results that may be misinterpreted as evidence for an excess of clonally derived granulocytes, an observation that limits the utility of XCIP analysis in this context. Lastly, we studied 4 patients with V617F+ myeloproliferative disorders who subsequently developed acute myeloid leukemia. In 3 patients the leukemic cells were V617F−, suggesting that in these patients the leukemia arose in a V617F− cell. (Blood. 2006;108: 3548-3555) © 2006 by The American Society of Hematology

Introduction

An acquired mutation in JAK2 has been described in nearly all patients with the myeloproliferative disorder (MPD) polycythemia vera (PV), and half those with essential thrombocythemia (ET) and idiopathic myelofibrosis (IMF).1,2 The V617F mutation arises in a multipotent progenitor,1 is associated with erythropoietin-independent growth of erythroid progenitors,1 confers constitutive activity on the kinase, with enhanced downstream signaling,2-4 and was sufficient for the development of erythrocytosis in a murine retroviral model.2 The V617F mutation was not found in an extensive survey of nonhematologic cancers and lymphoid malignancies and is relatively uncommon in myeloid malignancies other than the classic MPD.8-10

Analysis of prospective data from the PT-1 study11 has demonstrated that JAK2 status distinguishes 2 biologically distinct subtypes of ET, with the V617F+ subgroup exhibiting many laboratory and clinical similarities to PV.12 Similar observations have been reported by other groups.13,14 These results suggest that V617F+ ET and PV form a biologic continuum, with the degree of erythrocytosis determined by physiologic or genetic modifiers.12

The relationship of V617F− ET to V617F+ ET is unclear. It has been suggested that V617F− ET may represent an earlier phase of the same disease, with subsequent acquisition of the JAK2 mutation.4 In support of this concept it has been reported that patients with V617F+ MPD had a longer duration of disease compared to those lacking the mutation.4 In addition, the existence of rare families in whom multiple members have an MPD, which may be negative or positive for the V617F mutation, has been used to suggest the existence of a pre-JAK2 mutation.15 However, a prospective study of ET did not confirm a longer duration of disease in V617F+ patients and found no difference between mutation-positive and -negative patients in the frequency of features of advanced disease, such as splenomegaly, abnormal cytogenetics, and transformation rates.12 These considerations
suggest an alternative model in which JAK2-positive and -negative ET represent pathogenetically distinct diseases.

The MPDs are associated with several cytogenetic abnormalities, including trisomy 9, trisomy 8, and deletion of 20q and 13q. The rates of cytogenetic abnormalities have been reported to be comparable in V617F+ and V617F− MPDs, although the small number of patients preclude definitive conclusions. Such cytogenetic abnormalities may provide clues to the as yet unknown pathogenesis of V617F− MPDs and may illuminate the potential role of cooperating mutations in progression of V617F+ disease.

Both PV and ET may terminate in an accelerated phase, with patients experiencing falling blood counts, myelofibrosis, transformation, and progressive systemic symptoms, as well as frank acute leukemic transformation. However, neither is an inevitable consequence of the MPD, and acquisition of additional mutations seems likely to contribute to the evolution of these more aggressive stages. It is not known what role the JAK2 mutation plays in transformation to acute myeloid leukemia (AML). The V617F mutation is rare in de novo AML, although fusion genes involving JAK2 are associated with acute leukemia.

Here we have investigated the relationship of V617F− ET to V617F+ ET, the existence of a “pre-JAK2” phase of V617F+ MPDs, and the molecular mechanisms associated with disease progression.

### Patients, materials, and methods

#### Patients and samples

Granulocytes were prepared by centrifugation of whole blood through a Ficoll density gradient, and T cells were isolated from the mononuclear-cell layer by anti-CD2 magnetic beads, as described. Mean purity was greater than 95% for granulocytes and 91% for T cells. For samples from JAK2+ ET represent pathogenetically distinct diseases. The forward wild-type (WT) inner primer was labeled with FAM and were used in a modification of the 4-primer protocol published by Jones et al. The fluorescently labeled primers after overnight digestion with HsuI. The proportion of clonal granulocytes was estimated from the HUMARA assay, which permits the use of biologic samples and clinical data (Fulbourn, United Kingdom) for Causes of Clonal Haematological Disorders project, which permits the use of biologic samples and clinical data from patients with clonal hematologic disorders, and was carried out in accordance with the principles of the Declaration of Helsinki.

#### HUMARA and JAK2 quantitation

For quantitation of the JAK2 V617F mutation, fluorescently labeled primers were used in a modification of the 4-primer protocol published by Jones et al. The forward wild-type (WT) inner primer was labeled with FAM and the reverse mutation-specific inner primer with HEX, and the PCR products were run on an ABI Prism 3700 machine (Applied Biosystems, Foster City, CA). A dilution series of mutant and WT DNA was run with each reaction and used to estimate the proportion of V617F alleles in each patient’s DNA, as described in “Statistical analysis.” To calculate the proportion of V617F granulocytes from the V617F/WT allelic ratio, we assume that JAK2+ granulocytes are heterozygous for the mutation. Because a heterozygous cell contributes 1 WT and 1 mutant allele to the DNA sample, the estimated proportion of JAK2+ granulocytes is double the V617F/WT allelic ratio. The presence of both heterozygous and homoygous cells would lead to overestimation of the proportion of JAK2+ granulocytes. We have minimized the impact of this by excluding patients with known 9p loss of heterozygosity (LOH), trisomy 9, or V617F homozygosity (6 patients). We selected any ET patients (in whom homozygosity is rare) and focused on PV patients with low levels of JAK2 positivity, defined as mutation detectable by allele-specific PCR alone (3 patients), mutant peak less than 25% total height by sequencing (5 patients), or mutant peak height 25% to 50% (2 patients).

The human androgen receptor assay (HUMARA) was performed using fluorescently labeled primers after overnight digestion with HsuI. The proportion of clonal granulocytes was estimated from the HUMARA assay, which permits the use of biologic samples and clinical data (Fulbourn, United Kingdom) for Causes of Clonal Haematological Disorders project, which permits the use of biologic samples and clinical data from patients with clonal hematologic disorders, and was carried out in accordance with the principles of the Declaration of Helsinki.

#### Statistical analysis

The quantitation of V617F alleles used the logarithm of the ratio of peak areas for the mutant and WT peaks. A 3-parameter logistic curve was fitted to log(peak area ratio) versus V617F proportion from the dilution series. Parameter values were estimated by nonlinear least squares regression and point estimates of V617F proportion were calculated for patients. The measurement standard error for JAK2 and HUMARAs was estimated by variance components models.

For the Monte Carlo simulations of estimated proportions of clonal granulocytes under the null hypothesis of no mutation preceding JAK2 V617F, the data of Gale et al were used. The XCI proportions of paired T-cell and granulocyte samples were used to estimate the variability of granulocyte XCI for young (<50 years) and elderly (>75 years) women. A logit transform (defined as logit (p) = log(p/(1−p))) was taken of granulocyte and T-cell inactivation proportions, and as expected, these were linearly associated with slope 1 and normally distributed residuals. The age-specific standard deviation of the difference between granulocyte and T-cell XCI was used in the simulations (0.44 for women < 50 years, 1.25 for women > 75 years, and an interpolated estimate of 0.75 for women 50-75 years).

To perform the simulations, the logit of a given proportion of active X in T cells was used as the mean of a normal distribution for the logit of granulocyte XCI, with standard deviation as detailed. The JAK2 mutation was assumed to arise in a cell with an active maternal X chromosome with probability p, where p was the proportion of active maternal X chromosomes in granulocytes estimated from the previous step. For a given proportion of JAK2+ cells, the observed XCI in the mixed clonal and polyclonal granulocyte population could be calculated. The estimated proportion of clonal granulocytes could be calculated using the formulas described previously:

\[ G_C = \frac{R_T - R_G}{R_T + 1} \]

When \( R_C \leq R_G \), where \( G_C \) is the proportion of clonal granulocytes, and where \( R_T \) and \( R_G \) are the \( X^{TM}/X^T \) allele ratios for T cells and granulocytes, respectively. For each level of T-cell skewing, standard deviation and JAK2+ proportion, 50,000 simulated cases were used to generate the medians and 95% confidence intervals shown in Figure 2A. The simulations were used to assess whether the pattern we observed provided evidence for the hypothesis that JAK2 is associated with an increased proportion of clonal granulocytes.
against the null hypothesis of no pre-JAK2 phase. Under this hypothesis, the
centile of the observed proportion of clonal granulocytes compared to the
simulated population is uniformly distributed on [0,1], with mean 0.5. The
mean of the centiles for the 20 patients was the test statistic. Power
calculations show that a sample size of 20 would reject the null hypothesis
with 80% power if, on average, each patient fell on the upper third (ie,
≥ 67%) of the simulated population. This would equate to a 15%
population of clonal JAK2
granulocytes in patients with a 30% population of
JAK2
granulocytes, for example. Therefore, this sample size is
adequate to detect even modest populations of V617F
clonal granulocytes if they are present in most patients.

Hypothesis tests for whether there was any difference in proportions of
patients positive or negative for V617F with a given cytogenetic abnor-
mality were based on estimates of the frequency of V617F positivity in large
cohorts of the 3 MPD subtypes using appropriately sensitive detection
methods, namely, 97% for PV (pPV), 53% for ET (pET) and 55% for IMF
(pIMF). Assuming the number of patients with a given cytogenetic abnor-
mality is fixed as nPV, nET, and nIMF, then the probability that exactly x patients,
x = 0, 1, 2, . . . nPV + nET + nIMF, will be V617F
in the whole cohort is given by:

\[
p(x) = \sum_{k=0}^{\min(n_{PV}, n_{ET}, n_{IMF})} \binom{n_{PV} + n_{ET} + n_{IMF}}{k} \cdot \left( \frac{p_{PV}^k (1 - p_{PV})^{n_{PV} - k}}{k!} \right) \left( \frac{p_{ET}^k (1 - p_{ET})^{n_{ET} - k}}{k!} \right) \left( \frac{p_{IMF}^k (1 - p_{IMF})^{n_{IMF} - k}}{k!} \right)
\]

To calculate a 2-sided p value, values for P(x) were summed over 0...x and
nPV + nET + nIMF - x, . . . , nPV + nIMF + nET + nIMF.

**Results**

**Patients with V617F' ET do not subsequently become V617F**

To investigate the possibility that V617F' ET progresses into
V617F+ ET, we studied prospectively collected, paired DNA
samples from 50 patients with V617F' ET enrolled in the high-risk
PT-1 trial11 and the on-going low- and intermediate-risk trials.
Allele-specific PCR2 was used to detect the mutation in DNA from
unfractionated blood collected at trial entry and again after a
median follow-up of 77 months (range, 61-90 months). None of the
50 patients showed evolution from V617F’ to V617F+ ET (Figure
1A), suggesting that if it occurs at all, it is a rare phenomenon.
These data suggest that V617F’ and V617F’ thrombocytosis are
distinct disorders, rather than temporally linked phases of the
same disease.

**Comparison of XCIPs with proportion of V617F’ granulocytes**

The identification of V617F’ and V617F’ ET as separate disorders
does not exclude the possibility that the V617F mutation may
require one or more prior mutations to cause an overt MPD
phenotype. This scenario suggests that it might be possible to
detect a pre-JAK2 phase by comparing the proportion of clonally derived
granulocytes (using XCIPs) with the proportion of V617F’
granulocytes. We therefore assessed granulocyte and T-cell DNA from 20
informative women under the age of 75 who had a V617F’ MPD
(10 with ET and 10 PV). To calculate the proportion of V617F’
cells from the V617F/WT ratio, we assume that granulocytes are
heterozygous for the V617F mutation. Because 30% of PV patients
have evidence of 9p LOH and V617F homozygosity,1,3,4,30 we
excluded patients with known 9p LOH, trisomy 9, or a mutant peak
height greater than 50% of total peak height by sequencing. In addition,
we studied 10 patients with ET (in whom V617F homozygosity is
rare) and focused on PV patients with a low burden of disease.
HUMARA was used to calculate the proportion of clonal granulo-
cytes31 and a 4-primer allele-specific PCR method32 to quantify the
proportion of V617F’ cells. The method for quantifying the
V617F/WT ratio was reproducible and accurate, with little
evidence for interexperiment variability (Figure 1B), as was the case
for HUMARA (Figure 1C). The estimated standard errors of
measurement for the HUMARA and JAK2 assays were 6.7% and
5.5%, respectively.

Comparison between the proportions of clonal and V617F’
granulocytes showed 2 main points. First, the distribution of PV
patients was similar to ET patients, suggesting that the assumption
of heterozygosity had not substantially affected the pattern of
results for PV patients (Figure 1C). Second, some patients appeared
to have more clonal granulocytes than V617F’ cells. Two patients
(marked with A1 and A2 in the figure) had clonal granulocytes
estimated by XCIP analysis to be 70% to 85%, but V617F’
cells in the range 10% to 20%. These patients were 70 and 74 years old at
the time of sampling, and there has been nothing unusual about the
presentation or subsequent course of their MPDs. Six other
patients, marked with B1-6 in the figure, had clonal granulocytes estimated by HUMARA that exceeded the proportion of V617F+ cells, although the degree of discrepancy was less marked than for patients A1 and A2.

**Clonality studies: Monte Carlo modeling demonstrates unexpected variability and systematic bias**

These data might be taken to suggest the existence of a population of clonally derived granulocytes that are V617F+, and therefore used to support the concept of a pre-JAK2 phase of MPD development. However, the calculation of the proportion of clonally derived granulocytes using X-chromosome inactivation methods is based on a critical assumption, namely, that the pattern of X-chromosome inactivation in normal granulocytes is the same as that in T cells. This assumption underlies the estimation of the proportion of clonal granulocytes by any method of X-linked inactivation patterns, whether based on DNA or RNA, but, as has been shown in previous studies of healthy women, the actual proportion of granulocytes with a given X chromosome inactivated is distributed around the value for T cells, with the variability of the distribution increasing with age.24,29 We reasoned that this variability may have a significant impact on the accuracy of the calculated proportion of clonal granulocytes.

To assess whether discrepancy between granulocyte and T-cell XCIPs could explain why we found apparently clonal V617F+ granulocytes in some MPD patients, we undertook Monte Carlo simulations28 based on the null hypothesis of no pre-JAK2 phase. Using given values for the proportion of V617F+ granulocytes (the predefined “true” clonal proportion) and the T-cell XCIP together with the variance of granulocyte XCIP around the value for T cells calculated from healthy women,29 we modeled the resultant granulocyte XCIPs. These granulocyte XCIPs were then used to calculate the proportion of clonal granulocytes that would be obtained by XCIP analysis, thus allowing comparison of this estimated proportion with the predefined “true” proportion of clonal granulocytes.

Several observations emerged. First, the 95% confidence intervals for the population distribution of clonal granulocytes estimated from XCIPs were wide. As expected, this was more marked for older patients (Figure 2A). To see why discrepancies between granulocyte and T-cell XCIPs could explain why we found apparently clonal V617F+ granulocytes in some MPD patients, we undertook Monte Carlo simulations based on the null hypothesis of no pre-JAK2 phase. Using given values for the proportion of V617F+ granulocytes (the predefined “true” clonal proportion) and the T-cell XCIP together with the variance of granulocyte XCIP around the value for T cells calculated from healthy women, we modeled the resultant granulocyte XCIPs. These granulocyte XCIPs were then used to calculate the proportion of clonal granulocytes that would be obtained by XCIP analysis, thus allowing comparison of this estimated proportion with the predefined “true” proportion of clonal granulocytes.

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than would be expected under the null hypothesis, with a P value of 0.17. The 2 patients marked A in Figure 1C may well represent benign, age-related skewing, rather than a pre-JAK2 phase of disease. Our data therefore demonstrate that considerable caution must be exercised when using XCI analysis to quantify the proportion of clonal granulocytes.

**V617F+ and V617F− MPDs are associated with distinct patterns of cytogenetic abnormalities**

The concept that V617F+ and V617F− ET may represent pathogenetically distinct disorders raises the possibility that they may be associated with different patterns of cytogenetic abnormality. Previous studies assessing the relationship of cytogenetic abnormalities to JAK2 status have not shown any significant associations,1,12,17 although numbers have generally been too small to make definitive comment. We therefore assessed the studies of 20q and 13q deletions in MPDs.21

**Table 1. Cytogenetic abnormalities in V617F+ and V617F− patients with MPDs**

<table>
<thead>
<tr>
<th></th>
<th>V617F+</th>
<th>V617F−</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Del(20q) total</td>
<td>28</td>
<td>1</td>
<td>&lt;.001</td>
</tr>
<tr>
<td>PV</td>
<td>12</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>ET</td>
<td>5</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>IMF</td>
<td>10</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>MPD/MDS</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Del(13q) total</td>
<td>3</td>
<td>9</td>
<td>.17</td>
</tr>
<tr>
<td>PV</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>IMF</td>
<td>2</td>
<td>9</td>
<td></td>
</tr>
<tr>
<td>Translocations total</td>
<td>2</td>
<td>8</td>
<td>.12</td>
</tr>
<tr>
<td>ET</td>
<td>0</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>IMF</td>
<td>2</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Trisomy 9</td>
<td>10</td>
<td>0</td>
<td>.01</td>
</tr>
<tr>
<td>PV</td>
<td>3</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>ET</td>
<td>3</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>IMF</td>
<td>4</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Trisomy 8</td>
<td>6</td>
<td>1</td>
<td>.23</td>
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<td>PV</td>
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<td>0</td>
<td></td>
</tr>
<tr>
<td>ET</td>
<td>2</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>IMF</td>
<td>2</td>
<td>1</td>
<td></td>
</tr>
</tbody>
</table>

Data are pooled from several sources, including 3 prospective ET trials (599 patients with cytogenetic results)11,12, the European Myelofibrosis Network (71 patients)17, the Addenbrooke MPD clinic (89 patients),1 and previous collaborative studies of 20q and 13q deletions in MPDs.21

**V617F− AML in patients with a preceding V617F+ MPD**

To study the role of the JAK2 mutation in leukemic transformation, we identified 4 patients with V617F+ MPDs (2 ET, 2 PV) who subsequently transformed to AML. Patient PV1 was aged 48 years at diagnosis of PV, and received 32P, busulfan, and hydroxyurea before transformation to AML 25 years later. Interestingly, cytogenetics on 2 occasions before transformation to AML showed a del(20q) and a balanced t(1;9)(q21;q24) translocation, but cytogenetics after transformation to AML showed a complex karyotype, which did not include either the del(20q) or the t(1;9) translocation. Patient PV2 was aged 74 at diagnosis of PV and had the disease 12 years before AML transformation, during which time she received only hydroxyurea. Cytogenetics were normal at diagnosis of PV and not performed when the AML developed. The 2 ET patients, ET1 and ET2, were aged 75 and 70 years at diagnosis of ET and transformed to AML 26 and 44 months after diagnosis, respectively. Both had normal cytogenetics at diagnosis of ET, but ET1 had a 5q deletion at the time of AML transformation, whereas ET2 still had normal cytogenetics. Both had received only hydroxyurea before developing AML.

Paired samples before and after AML transformation were available for all 4 patients and were used to assess JAK2 V617F mutation status (Figure 3). A panel of microsatellite markers on chromosome 20 was used to confirm that the paired DNA samples from each patient did indeed have the same genotype (data not shown). For patient PV1, granulocytes taken during the PV phase showed a predominantly mutant sequencing trace, but DNA from the AML bone marrow sample was WT (Figure 3A). This finding is consistent with the cytogenetic evidence for the appearance of a distinct clone at the time of transformation. Patient PV2 also had a mixed sequence trace in granulocytes but subsequently a WT trace in AML peripheral-blood blasts (Figure 3A). For the ET patients, V617F positivity was demonstrated in pre-transformation samples using allele-specific PCR (data not shown). Only the WT allele was detected in the AML sample of patient ET1, whereas the V617F allele predominated in the sample from patient ET2 (Figure 3B).

Thus, in 3 of 4 patients with a V617F+ MPD who transformed to AML, the leukemic cells were V617F−. There are 3 possible models to explain this unexpected finding (Figure 4A). First, the mutations responsible for transformation to AML may have developed in a V617F+ clone that subsequently reverted to V617F− negativity. Loss of the V617F mutation may provide a growth advantage to leukemic cells if, for example, the V617F mutation is associated with a strong differentiation signal. Second, if mutation of JAK2 is not the initiating event in some MPDs, the AML may result from transformation within the pre-JAK2 clone. Third, AML may result from transformation of a normal stem cell, perhaps as a consequence of mutagenic therapy.

Evidence for the first model (reversion) was sought using cytogenetic analysis and microsatellite PCR. No deletion of chromosome 9p was detected by G-banding in the 3 patients for whom metaphases were available at the time of their AML. Microsatellite PCR was performed on samples from patients PV1 (data not shown) and PV2 (Figure 4B). In the PV phase of the disease, both patients exhibited LOH for 9p markers. By contrast, the AML samples from both patients showed retention of heterozygosity for markers on 9p, thus excluding mitotic recombination as a mechanism for reversion to WT JAK2. Unfortunately, the 2 women (PV2 and ET1) were uninformative at the androgen...
receptor locus, preventing us from testing whether model 3 was operative. Our results therefore demonstrate that model 1 (reversion) is unlikely and suggest that, in patients with a V617F/H11001 MPD, AML can arise in a V617F/H11002 cell.

Discussion

We have addressed several issues raised by the discovery of the JAK2 V617F mutation, including the relationship between V617F/H11001 and V617F/H11002 subtypes of ET, the timing of the JAK2 mutation, and the molecular mechanisms associated with leukemia transformation.

We have previously demonstrated that the V617F/H11001 and V617F/H11002 subtypes of ET exhibit multiple laboratory and clinical differences and have suggested that the 2 subtypes represent pathogenetically distinct diseases rather than sequential phases of the same disease.12 We now provide direct evidence for this model. Comparison of paired samples from 50 patients with V617F/H11002 ET showed no evidence that they subsequently acquire a JAK2 V617F mutation. In addition, we demonstrate that V617F+ and V617F− MPD patients exhibit very different patterns of cytogenetic abnormalities. In particular, the demonstration that 28 of 29 patients with a 20q deletion were V617F+ provides striking evidence for cooperation between the JAK2 mutation and gene(s) located on the long arm of chromosome 20.

Kralovics and colleagues have proposed a “sequential disorder” model in which V617F/H11002 MPDs represent an earlier phase of V617F/H11001 disease.4 Support for this model came from 2 lines of evidence. First, they found that V617F+ patients had a longer duration of disease.4 The discrepancy between this result and data from the PT-1 trial12 may reflect methodologic differences. Kralovics and colleagues used sequence analysis that is now recognized to be less sensitive than allele-specific PCR.12 Because the proportion of V617F+ granulocytes increases with time,31 sequence analysis will preferentially detect patients relatively late in the course of their disease, whereas patients in the early stage may be falsely labeled as V617F+. This bias may produce an apparent difference in the duration of the disease between the 2 subtypes of ET. The second line of evidence is that familial MPD pedigrees have both V617F/H11001 and V617F/H11002 members. However, it is not clear whether the genetic lesion that predisposes to an MPD in such families contributes to the pathogenesis of sporadic MPDs.

Our results highlight several issues that limit the ability of XCIP analysis to demonstrate a pre-JAK2 clone of V617F− cells in V617F+ patients. First, several groups have demonstrated small differences in XCIPs from T cells and granulocytes in healthy subjects.24,29,32,33 We show here that these differences result in wide confidence limits for the calculated proportion of V617F− cells that are apparently clonally derived. Importantly, this variability is systematically biased toward overestimating the proportion of clonally derived granulocytes. These problems result from inherent differences in granulocyte and T-cell XCIPs (due to selection for X-linked polymorphisms that affect stem-cell behavior24,34) and therefore apply to both DNA and RNA methods of XCIP analysis. Second, when estimating the proportion of clonal cells, it is
AML in majority of patients, have balanced X-inactivation patterns.35,36 9p either side of 1992) and blasts from leukemic transformation (2004) for 2 markers on chromosome on peripheral-blood granulocytes and T cells from the PV phase of disease (taken in JAK2 potential explanation for our striking observation that several abnormalities of AML evolving from preceding myelodysplasia the proportion of JAK2 granulocytes are heterozygous. A mixed population of homozygous, heterozygous, and WT cells would lead to overestimation of granulocytes is rare), by excluding PV patients with a minized the impact of this by studying patients with ET (in chromosome 9p either side of JAK2 from patient PV2.

assumed that T cells are not involved in the malignant clone. In support of this, T cells lack the JAK2 mutation1,2,4,25-27 and, in the majority of patients, have balanced X-inactivation patterns.35,36 However, T-cell involvement by a pre-JAK2 clone in a minority of patients cannot be excluded. The third important assumption is that granulocytes are heterozygous. A mixed population of homozygous, heterozygous, and WT cells would lead to overestimation of the proportion of JAK2+ granulocytes. In this report, we have minimized the impact of this by studying patients with ET (in whom homozygosity is rare), by excluding PV patients with a homozygous sequence trace, and by selecting patients with a low V617F/WT ratio. Nevertheless, such a phenomenon may explain patient C in Figure 1C and remains a further caveat to the use of XCIPs to identify a pre-JAK2 phase.

These problems inherent in comparisons between JAK2 quantitation and XCIPs make it difficult to draw meaningful conclusions about the existence of a pre-JAK2 clone. However, it is important to emphasize that these considerations do not exclude a pre-JAK2 phase of disease in V617F+ patients. Indeed, this remains a potential explanation for our striking observation that several patients with a V617F+ MPD transformed to a V617F- AML. An analogous sequence of events is highly unusual in other hematologic malignancies. For example, the blast transformation of chronic myeloid leukemia is BCR-ABL+ and the cytogenetic abnormalities of AML evolving from preceding myelodysplasia include those of the original myelodysplastic clone.37 Our observations in V617F+ MPDs extend the findings of Jelinkova et al.,10 who found that the prevalence of the JAK2 mutation was lower in samples from patients with AML transformed from antecedent PV and IMF than in their cohort of PV and IMF patients without transformation.

There are 3 possible models for the development of a V617F- AML in a patient with V617F+ MPD (Figure 4A). First, leukemic transformation may have occurred in a V617F+ cell that subsequently became V617F-. It is possible that the JAK2 V617F mutation provides a strong differentiating signal to hematopoietic progenitors in which case leukemic blasts that lose this signal may gain a growth advantage. However, this model seems unlikely because, in patient PV1, the leukemic cells did not have either the 20q deletion or the t(1;9) translocation that were present in the PV phase. Furthermore, we were unable to find any evidence for mitotic recombination or deletion of the originally mutated JAK2 gene in either patient PV1 or PV2 (Figure 4B). We cannot exclude the possibility that point mutation could have caused reversion to WT JAK2, but overall there seems little evidence in favor of this model.

Another possibility is that the leukemia could have developed from a normal stem cell, not part of the original clone. This could explain patient PV1, because he received known mutagens (C3 and busulphan). However, the other patients received only hydroxyurea. Although there is controversy over the leukemogenicity of hydroxyurea in MPDs, extensive experience with the drug in sickle cell anemia suggests that hydroxyurea does not commonly induce leukemic transformation of normal stem cells.38 It is therefore difficult to explain why patients PV2 and ET1 would develop leukemia in a normal stem cell following therapy with hydroxyurea alone.

The third model to explain the development of V617F- AML is that, in these patients, the JAK2 mutation followed an initial pre-JAK2 phase of their disease, which resulted from an unidentified initial mutation. Such an initiating mutation could either confer a growth or survival advantage in cooperation with the JAK2 and the AML mutations or, alternatively, could promote genomic instability, thus predisposing the target cell to the acquisition of further mutations. This model raises the question of why the AML did not develop in a stem cell with both the initiating mutation and the V617F mutation, because with increasing time the V617F+ cells come to predominate. One possibility is that the V617F mutation selects against proliferation of immature myeloblasts, perhaps by providing a strong differentiation signal, although it then becomes difficult to explain both patient ET2 who actually evolved toward a homozygous V617F pattern in her leukemic cells, and rare occurrences of V617F+ de novo AML.7,9,10

Our results argue against the first model to explain the absence of the JAK2 mutation in the leukemic phase of V617F+ MPDs and demonstrate that distinguishing between models 2 and 3 will be difficult. Importantly, confirmation of model 3 will require identification of the putative initiating mutation since indirect methods based on XCIP analysis are too sensitive to departures from the assumption of equal XCIPs in T cells and granulocytes.

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References


