

Brief report

Altered gene expression in myeloproliferative disorders correlates with activation of signaling by the V617F mutation of Jak2

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We identified 13 new gene expression markers that were elevated and one marker, *ANKRD15*, that was down-regulated in patients with polycythemia vera (PV). These 14 markers, as well as the previously described *PRV1* and *NF-E2*, exhibited the same gene expression alterations also in patients with exogenously activated granulocytes due to sepsis or granulocyte colony-stimulating factor (G-CSF) treatment. The recently described

V617F mutation in the Janus kinase 2 (*JAK2*) gene allows defining subclasses of patients with myeloproliferative disorders based on the *JAK2* genotype. Patients with PV who were homozygous or heterozygous for *JAK2-V617F* exhibited higher levels of expression of the 13 new markers, *PRV1*, and *NF-E2* than patients without *JAK2-V617F*, whereas *ANKRD15* was down-regulated in these patients. Our results suggest that the alterations in

expression of the markers studied are due to the activation of the Jak/signal transducer and activator of transcription (STAT) pathway through exogenous stimuli (sepsis or G-CSF treatment), or endogenously through the *JAK2-V617F* mutation. (Blood. 2005;106:3374-3376)

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Introduction

Myeloproliferative disorders (MPDs) are a heterogeneous group of diseases characterized by increased hematopoiesis leading to elevated numbers of nonlymphoid cells or platelets in the peripheral blood. Diagnostic criteria for polycythemia vera (PV), essential thrombocythemia (ET), and idiopathic myelofibrosis (IMF) have been defined by the Polycythemia Vera Study Group (PVSG) and more recently by the World Health Organization (WHO).¹⁻³ The Janus kinase (Jak) family of proteins mediate the effects of hematopoietic cytokines, for example, erythropoietin and granulocyte colony-stimulating factor (G-CSF), by phosphorylating cytoplasmic targets, including the signal transducers and activators of transcription (STATs).⁴ Recently, a mutation exchanging valine to phenylalanine at position 617 (V617F) of the Jak2 protein has been identified in patients with MPDs.⁵⁻⁸ This mutation results in the activation of the Jak2 kinase. Comparison of granulocyte mRNA expression by differential display or microarrays has been used to define biomarkers for MPDs.⁹⁻¹¹ The value of markers, such as elevated expression of mRNAs for polycythemia rubra vera 1 (*PRV1*) and nuclear factor erythroid-derived 2 (*NF-E2*) in granulocytes,^{10,11} in the diagnostic workup of patients with suspected MPDs remains to be established. Here we analyzed 14 new gene expression markers as well as *PRV1* and *NF-E2* by quantitative

polymerase chain reaction (PCR) in patients with MPDs classified according to the *JAK2-V617F* mutation status and in patients with exogenous stimulation of granulocytes by cytokines.

Study design

Patients

We studied 98 patients with MPDs (54 PV, 33 ET, 11 IMF); 30 patients with PV were from Italy, and the remaining 68 patients with MPD were from Switzerland. The PVSG criteria were applied for the Italian patients with PV, whereas the WHO diagnostic criteria were followed for all patients with MPD in the Swiss cohort.¹⁻³ Four individuals with secondary erythrocytosis (SE) with elevated serum erythropoietin due to pulmonary dysfunction, 4 with secondary neutrophilia (3 due to sepsis and 1 postsurgical neutrophilia), and 28 healthy individuals were included. In addition, 3 healthy donors were examined before and after G-CSF treatment for stem-cell mobilization. The study was approved by the ethics committee of Basel (Ethikkommission Beider Basel), Switzerland. Patients provided informed consent in accordance with the Declaration of Helsinki.

RNA and DNA analyses

Isolation of granulocytes and RNA and cDNA preparation were performed as described.¹² The primer sequences are listed in Table S1 (available at the

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Submitted May 10, 2005; accepted July 11, 2005. Prepublished online as *Blood* First Edition Paper, August 4, 2005; DOI 10.1182/blood-2005-05-1889.

Supported by grants from the Swiss National Science Foundation (3100-066949.01), the Swiss Cancer League (OCS-01411-08-2003), the Lichtenstein Stiftung (R.C.S.), the Krebsliga beider Basel (R.K.), and by a grant from the Associazione Italiana per la Ricerca sul Cancro (AIRC), Milan, Italy (M.C.).

R.K. designed and performed research and wrote the article; S.-S.T., A.S.B., R.T., and D.P. performed research; M.B. contributed vital analytical tools and performed statistical analysis; A.T. contributed vital analytical tools and

samples; F.P. performed research and contributed vital samples; M.C. designed research and contributed vital samples; and R.C.S. designed research and wrote the article.

An Inside *Blood* analysis of this article appears in the front of this issue.

The online version of the article contains a data supplement.

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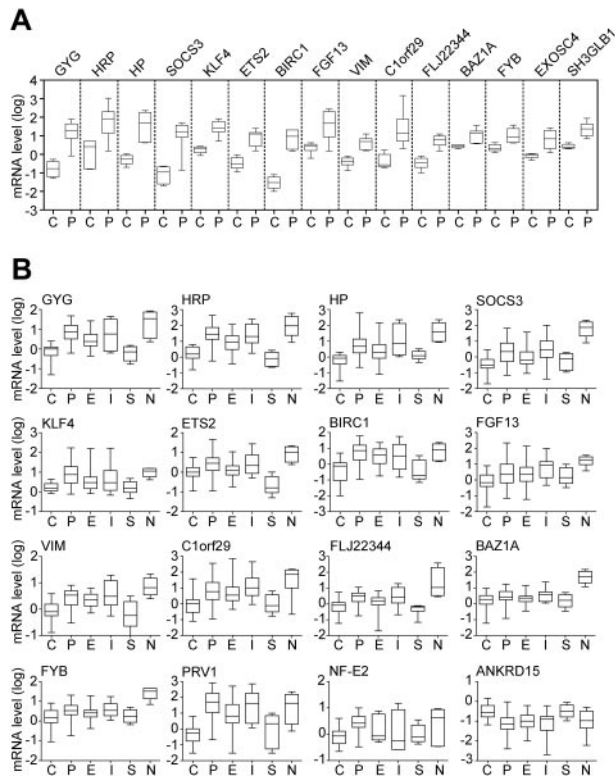


Figure 1. Validation of gene expression changes by quantitative PCR. (A) Marker expression in the learning cohort. Fifteen differentially expressed genes identified by microarray analysis were re-examined by real-time PCR in 4 healthy controls (C) and 7 patients with polycythemia vera (P). Boxes represent the interquartile range that contains 50% of the values; the horizontal line in the box marks the median and bars indicate the range of values. Relative gene expression is shown on a logarithmic scale (\log_{10}) and the values represent the mRNA expression relative to a healthy control calibrator sample, calculated by the $\Delta\Delta C_T$ method. All 15 genes examined showed a statistically significant difference ($P < .05$; Mann-Whitney *U* test) between controls and PV. (B) Marker expression in the test cohort, consisting of 28 healthy controls (C), 47 patients with polycythemia vera (P), 33 patients with essential thrombocythemia (E), 11 patients with idiopathic myelofibrosis (I), 4 patients with secondary erythrocytosis (S), and 4 patients with secondary neutrophilia (N). Annotation as indicated in panel A.

Blood website; click on the Supplemental Table link at the top of the online article). Quantitative PCR was performed with the SYBR green master mix in duplicate (Applied Biosystems, Foster City, CA). The differences of threshold cycles (ΔC_T) were derived by subtracting the C_T value for the internal reference, ribosomal protein L19 (*RPL19*), from the C_T values of the marker genes.^{13,14} One of the healthy control cDNAs was chosen as a calibrator for calculating the $\Delta\Delta C_T$ values. The *JAK2* genotyping and the quantification of the *PRV1* mRNA were performed as described.^{13,14}

Microarray analysis

Total RNA from granulocytes was purified by the RNeasy total RNA isolation kit (Qiagen, Hilden, Germany). The U133A Human Genomic arrays (Affymetrix, Santa Clara, CA) were used for gene profiling as described.¹⁵

Results and discussion

Using microarray analysis, we screened for differentially expressed genes in granulocyte RNA from 7 patients with PV and 4 healthy controls. A total of 280 significant expression differences ($P < .05$) were observed (data not shown). The 15 most elevated genes in the microarrays were confirmed by quantitative PCR in the same 7 patients with PV and 4 controls, which constituted the learning

cohort (Figure 1A). These genes encode transcription factors (*ETS2*, *KLF4*, *BAZ1A*), a cytokine (*FGF13*), proteins involved in signaling and apoptosis (*SOCS3*, *FYB*, *SH3GLB1*, *BIRC1*), a glycogen metabolism component (*GYG*), haptoglobin (*HP*) and haptoglobin-related protein (*HRP*), vimentin (*VIM*), the exosome component *EXOSC4*, and genes encoding proteins of unknown function (*C1orf29*, *FLJ22344*).

These results were validated in an independent test cohort consisting of 47 patients with PV and 28 healthy individuals. Thirteen of the 15 markers showed significant differences between controls and PV (Figure 1B). None of the observed changes were specific for PV, because the markers were also altered in some patients with IMF and ET. The marker expression in patients with SE and healthy controls was comparable (Figure 1B). We also examined the expression of *PRV1* and *NF-E2*, 2 markers previously shown to be elevated in MPDs,^{10,11,14,16-18} and *ANKRD15*, a putative tumor suppressor gene located within the minimal 9pLOH region.^{7,19} Consistent with the previous reports,^{10,11,14,16-18} *PRV1* and *NF-E2* exhibited elevated expression in PV, IMF, and ET, whereas *ANKRD15* mRNA was decreased in PV and IMF (Figure 1B).

Because granulocytes from patients with MPDs were shown to be functionally activated,²⁰ we examined the possibility that the

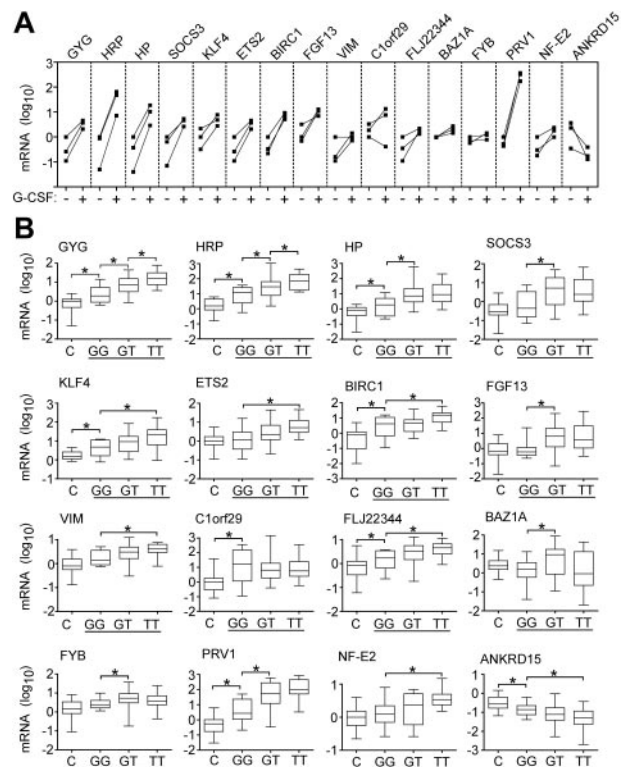


Figure 2. Effects of cytokine stimulation and *JAK2* mutation on marker expression. (A) Expression of markers in granulocytes of 3 healthy donors before and after stem cells mobilization by G-CSF. For each individual, the gene expression is shown before (–) and after (+) G-CSF administration and the corresponding values are connected by solid lines. The mRNA levels of the markers were determined by quantitative PCR. Relative gene expression is shown on a logarithmic scale (\log_{10}) and the values represent the mRNA expression relative to a healthy control calibrator sample, calculated by the $\Delta\Delta C_T$ method. (B) Marker expression in patients with the *JAK2-V617F* mutation. The mRNA level of individual markers was determined in 28 healthy controls (C) and in 54 patients with PV (horizontal line) grouped according to the *JAK2* genotype. Ten patients with wild-type *JAK2* (GG), 21 patients heterozygous for the *JAK2-V617F* mutation (GT), and 23 patients homozygous for the *JAK2-V617F* mutation (TT) were examined. Bars with asterisks indicate statistically significant differences between groups ($P < .05$; Mann-Whitney *U* test).

altered gene expression is caused by cytokine stimulation. Granulocytes from 4 patients with secondary neutrophilia showed elevated expression of all markers examined (Figure 1B), suggesting that the observed gene expression changes could be induced by cytokines. To examine the possibility that the Jak/STAT signaling pathway is involved, we determined the marker expression in granulocytes of healthy stem-cell donors before and after G-CSF administration. *PRV1* was previously shown to increase after G-CSF treatment.¹⁰ We observed increased expression of all markers after G-CSF, whereas *ANKRD15* mRNA was decreased (Figure 2A). The results obtained in neutrophilia and after G-CSF treatment indicate that exogenous cytokine stimulation can cause the same concerted alterations in gene expression as MPD.

Because the *JAK2-V617F* mutation caused intrinsically activated Jak/STAT signaling in hematopoietic cell lines,⁵⁻⁷ the altered gene expression detected in patients with MPDs could be a consequence of the presence of the *JAK2-V617F* mutation. Therefore, we examined whether the expression of the markers correlates with the *JAK2* mutation status in PV (Figure 2B). Six of the new markers and *PRV1* exhibited significantly higher mRNA levels in patients heterozygous for the *JAK2-V617F* mutation compared to patients with PV who had wild-type *JAK2*. In the case of *ETS2*, *KLF4*, *HRP*, *BIRC1*, *FLJ22344*, *VIM*, and *NF-E2*, significant elevation of expression, and in the case of *ANKRD15* significant decrease, were observed only when patients homozygous for *JAK2-V617F* were compared to patients with the wild-type *JAK2*. Although several markers exhibited a gradual alteration of expression dependent on the dosage of the mutated *JAK2* gene, the gene expression differences between patients with PV who were heterozygous and homozygous for *JAK2-V617F* were statistically signifi-

cant only in case of *HRP* and *GYG* (Figure 2B). Patients with PV who did not have mutation in *JAK2* when compared to healthy controls showed significantly altered expression levels for *HP*, *HRP*, *GYG*, *KLF4*, *BIRC1*, *C1orf29*, *FLJ22344*, *PRV1*, and *ANKRD15*. This could be due to the presence of a small percentage of granulocytes with *JAK2-V617F* that contribute to the altered marker expression, which was not detected by sequencing. The presence of minor cell populations with *JAK2-V617F* in patients with PV was reported using allele-specific PCR.⁸ Alternatively, the patients with PV who did not have *JAK2-V617F* may carry a mutation in another component of the same signaling pathway. Interestingly, expression of *SOCS3*, a transcriptional target of STATs,²¹ was not increased in patients without *JAK2-V617F*.

Our results suggest that the alterations in expression of the 13 markers and *ANKRD15* described in this report, as well as the 2 previously described markers *PRV1* and *NF-E2*, are responsive to the activation of the Jak/STAT pathway through exogenous stimuli (secondary neutrophilia or G-CSF treatment), or endogenously through a gain-of-function mutation in *JAK2*. Thus, determining the presence or absence of the *JAK2-V617F* mutation will be the primary diagnostic assay and it remains to be determined how much additional information can be gained by measuring expression of biomarkers in MPDs.

Acknowledgments

We thank Philippe Demougin for assistance with the microarray analysis and Jürg Schwaller for helpful comments on the manuscript.

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2005 106: 3374-3376

doi:10.1182/blood-2005-05-1889 originally published online
August 4, 2005

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