

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
6 May 2010 (06.05.2010)

(10) International Publication Number
WO 2010/051214 A1

- (51) International Patent Classification:
C12Q 1/68 (2006.01) *G01N 33/53* (2006.01)
- (21) International Application Number:
PCT/US2009/061691
- (22) International Filing Date:
22 October 2009 (22.10.2009)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
61/110,501 31 October 2008 (31.10.2008) US
12/503,318 15 July 2009 (15.07.2009) US
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- (81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.
- (84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— with international search report (Art. 21(3))

(54) Title: COMPOSITIONS AND METHODS FOR DETECTING MUTATIONS IN JAK2 NUCLEIC ACID

Series of Representative Sequencing Chromatograms

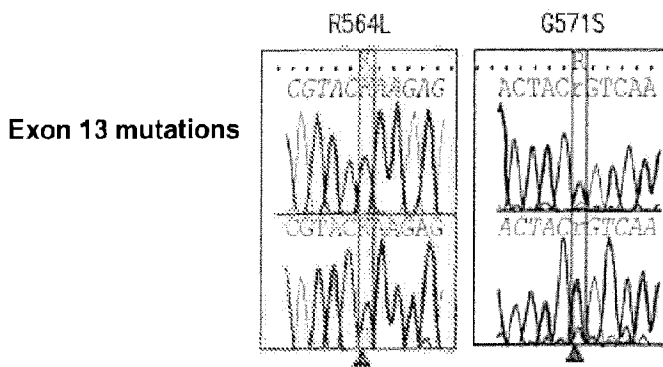


FIG. 1(A)

(57) Abstract: The invention disclosed herein is based on the identification of novel mutations in the JAK2 gene and JAK2 protein. The invention provides compositions and methods useful for diagnosing hematopoietic diseases including, for example, myeloproliferative diseases. The invention also provides compositions and methods useful for determining a prognosis of an individual diagnosed as having a hematopoietic disease.

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COMPOSITIONS AND METHODS FOR DETECTING MUTATIONS IN JAK2 NUCLEIC ACID

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Applications 61/110,501, filed October 31, 2008 and 12/503,318, filed July 15, 2009, each of which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0002] This invention relates to the field of disease detection and more specifically to compositions and diagnostic methods useful for patients having hematopoietic disorders such as a myeloproliferative disease.

BACKGROUND OF THE INVENTION

[0003] The following discussion of the background of the invention is merely provided to aid the reader in understanding the invention and is not admitted to describe or constitute prior art to the invention.

[0004] The Janus kinases are a family of tyrosine kinases that play a role in cytokine signaling. For example, JAK2 kinase acts as an intermediary between membrane-bound cytokine receptors such as the erythropoietin receptor (EpoR), and down-stream members of the signal transduction pathway such as STAT5 (Signal Transducers and Activators of Transcription protein 5). *See, e.g.*, Schindler, C.W., *J. Clin Invest.* 109:1133-1137 (2002); Tefferi and Gilliland, *Mayo Clin. Proc.* 80:947-958 (2005); Giordanetto and Kroemer, *Protein Engineering*, 15(9):727-737 (2002). JAK2 is activated when cytokine receptor/ligand complexes phosphorylate the associated JAK2 kinase. *Id.* JAK2 can then phosphorylate and activate its substrate molecule, for example STAT5, which enters the nucleus and interacts with other regulatory proteins to affect transcription. *Id.*; Nelson, M.E., and Steensma, D.P., *Leuk. Lymphoma* 47:177-194 (2006).

[0005] Certain hematopoietic diseases including non-CML myeloproliferative diseases (MPDs) such as polycythemia vera (PV), essential thrombocythemia (ET), and chronic idiopathic myelofibrosis (IMF) and as of yet unclassified myeloproliferative diseases (MPD-

NC) are characterized by an aberrant increase in blood cells. *See e.g.*, Vainchenker and Constantinescu, *Hematology* (American Society of Hematology), 195-200 (2005). This increase is generally initiated by a spontaneous mutation in a multipotent hematopoietic stem cell located in the bone marrow. *Id.* Due to the mutation, the stem cell produces far more blood cells of a particular lineage than normal, resulting in the overproduction of cells such as erythroid cells, megakaryocytes, granulocytes and monocytes. Some symptoms common to patients with MPD include enlarged spleen, enlarged liver, elevated white, red and/or platelet cell count, blood clots (thrombosis), weakness, dizziness and headache. Diseases such as PV, ET and IMF may presage leukemia, however the rate of transformation (*e.g.*, to blast crisis) differs with each disease. *Id.* It has long been postulated that perturbation of protein tyrosine kinase (PTK) signaling by mutations and other genetic alterations is associated with MPDs. Mutant PTKs such as, for example, Janus kinase 2 (JAK2) gene mutations, can lead to constitutive activity in patients with MPDs.

[0006] The specific gene and concomitant mutation or mutations responsible for many MPDs is not known. However, a mutation in the Janus kinase 2 (JAK2) gene, a cytoplasmic, nonreceptor tyrosine kinase, has been identified in a number of MPDs. The discovery of the JAK2 V617F mutation was a milestone in unveiling the molecular pathogenesis of MPDs. For example, this mutation has been reported in up to 97% of patients with PV, and in greater than 40% of patients with either ET or IMF. *See e.g.*, Baxter *et al.*, *Lancet* 365:1054-1060 (2005); James *et al.*, *Nature* 438:1144-1148 (2005); Zhao, *et al.*, *J. Biol. Chem.* 280(24):22788-22792 (2005); Levine *et al.*, *Cancer Cell*, 7:387-397 (2005); Kralovics, *et al.*, *New Eng. J. Med.* 352(17):1779-1790 (2005); Jones, *et al.*, *Blood* 106:2162-2168 (2005); Steensma, *et al.*, *Blood* 106:2107-2109 (2005).

[0007] A variety of different approaches and a large body of evidence suggest that, when present, the JAK2 V617F mutation contributes to the pathogenesis of MPD. *See e.g.*, Kaushansky, *Hematology* (Am Soc Hematol Educ Program), 533-7 (2005). The mutation has been detected from blood samples, bone marrow and buccal samples (*see, e.g.*, Baxter *et al.*, *Lancet* 365:1054-1060 (2005); James *et al.*, *Nature* 438:1144-1148 (2005); Zhao, *et al.*, *J. Biol. Chem.* 280(24):22788-22792 (2005); Levine *et al.*, *Cancer Cell*, 7:387-397 (2005); Kralovics, *et al.*, *New Eng. J. Med.* 352(17):1779-1790 (2005)), and homozygous and

heterozygous cell populations have been reported in MPD patients. Baxter *et al.*, *Lancet* 365:1054-1060 (2005).

[0008] The JAK2 V617F substitution, which is located in the pseudokinase domain of JAK2, relieves the auto-inhibition of its kinase activity, leading to a constitutively active kinase and augments downstream JAK2-STAT signaling pathways (*see e.g.*, Saharinen *et al.*, *Mol Cell Biol* 20:3387-3395 (2000); Saharinen *et al.*, *Mol. Biol Cell* 14:1448-1459 (2003). Other *JAK2* mutations in humans including translocations, point mutations, deletions, and insertions have been reported. *See e.g.*, Scott *et al.*, *N Engl J Med* 356:459-468 (2007); Li *et al.*, *Blood* 111:3863-3866 (2008).

SUMMARY OF THE INVENTION

[0009] The invention is based on the identification of previously unknown mutations in the JAK2 gene and JAK2 protein. Specifically, the JAK2 gene and protein mutations include the mutations shown in Table 2. The invention further provides compositions and methods useful in the diagnosis and prognosis of hematopoietic diseases including, for example, myeloproliferative diseases.

[0010] In one aspect, the invention provides an isolated nucleic acid of at least 17 nucleotides of SEQ ID NO: 1, in which the fragment has a mutation selected from the mutations shown in Table 2, and the isolated nucleic acid is less than 5000 nucleotides. In one embodiment, the isolated nucleic acid includes at least one additional mutation shown in Table 2. In another embodiment, the isolated nucleic acid is labeled with a detectable label.

[0011] In a second aspect, the invention provides a polypeptide of at least 10 contiguous amino acids of SEQ ID NO: 2 in which the polypeptide has a mutation selected from the mutations shown in Table 2, and the polypeptide is less than 1100 amino acids. In one embodiment, the polypeptide includes at least one additional mutation shown in Table 2. In another embodiment, the fragment is labeled with a detectable label.

[0012] In another aspect, the invention provides a method for diagnosing a hematopoietic disease in an individual comprising: a) providing a sample from said individual, wherein said sample comprises JAK2 nucleic acid, b) evaluating a sample from the individual for the presence or absence of one or more mutations in JAK2 nucleic acid in which one or more

mutations is selected from the group consisting of the mutations of Table 2, and c) identifying the individual as having a hematopoietic disease when the JAK2 nucleic acid comprises at least one of the mutations.

[0013] In another aspect, the invention provides a method of determining a prognosis of an individual diagnosed with a hematopoietic disease, the method comprising: (a) determining the presence or absence of one or more mutations in a JAK2 nucleic acid sample in which one or more mutations is selected from the group consisting of the mutations of Table 2; and (b) identifying the individual as having poor prognosis when one or more mutations are present in the JAK2 nucleic acid sample.

[0014] In another aspect, the invention provides a method for selecting therapy for an individual with a hematopoietic disorder comprising evaluating a sample containing nucleic acids from the individual for the presence or absence of one or more mutations in JAK2 nucleic acid in which one or more mutations is selected from the group consisting of the mutations shown in Table 2 and selecting the therapy based on mutations in JAK2 nucleic acid.

[0015] In some embodiments of any of the above aspects of the invention, the JAK2 nucleic acid is RNA. In other embodiments of any of the above aspects of the invention, the presence or absence of one or more mutations may be determined relative to SEQ ID NO: 1. In certain embodiments of any of the above aspects of the invention, the JAK2 nucleic acid includes two or more of the mutations shown in Table 2.

[0016] In still other embodiments of any of the above aspects of the invention, evaluating or determining the presence or absence of one or more mutations in a JAK2 nucleic acid sample includes amplifying JAK2 nucleic acid and hybridizing the amplified JAK2 nucleic acid with a detection oligonucleotide that is capable of specifically detecting a JAK2 nucleic acid mutant sequence under hybridization conditions. In other embodiments of any of the above aspects of the invention, evaluating or determining the presence or absence of one or more mutations in a JAK2 nucleic acid sample includes amplifying JAK2 nucleic acid and performing direct sequencing analysis of the amplified nucleic acid.

[0017] In another aspect, the invention provides a method for diagnosing a hematopoietic disease in an individual comprising: a) evaluating a sample containing polypeptides from the

individual for the presence or absence of one or more mutations in JAK2 polypeptide in which one or more mutations is selected from the group consisting of the mutations of Table 2, and b) identifying the individual as having a hematopoietic disease when the JAK2 polypeptide comprises at least one of the mutations.

[0018] In another aspect, the invention provides a method of determining a prognosis of an individual diagnosed with a hematopoietic disease, the method comprising: (a) determining the presence or absence of one or more mutations in a JAK2 polypeptide sample in which one or more mutations is selected from the group consisting of the mutations of Table 2; and (b) identifying the individual as having poor prognosis when one or more mutations are present in the JAK2 polypeptide.

[0019] In one aspect, the invention provides a method for selecting therapy for an individual with a hematopoietic disorder comprising evaluating a sample containing polypeptides from the individual for the presence or absence of one or more mutations in JAK2 polypeptide in which one or more mutations is selected from the group consisting of the mutations shown in Table 2 and selecting the therapy based on mutations in JAK2 polypeptide.

[0020] In some embodiments of the above aspects of the invention, the presence or absence of one or more mutations may be determined relative to SEQ ID NO: 2. In certain embodiments of the above aspects, the JAK2 polypeptide includes 2 or more of the mutations shown in Table 2. In certain embodiments of the above aspects, evaluating a sample or determining the presence or absence of one or more mutations in a JAK2 polypeptide sample includes using an antibody that specifically binds to the mutated JAK2 polypeptide.

[0021] In some embodiments of any of the above aspects of the invention, the JAK2 nucleic acid and/or polypeptide sample is from a biological fluid from the patient, preferably the sample is blood, serum, or plasma.

[0022] In certain embodiments of any of the above aspects of the invention, the disease is a myeloproliferative disease; more preferably, the myeloproliferative disease is polycythemia vera, essential thrombocythemia, idiopathic myelofibrosis, or an unclassified myeloproliferative disease.

[0023] The term “neoplastic disease” refers to a condition characterized by an abnormal growth of new cells such as a tumor. A neoplasm includes solid and non-solid tumor types such as a carcinoma, sarcoma, leukemia and the like. A neoplastic disease may be malignant or benign.

[0024] The term “myeloproliferative disease (MPD)” or “myeloproliferative disorder” is meant to include non-lymphoid dysplastic or neoplastic conditions arising from a hematopoietic stem cell or its progeny. “MPD patient” includes a patient who has been diagnosed with an MPD. “Myeloproliferative disease” is meant to encompass the specific, classified types of myeloproliferative diseases including polycythemia vera (PV), essential thrombocythemia (ET) and idiopathic myelofibrosis (IMF). Also included in the definition are hypereosinophilic syndrome (HES), chronic neutrophilic leukemia (CNL), myelofibrosis with myeloid metaplasia (MMM), chronic myelomonocytic leukemia (CMML), juvenile myelomonocytic leukemia, chronic basophilic leukemia, chronic eosinophilic leukemia, and systemic mastocytosis (SM). “Myeloproliferative disease” is also meant to encompass any unclassified myeloproliferative diseases (UMPD or MPD-NC).

[0025] As used herein the terms “diagnose” or “diagnosis” or “diagnosing” refer to distinguishing or identifying a disease, syndrome or condition or distinguishing or identifying a person having a particular disease, syndrome or condition.

[0026] “Determining a prognosis” as used herein refers to the process in which the course or outcome of a condition in a patient is predicted. The term “prognosis” does not refer to the ability to predict the course or outcome of a condition with 100% accuracy. Instead, the term refers to identifying an increased or decreased probability that a certain course or outcome will occur in a patient exhibiting a given condition/marker, when compared to those individuals not exhibiting the condition. The nature of the prognosis is dependent upon the specific disease and the condition/marker being assessed. For example, a prognosis may be expressed as the amount of time a patient can be expected to survive, the likelihood that the disease goes into remission, or to the amount of time the disease can be expected to remain in remission.

[0027] As used herein, the term “treatment,” “treating,” or “treat” refers to care by procedures or application that are intended to relieve illness or injury. Although it is

preferred that treating a condition or disease such as a myeloproliferative disease will result in an improvement of the condition, the term treating as used herein does not indicate, imply, or require that the procedures or applications are at all successful in ameliorating symptoms associated with any particular condition. Treating a patient may result in adverse side effects or even a worsening of the condition which the treatment was intended to improve.

[0028] By “subject” is meant a human or any other animal which contains a JAK2 gene that can be amplified using the primers and methods described herein. A subject can be a patient, which refers to a human presenting to a medical provider for diagnosis or treatment of a disease. A human includes pre and post natal forms.

[0029] As used herein, the term “patient” refers to one who receives medical care, attention or treatment. As used herein, the term is meant to encompass a person diagnosed with a disease such as myeloproliferative disease as well as a person who may be symptomatic for a disease but who has not yet been diagnosed.

[0030] The term “sample” or “patient sample” is meant to include biological samples such as tissues and bodily fluids. “Bodily fluids” may include, but are not limited to, blood, serum, plasma, saliva, cerebral spinal fluid, pleural fluid, tears, lactal duct fluid, lymph, sputum, urine, amniotic fluid, and semen. A sample may include a bodily fluid that is “acellular.” An “acellular bodily fluid” includes less than about 1% (w/w) whole cellular material. Plasma or serum are examples of acellular bodily fluids. A sample may include a specimen of natural or synthetic origin.

[0031] The term “nucleic acid” or “nucleic acid sequence” refers to an oligonucleotide, nucleotide or polynucleotide, and fragments or portions thereof, which may be single or double stranded, and represent the sense or antisense strand. A nucleic acid may include DNA or RNA, and may be of natural or synthetic origin. For example, a nucleic acid may include mRNA, genomic DNA or cDNA. Nucleic acid may include nucleic acid that has been amplified (*e.g.*, using polymerase chain reaction). The convention “NTwt###NTmut” is used to indicate a mutation that results in the wild-type nucleotide NTwt at position ### in the nucleic acid being replaced with mutant NTmut.

[0032] For the JAK2 nucleic acid sequence, a “mutation” means a JAK2 nucleic acid sequence that includes at least one nucleic acid variation as compared to reference sequence

GenBank accession number NM_004972 (SEQ ID NO: 1). A mutation in JAK2 nucleic acid may result in a change in the encoded polypeptide sequence or the mutation may be silent with respect to the encoded polypeptide sequence. A change in an amino acid sequence may be determined as compared to SEQ ID NO: 2, as a reference amino acid sequence.

[0033] The term “zygosity status” as used herein refers to a sample, a cell population, or an organism as appearing heterozygous, homozygous, or hemizygous as determined by testing methods known in the art and described herein. The term “zygosity status of a nucleic acid” means determining whether the source of nucleic acid appears heterozygous, homozygous, or hemizygous. The “zygosity status” may refer to differences in a single nucleotide in a sequence. In some methods, the zygosity status of a sample with respect to a single mutation may be categorized as homozygous wild-type, heterozygous (*i.e.*, one wild-type allele and one mutant allele), homozygous mutant, or hemizygous (*i.e.*, a single copy of either the wild-type or mutant allele). Because direct sequencing of plasma or cell samples as routinely performed in clinical laboratories does not reliably distinguish between hemizygosity and homozygosity, in some embodiments, these classes are grouped. For example, samples in which no or a minimal amount of wild-type nucleic acid is detected are termed “hemizygous/homozygous mutant.” In some embodiments, a “minimal amount” may be between about 1-2%. In other embodiments, a minimal amount may be between about 1-3%. In still other embodiments, a “minimal amount” may be less than 1%.

[0034] The term “substantially all” as used herein means at least about 60%, about 70%, about 80%, about 90%, about 95%, about 99%, or 100%.

[0035] “Substantially pure” as used herein in the context of nucleic acid represents at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or at least 99% of the nucleic acid in a sample. The nucleic acid sample may exist in solution or as a dry preparation.

[0036] By “isolated”, when referring to a nucleic acid (e.g., an oligonucleotide such as RNA, DNA, or a mixed polymer) is meant a nucleic acid that is apart from a substantial portion of the genome in which it naturally occurs and/or is substantially separated from other cellular components which naturally accompany such nucleic acid. For example, any nucleic acid that has been produced synthetically (e.g., by serial base condensation) is considered to

be isolated. Likewise, nucleic acids that are recombinantly expressed, cloned, produced by a primer extension reaction (c.g., PCR), or otherwise excised from a genome are also considered to be isolated.

[0037] As used herein, a "fragment" means a polynucleotide that is at least about 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 200, 300, 400, 500, 1000 nucleotides or more in length.

[0038] "Specific hybridization" is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after any subsequent washing steps. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may occur, for example, at 65°C in the presence of about 6×SSC. Stringency of hybridization may be expressed, in part, with reference to the temperature under which the wash steps are carried out. Such temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Equations for calculating T_m and conditions for nucleic acid hybridization are known in the art.

[0039] By "substantially complementary" is meant that two sequences that will specifically hybridize. The skilled artisan will understand that substantially complementary sequences need not hybridize along their entire length.

[0040] Oligonucleotides used as primers or probes for specifically amplifying (*i.e.*, amplifying a particular target nucleic acid sequence) or specifically detecting (*i.e.*, detecting a particular target nucleic acid sequence) a target nucleic acid generally are capable of specifically hybridizing to the target nucleic acid.

[0041] The term "oligonucleotide" is understood to be a molecule that has a sequence of bases on a backbone comprised mainly of identical monomer units at defined intervals. The bases are arranged on the backbone in such a way that they can enter into a bond with a nucleic acid having a sequence of bases that are complementary to the bases of the oligonucleotide. The most common oligonucleotides have a backbone of sugar phosphate units. A distinction may be made between oligodeoxyribonucleotides that do not have a hydroxyl group at the 2' position and oligoribonucleotides that have a hydroxyl group in this

position. Oligonucleotides also may include derivatives, in which the hydrogen of the hydroxyl group is replaced with organic groups, *e.g.*, an allyl group. Oligonucleotides of the method which function as primers or probes are generally at least about 10-15 nucleotides long and more preferably at least about 15 to 25 nucleotides long, although shorter or longer oligonucleotides may be used in the method. The exact size will depend on many factors, which in turn depend on the ultimate function or use of the oligonucleotide. The oligonucleotide may be generated in any manner, including, for example, chemical synthesis, DNA replication, reverse transcription, PCR, or a combination thereof. The oligonucleotide may be modified. For example, the oligonucleotide may be labeled with an agent that produces a detectable signal (*e.g.*, a fluorophore).

[0042] The term “detectable label” as used herein refers to a molecule or a compound or a group of molecules or a group of compounds associated with a nucleic acid or a polypeptide and is used to identify the nucleic acid or the polypeptide. In some cases, the detectable label may be detected directly. In other cases, the detectable label may be a part of a binding pair, which can then be subsequently detected. Signals from the detectable label may be detected by various means and will depend on the nature of the detectable label. Detectable labels may be isotopes, fluorescent moieties, colored substances, and the like. Examples of means to detect detectable label include but are not limited to spectroscopic, photochemical, biochemical, immunochemical, electromagnetic, radiochemical, or chemical means, such as fluorescence, chemifluorescence, or chemiluminescence, or any other appropriate means.

[0043] By “antibody that specifically binds to the mutated JAK2 polypeptide” is meant that the antibody preferentially binds to mutated JAK2 polypeptide and not to the wild type JAK2 polypeptide. Preferential binding of the antibody is meant to include at least 90% of the times the antibody will bind to mutated JAK2 polypeptide and discriminate between mutated and wild type JAK2 polypeptides.

[0044] As used herein, the term “activation domain” in reference to JAK2 refers generally to a domain involved in cell activation such as, for example, cell proliferation. An example of an activation domain is a kinase or pseudokinase domain.

[0045] As used herein, the term “pseudokinase domain” refers to a portion of a polypeptide or nucleic acid that encodes a portion of the polypeptide, where the portion shows homology

to a functional kinase but possesses no catalytic activity. A pseudokinase domain may also be referred to as a “kinase-like domain.” An example of a pseudokinase domain is the JAK2 pseudokinase domain, also termed the JH2 domain. The N-terminal part of JAK2 pseudokinase domain (JH2) is a regulatory domain that negatively regulates the activity of JAK2.

[0046] The term “kinase domain” refers to a portion of a polypeptide or nucleic acid that encodes a portion of the polypeptide, where the portion is required for kinase activity of the polypeptide (*e.g.*, tyrosine kinase activity).

[0047] In some methods of the invention, mutations may “affect JAK2 kinase activity.” The affected JAK2 kinase activity may include kinase activity that increases, decreases, becomes constitutive, stops completely or affects greater, fewer or different targets. A mutation that affects kinase activity may be present in a kinase domain or in a domain associated with a kinase domain such as the JAK2 pseudokinase domain.

[0048] As used herein, the term “including” has the same meaning as the term comprising.

BRIEF DESCRIPTION OF THE FIGURES

[0049] FIG. 1 is a series of representative sequencing chromatograms of Exon 13 mutations (FIG. 1A), Exon 14 deletion (FIG. 1B), and Exon 15 mutation (FIG. 1C). Arrows indicate positions of mutant nucleotides and dots indicate deleted nucleotides.

[0050] FIG. 2 is a schematic diagram of the JAK2 gene structure with some of the mutated residues in exons 12-15 shown.

DETAILED DESCRIPTION OF THE INVENTION

[0051] The present invention is based on the discovery of previously unknown mutations in the JAK2 nucleic acid and protein which have been associated with myeloproliferative diseases. The mutations are shown in Table 2.

[0052] JAK2 nucleic acid

[0053] JAK2 genomic nucleic acid is located in human chromosome 9. Exemplary sequences of human JAK2 genomic sequences include but are not limited to GenBank

Accession numbers: NG_009904, CM000260, CM000671, GL000069. These sequences are incorporated herein by reference.

[0054] Exemplary sequences of all or portions of human JAK2 mRNA include but are not limited to GenBank Accession numbers: NM_004972, human JAK2 mRNA. These sequences are incorporated herein by reference. Exemplary sequence of JAK2 mRNA is provided in SEQ ID NO: 1.

[0055] The JAK2 nucleic acids of this invention include, for example, nucleic acids that are substantially identical to a portion of the JAK2 nucleotide sequence of SEQ ID NO: 1 and further comprise one or more of the following mutations listed in Table 2. In some embodiments, the JAK2 nucleic acids have at least 10, 12, 14, 16, 18, 20, 25, 30, 40, 50, 75, 100, or more nucleotides in length. In some other embodiments, the JAK2 nucleic acids are less than 6000, 5000, 4000, 3000, 2000, 1000, 750, 500, 400, 300, or 200 nucleotides in length.

[0056] **Biological Sample Collection and Preparation**

[0057] The methods and compositions of this invention may be used to detect mutations in the JAK2 gene and/or JAK2 protein using a biological sample obtained from an individual. The nucleic acid (DNA or RNA) may be isolated from the sample according to any methods well known to those of skill in the art. If necessary the sample may be collected or concentrated by centrifugation and the like. The cells of the sample may be subjected to lysis, such as by treatments with enzymes, heat, surfactants, ultrasonication, or a combination thereof. The lysis treatment is performed in order to obtain a sufficient amount of nucleic acid derived from the individual's cells to detect using polymerase chain reaction.

Alternatively, mutations in the JAK2 gene may be detected using an acellular bodily fluid according to the methods described in U.S. Patent Application 11/408,241 (Publication No. US 2007-0248961), hereby incorporated by reference.

Plasma or Serum Preparation Methods

[0058] Methods of plasma and serum preparation are well known in the art. Either "fresh" blood plasma or serum, or frozen (stored) and subsequently thawed plasma or serum may be used. Frozen (stored) plasma or serum should optimally be maintained at storage conditions of -20 to -70 degrees centigrade until thawed and used. "Fresh" plasma or serum should be

refrigerated or maintained on ice until used, with nucleic acid (e.g., RNA, DNA or total nucleic acid) extraction being performed as soon as possible. Exemplary methods are described below.

[0059] Nucleic Acid Extraction and Amplification

[0060] The nucleic acid to be amplified may be from a biological sample such as an organism, cell culture, tissue sample, and the like. The biological sample can be from a subject which includes any animal, preferably a mammal. A preferred subject is a human, which may be a patient presenting to a medical provider for diagnosis or treatment of a disease. The biological sample may be obtained from a stage of life such as a fetus, young adult, adult, and the like. Particularly preferred subjects are humans being tested for the existence of a JAK2 mutation.

[0061] Various methods of extraction are suitable for isolating the DNA or RNA. Suitable methods include phenol and chloroform extraction. See Maniatis et al., *Molecular Cloning, A Laboratory Manual*, 2d, Cold Spring Harbor Laboratory Press, page 16.54 (1989). Numerous commercial kits also yield suitable DNA and RNA including, but not limited to, QIAamp™ mini blood kit, Agencourt Genfind™, Roche Cobas® Roche MagNA Pure® or phenol:chloroform extraction using Eppendorf Phase Lock Gels®, and the NucliSens extraction kit (Biomérieux, Marcy l'Etoile, France). In other methods, mRNA may be extracted from patient blood/bone marrow samples using MagNA Pure LC mRNA HS kit and Mag NA Pure LC Instrument (Roche Diagnostics Corporation, Roche Applied Science, Indianapolis, IN).

[0062] Numerous methods are known in the art for isolating total nucleic acid, DNA and RNA from blood, serum, plasma and bone marrow or other hematopoietic tissues. In fact, numerous published protocols, as well as commercial kits and systems are available. By way of example but not by way of limitation, examples of such kits, systems and published protocols are described below. Commercially available kits include Qiagen products such as the QiaAmp DNA Blood MiniKit (Cat.# 51104, Qiagen, Valencia, CA), the QiaAmp RNA Blood MiniKit (Cat.# 52304, Qiagen, Valencia, CA); Promega products such as the Wizard Genomic DNA Kit (Cat.# A1620, Promega Corp. Madison, WI), Wizard SV Genomic DNA Kit (Cat.# A2360, Promega Corp. Madison, WI), the SV Total RNA Kit (Cat.# X3100,

Promega Corp. Madison, WI), PolyATract System (Cat.# Z5420, Promega Corp. Madison, WI), or the PurYield RNA System (Cat.# Z3740, Promega Corp. Madison, WI).

Extraction of RNA from Plasma or Serum

[0063] Plasma RNA is highly sensitive and may replace DNA-based testing because of the relative abundance of the RNA and the ease in detecting deletions such as, for example, deletion of Exon 14. Circulating extracellular deoxyribonucleic acid (DNA), including tumor-derived or associated extracellular DNA, is also present in plasma and serum. *See* Stroun, M., *et al.*, *Oncology* 46:318-322, (1989). Since this DNA will additionally be extracted to varying degrees during the RNA extraction methods described above, it may be desirable or necessary (depending upon clinical objectives) to further purify the RNA extract and remove trace DNA prior to proceeding to further RNA analysis. This may be accomplished using DNase, for example by the method as described by Rashtchian, A., *PCR Methods Applic.* 4:S83-S91, (1994), as follows.

[0064] Glass beads, Silica particles or Diatom Extraction: RNA may be extracted from plasma or serum using silica particles, glass beads, or diatoms, as in the method or adaptations of Boom, R., *et al.*, *J. Clin. Micro.* 28:495-503, (1990); Cheung, R. C., *et al.*, *J. Clin Micro.* 32:2593-2597, (1994).

[0065] Acid Guanidinium Thiocyanate-Phenol-Chloroform Extraction: As an alternative method, RNA may be extracted from plasma or serum using the Acid Guanidinium Thiocyanate-Phenol-chloroform extraction method described by Chomczynski, P. and Sacchi, N., *Analytical Biochemistry* 162:156-159, (1987), as follows.

[0066] Alternative Nucleic Acid Extraction Methods: Alternative methods may be used to extract RNA from body fluids including but not limited to centrifugation through a cesium chloride gradient, including the method as described by Chirgwin, J. M., *et al.*, *Biochemistry* 18:5294-5299, (1979), and co-precipitation of extracellular RNA from plasma or serum with gelatin, such as by adaptations of the method of Fournie, G. J., *et al.*, *Analytical Biochemistry* 158:250-256, (1986), to RNA extraction.

Alternative Nucleic Acid Amplification Methods

[0067] Alternative methods of nucleic acid amplification which may be used include variations of RT-PCR, including quantitative RT-PCR, for example as adapted to the method described by Wang, A. M. et al., Proc. Natl. Acad. Sci. USA 86:9717-9721, (1989), or by Karet, F. E., et al., Analytical Biochemistry 220:384-390, (1994). Another method of nucleic acid amplification or mutation detection which may be used is ligase chain reaction (LCR), as described by Wiedmann, et al., PCR Methods Appl. 3:551-564, (1994). An alternative method of amplification or mutation detection is allele specific PCR (ASPCR). ASPCR which utilizes matching or mismatching between the template and the 3' end base of a primer well known in the art. See e.g., U.S. Patent 5,639,611.

[0068] Another method of mutation detection is nucleic acid sequencing. Sequencing can be performed using any number of methods, kits or systems known in the art. One example is using dye terminator chemistry and an ABI sequencer (Applied Biosystems, Foster City, CA). Sequencing also may involve single base determination methods such as single nucleotide primer extension ("SNaPshot®" sequencing method) or allele or mutation specific PCR. The SNaPshot® Multiplex System is a primer extension-based method that enables multiplexing up to 10 SNPs (single nucleotide polymorphisms). The chemistry is based on the dideoxy single-base extension of an unlabeled oligonucleotide primer (or primers). Each primer binds to a complementary template in the presence of fluorescently labeled ddNTPs and AmpliTaq® DNA Polymerase, FS. The polymerase extends the primer by one nucleotide, adding a single ddNTP to its 3' end. SNaPshot® Multiplex System is commercially available (ABI PRISM® SNaPshot® Multiplex kit, Applied Biosystems Foster City, CA). Products generated using the ABI PRISM® SNaPshot® Multiplex kit can be analyzed with GeneScan® Analysis Software version 3.1 or higher using ABI PRISM®310 Genetic Analyzer, ABI PRISM® 3100 Genetic Analyzer or ABI PRISM® 3700 DNA Analyzer.

[0069] Exemplary Methods for Detection of JAK2 DNA and RNA Mutations

[0070] Nucleic acid (e.g., total nucleic acid) may be extracted from patient's biological sample using any appropriate method. Next, an RT-PCR reaction may be performed using either the total nucleic acid preparation or the RNA preparation to specifically amplify a portion of the patient RNA. An exemplary one-step RT-PCR system is the Superscript III

System (Invitrogen, Carlsbad, CA). Other methods and systems for RT-PCR reactions are well known in the art and are commercially available. By way of example, but not by way of limitation, a primer pair for JAK2 may be 5'-TGT AAA ACG ACG GCC AGT CTA AAT GCT GTC CCC CAA AG-3' (forward primer, SEQ ID NO: 6) and 5'-CAG GAA ACA GCT ATG ACC CCA TGC CAA CTG TTT AGC AA-3' (reverse primer, SEQ ID NO: 7). The RT-PCR product may then be purified, for example by gel purification, and the resulting purified product may be sequenced. Nucleic acid sequencing methods are known in the art; an exemplary sequencing method includes the ABI Prism BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Foster City, CA). The sequencing data may then be analyzed for the presence or absence of one or more mutations in JAK2 nucleic acid. The sequencing data may also be analyzed to determine the proportion of wild-type to mutant nucleic acid present in the sample.

[0071] The presence or absence of JAK2 mutations can be determined in a nucleic acid by sequencing appropriate portions of the JAK2 gene containing the mutations sought to be detected. For example, each amplicon of the JAK2 gene is sequenced with forward and reverse primers. In another approach, JAK2 mutations that change susceptibility to digestion by one or more endonuclease restriction enzymes may be used to detect the mutations. In another embodiment, the presence of one or more JAK2 mutations can be determined by allele specific amplification. In yet another embodiment, the presence of one or more JAK2 mutations can be determined by primer extension. In yet a further embodiment, the presence of one or more JAK2 mutations can be determined by oligonucleotide ligation. In another embodiment, the presence of one or more JAK2 mutations can be determined by hybridization with a detectably labeled probe containing the mutant JAK2 sequence. The presence or absence of JAK2 mutations can be determined by any known or future method.

[0072] **Detection of Mutated JAK2 Proteins**

[0073] According to the invention, the presence or absence of JAK2 mutations can also be determined by analyzing the JAK2 protein (SEQ ID NO: 2) encoded by the mutated JAK2 gene. The mutations include those shown in Table 2. Detection of JAK2 mutations at the protein level can be detected by any method well known in the field. In one embodiment, detection of JAK2 mutations is carried out by isolating JAK2 protein and subjecting it to amino acid sequence determination. This may require fragmenting the protein by proteolytic

or chemical means prior to sequencing. Methods of determining an amino acid sequence are well known in the art.

[0074] Detection of mutated JAK2 proteins can be accomplished using, for example, antibodies, aptamers, ligands/substrates, other proteins or protein fragments, other protein-binding agents, or mass spectrometry analysis of fragments. Preferably, protein detection agents are specific for the mutated JAK2 protein of the present invention and can therefore discriminate between a mutated protein and the wild-type protein or another variant form. This can generally be accomplished by, for example, selecting or designing detection agents that bind to the region of a protein that differs between the variant and wild-type protein.

[0075] One preferred agent for detecting a mutated JAK2 protein is an antibody capable of selectively binding to a variant form of the protein. Antibodies capable of distinguishing between wild-type and mutated JAK2 protein may be created by any suitable method known in the art. The antibodies may be monoclonal or polyclonal antibodies, single chain or double chain, chimeric or humanized antibodies or portions of immunoglobulin molecules containing the portions known in the state of the art to correspond to the antigen binding fragments.

[0076] Methods for manufacturing polyclonal antibodies are well known in the art. Typically, antibodies are created by administering (e.g., via subcutaneous injection) the mutated JAK2 protein immunogenic fragment containing the mutation to white New Zealand rabbits. The JAK2 antigen is typically injected at multiple sites and the injections are repeated multiple times (e.g., approximately bi-weekly) to induce an immune response. Desirably, the rabbits are simultaneously administered an adjuvant to enhance anti-JAK2 immunity. The polyclonal antibodies are then purified from a serum sample, for example, by affinity chromatography using the same JAK2 antigen to capture the antibodies. The antibodies can be made specific to the mutation by removing antibodies cross-reacting with native JAK2.

[0077] In vitro methods for detection of the mutated JAK2 proteins also include, for example, enzyme linked immunosorbent assays (ELISAs), radioimmunoassays (RIA), Western blots, immunoprecipitations, immunofluorescence, and protein arrays/chips (e.g., arrays of antibodies or aptamers). For further information regarding immunoassays and related protein detection methods, see Current Protocols in Immunology, John Wiley & Sons,

N.Y., and Hage, "Immunoassays", *Anal Chem.* 1999 Jun. 15; 71(12):294R-304R. Additional analytic methods of detecting amino acid variants include, but are not limited to, altered electrophoretic mobility (e.g., 2-dimensional electrophoresis), altered tryptic peptide digest, altered JAK2 kinase activity in cell-based or cell-free assay, alteration in ligand or antibody-binding pattern, altered isoelectric point, and direct amino acid sequencing.

[0078] Diagnostic Tools

[0079] JAK2 nucleic acid may be used as tools to diagnose an individual as having (or as likely to develop) a myeloproliferative disease. Alternatively, the JAK2 mutation status, used alone or in combination with other clinical parameters, also may be used to determine a prognosis for a patient diagnosed as having a myeloproliferative disease. Exemplary mutations in JAK2 nucleic acid is listed in Tables 1 and 2.

[0080] In some embodiments, the JAK2 nucleic acids further comprise a detectable label and are used as a probe ("JAK2 probe") to detect mutated JAK2 nucleic acids in a patient sample. The JAK2 probe may be detectably labeled by methods known in the art. Useful labels include, for example, fluorescent dyes (e.g., Cy5®, Cy3®, FITC, rhodamine, lanthamide phosphors, Texas red, FAM, JOE, Cal Fluor Red 610®, Quasar 670®), radioisotopes (e.g., ³²P, ³⁵S, ³H, ¹⁴C, ¹²⁵I, ¹³¹I), electron-dense reagents (e.g., gold), enzymes (e.g., horseradish peroxidase, beta-galactosidase, luciferase, alkaline phosphatase), colorimetric labels (e.g., colloidal gold), magnetic labels (e.g., Dynabeads™), biotin, dioxigenin, or haptens and proteins for which antisera or monoclonal antibodies are available. Other labels include ligands or oligonucleotides capable of forming a complex with the corresponding receptor or oligonucleotide complement, respectively. The label can be directly incorporated into the nucleic acid to be detected, or it can be attached to a probe (e.g., an oligonucleotide) or antibody that hybridizes or binds to the nucleic acid to be detected.

[0081] In other embodiments, the JAK2 probes are TaqMan® probes, molecular beacons, and Scorpions (e.g., Scorpion™ probes). These types of probes are based on the principle of fluorescence quenching and involve a donor fluorophore and a quenching moiety. The term "fluorophore" as used herein refers to a molecule that absorbs light at a particular wavelength (excitation frequency) and subsequently emits light of a longer wavelength (emission frequency). The term "donor fluorophore" as used herein means a fluorophore that, when in close proximity to a quencher moiety, donates or transfers emission energy to the quencher.

As a result of donating energy to the quencher moiety, the donor fluorophore will itself emit less light at a particular emission frequency that it would have in the absence of a closely positioned quencher moiety.

[0082] The term “quencher moiety” as used herein means a molecule that, in close proximity to a donor fluorophore, takes up emission energy generated by the donor and either dissipates the energy as heat or emits light of a longer wavelength than the emission wavelength of the donor. In the latter case, the quencher is considered to be an acceptor fluorophore. The quenching moiety can act via proximal (i.e., collisional) quenching or by Förster or fluorescence resonance energy transfer (“FRET”). Quenching by FRET is generally used in TaqMan® probes while proximal quenching is used in molecular beacon and Scorpion™ type probes. Suitable quenchers are selected based on the fluorescence spectrum of the particular fluorophore. Useful quenchers include, for example, the Black Hole™ quenchers BHQ-1, BHQ-2, and BHQ-3 (Biosearch Technologies, Inc.), and the ATTO-series of quenchers (ATTO 540Q, ATTO 580Q, and ATTO 612Q; Atto-Tec GmbH).

[0083] With Scorpion primers, sequence-specific priming and PCR product detection is achieved using a single molecule. The Scorpion primer maintains a stem-loop configuration in the unhybridized state. The fluorophore is attached to the 5' end and is quenched by a moiety coupled to the 3' end, although in suitable embodiments, this arrangement may be switched. The 3' portion of the stem also contains sequence that is complementary to the extension product of the primer. This sequence is linked to the 5' end of a specific primer via a non-amplifiable monomer. After extension of the primer moiety, the specific probe sequence is able to bind to its complement within the extended amplicon thus opening up the hairpin loop. This prevents the fluorescence from being quenched and a signal is observed. A specific target is amplified by the reverse primer and the primer portion of the Scorpion primer, resulting in an extension product. A fluorescent signal is generated due to the separation of the fluorophore from the quencher resulting from the binding of the probe element (e.g., the JAK2 probe) of the Scorpion primer to the extension product.

[0084] TaqMan® probes (Heid, et al., Genome Res 6: 986-994, 1996) use the fluorogenic 5' exonuclease activity of Taq polymerase to measure the amount of target sequences in cDNA samples. TaqMan® probes are oligonucleotides that contain a donor fluorophore usually at or near the 5' base, and a quenching moiety typically at or near the 3' base. The quencher moiety may be a dye such as TAMRA or may be a non-fluorescent molecule such

as 4-(4 -dimethylaminophenylazo) benzoic acid (DABCYL). See Tyagi, et al., 16 Nature Biotechnology 49-53 (1998). When irradiated, the excited fluorescent donor transfers energy to the nearby quenching moiety by FRET rather than fluorescing. Thus, the close proximity of the donor and quencher prevents emission of donor fluorescence while the probe is intact.

[0085] TaqMan® probes are designed to anneal to an internal region of a PCR product. When the polymerase (e.g., reverse transcriptase) replicates a template on which a TaqMan® probe is bound, its 5' exonuclease activity cleaves the probe. This ends the activity of the quencher (no FRET) and the donor fluorophore starts to emit fluorescence which increases in each cycle proportional to the rate of probe cleavage. Accumulation of PCR product is detected by monitoring the increase in fluorescence of the reporter dye (note that primers are not labeled). If the quencher is an acceptor fluorophore, then accumulation of PCR product can be detected by monitoring the decrease in fluorescence of the acceptor fluorophore.

[0086] The JAK2 polypeptides of this invention include, for example, polypeptides that are substantially identical to a portion of the JAK2 amino acid sequence of SEQ ID NO: 2 and further comprise one or more of the following mutations listed in Table 2. These polypeptides may be used as tools to diagnose an individual as having (or as likely to develop) a myeloproliferative disease. Alternatively, the JAK2 mutation status, used alone or in combination with other clinical parameters, also may be used to determine a prognosis for a patient diagnosed as having a myeloproliferative disease. In some embodiments, the JAK2 polypeptides have at least 10, 12, 14, 16, 18, 20, 25, 30, 40, 50, 75, 100, or more amino acids. In some embodiments, the JAK2 polypeptide is less than 1100, 1000, 900, 800, 700, 600, 500, or 400 amino acids.

[0087] Kits For Detecting JAK2 Mutations

[0088] The invention also provides kits for detecting JAK2 mutations. The kits will contain at least a primer pair capable of amplifying a target JAK2 nucleic acid sequence of SEQ ID NO: 1 and a means for detecting a JAK2 mutation in the target. Preferably, the amplification using the primer pair of the kit results in a reaction product having at least 20, 40, 60, 80, 100, 125, 150, 200, 300, 500, or more nucleotides. Suitable primer pairs include, for example, primers having the sequence of SEQ ID NOs: 6 and 7. Suitable means for detecting a JAK2 mutation in the reaction product make use of a detectably labeled JAK2 probe, such as those described herein.

[0089] Diagnosis, Detection, and Prognosis

[0090] The presence of the JAK2 mutations, such as, for example, the mutations listed in Table 2 alone, in combination with each other, or in combination with other JAK2 mutations can be as an indicator of disease.

[0091] Without wishing to be bound by any theory, it is believed that the JAK2 mutations allow the activation loop of the kinase domain to move away from the pseudokinase domain, thus leading to constitutive activation of the JAK2-STAT pathway. Mutations in the pseudokinase domain are expected to inactivate the auto-inhibitory function of the pseudokinase domain on the kinase activity. A considerable portion of activating mutations in tyrosine kinases associated with human cancer are loss-of-function alleles residing in the auto-inhibitory domains, for example, point mutations and deletions that result in constitutive tyrosine kinase activation. Therefore, testing for JAK2 mutations should include most of the pseudokinase domain.

[0092] Without wishing to be bound by any theory, it has been suggested from homology modeling approaches that residues 537 through 543 (mutation hot spots in exon 12) lie within a loop region bridging the SH2 and JH2 domains of JAK2. In the predicted model, positive polar or hydrophobic interactions between D407–K655, S411–E653, K415–E685 and F408–H608 from the SH2 and the JH2 domains, respectively, are closely packed in the predicted interface that further supported the JH2-JH1 interaction (21). Therefore, mutations in this loop area may disrupt JH2-JH1 interaction leading to constitutive kinase activation, e.g., del/F537-K539ins/L, del/N542-E543, H538QK539L and K539L, all displayed increased JAK2 activation, cytokine-independent hypersensitive proliferation, and in the case of K539L, developed a myeloproliferative phenotype. See e.g., Scott *et al.*, N Engl J Med 356:459-468 (2007).

[0093] One or more of the following determinations may be used to diagnose a patient: determining the presence or absence of a specific JAK2 mutation, determining the zygosity status of the sample, and determining the ratio of mutant to wild-type JAK2 nucleic acid or mRNA in the sample. For example, patients found to carry a specific JAK2 mutation by the methods of the invention may be recommended for further testing to verify an MPD diagnosis, or detection of the mutation may be used to finally confirm a preliminary diagnosis of MPD (e.g., if a patient is symptomatic for an MPD and also tests positive for a specific

JAK2 mutation known to be indicative of a particular MPD, the patient may be finally diagnosed with an MPD such as PV). Similarly, methods of the invention may be used to diagnose patients who are asymptomatic for MPD, for example patients who are in the very early stages of an MPD. JAK2 mutations may also be detected in MPD patients who are undergoing treatment; if the ratio of mutant to wild-type JAK2 nucleic acid or the zygosity status of the sample changes during treatment, a different diagnosis may be made.

[0094] One or more of the following determinations may be used to treat a patient: determining the presence or absence of a specific JAK2 mutation, determining the zygosity status of the sample, and determining the ratio of mutant to wild-type JAK2 nucleic acid in a sample. A physician or treatment specialist may administer, forego or alter a treatment or treatment regime based on one or more of the determinations. Further, the number of cancerous cells carrying the mutation may change during the course of an MPD and monitoring the ratio, the zygosity status, and/or the presence or absence of a JAK2 mutation may be an indication of disease status or treatment efficacy. For example, treatment may reduce the number of mutant cancerous cells, or the disease may become worse with time, and the number of diseased cells may increase. Additionally, one or more of the determinations may aid in patient prognosis and quality of life decisions. For example, decisions about whether to continue - or for how long to continue - a painful, debilitating treatment such as chemotherapy may be made.

[0095] The zygosity status and the ratio of wild-type to mutant nucleic acid in a sample may be determined by methods known in the art including sequence-specific, quantitative detection methods. Other methods may involve determining the area under the curves of the sequencing peaks from standard sequencing electropherograms, such as those created using ABI Sequencing Systems, (Applied Biosystems, Foster City CA). For example, the presence of only a single peak such as a "G" on an electropherogram in a position representative of a particular nucleotide is an indication that the nucleic acids in the sample contain only one nucleotide at that position, the "G." The sample may then be categorized as homozygous because only one allele is detected. The presence of two peaks, for example, a "G" peak and a "T" peak in the same position on the electropherogram indicates that the sample contains two species of nucleic acids; one species carries the "G" at the nucleotide position in

question, the other carries the “T” at the nucleotide position in question. The sample may then be categorized as heterozygous because more than one allele is detected.

[0096] The sizes of the two peaks may be determined (*e.g.*, by determining the area under each curve), and a ratio of the two different nucleic acid species may be calculated. A ratio of wild-type to mutant nucleic acid may be used to monitor disease progression, determine treatment, or to make a diagnosis. For example, the number of cancerous cells carrying a specific JAK2 mutation may change during the course of an MPD. If a base line ratio is established early in the disease, a later determined higher ratio of mutant nucleic acid relative to wild-type nucleic acid may be an indication that the disease is becoming worse or a treatment is ineffective; the number of cells carrying the mutation may be increasing in the patient. A lower ratio of mutant relative to wild-type nucleic acid may be an indication that a treatment is working or that the disease is not progressing; the number of cells carrying the mutation may be decreasing in the patient.

EXAMPLES

[0097] EXAMPLE 1: Detection of the JAK2 Mutations

[0098] Approximately 20,000 patient samples with suspicious diagnosis of MPD over a period of 7 months (from November, 2007 through June, 2008) were collected and screened for *JAK2* gene mutation through the region of entire exons 12-15. Five milliliters of blood in Lavender (purple top tubes) containing ethylenediaminetetraacetic acid (EDTA) anticoagulant were required for analysis. Blood samples were refrigerated (not frozen) or kept at room temperature no more than 48 hr if immediate nucleic acid extraction was not possible.

[0099] Total nucleic acids were isolated from peripheral blood plasma by the NucliSens extraction kit (bioMerieux Inc., Durham, NC, USA) according to the manufacturer's instructions. First strand cDNAs were then prepared by reverse transcription of total RNAs with random primers at 55°C for 30 min, followed by PCR reactions using SuperSript III one-step RT-PCR system with Platinum Taq DNA polymerase (Invitrogen, Carlsbad, CA, USA). For amplification of the *JAK2* exons 12-15, the following primer set and conditions were used: 5'-TGT AAA ACG ACG GCC AGT CTA AAT GCT GTC CCC CAA AG-3' (forward primer, SEQ ID NO: 6) and 5'-CAG GAA ACA GCT ATG ACC CCA TGC CAA

CTG TTT AGC AA-3' (reverse primer, SEQ ID NO: 7); initial step of 2 min at 94 °C, followed by 40 cycles of 94 °C for 15 sec, 60 °C for 30 sec, and 68 °C for 1 min, and ending with one step of 68 °C for 7 min. The 491-bp amplified products were filter-purified by Multiscreen PCR plates (Millipore, Billerica, MA, USA) and sequenced in both directions using the ABI Prism BigDye® Terminator v3.1 Cycle Sequencing Kit and detected by ABI PRISM 3100 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA). Sequence data was then base-called, assembled and analyzed by ABI Prism® SeqScape software (Applied Biosystems, Foster City, CA, USA) using the *JAK2* sequence (accession number NM004972) as a reference.

[0100] Table 1 presents a mutation analysis of *JAK2* gene exon 12 (SEQ ID NO: 3), exon 13 (SEQ ID NO: 4), exon 14 (SEQ ID NO: 5), and exon 15 from a large group of suspected MPD blood samples.

Table 1: Mutation Analysis

Exon*	Mutation	Codon change	No. of cases	Pattern on sequencing#
12	Silent	H531	1	Heterozygous
12	Duplication	dupl/V536-F547	2	Heterozygous
12	Deletion	del H538	1	Heterozygous
12	Deletion	dcl/H538-K539	1	Heterozygous
12	Deletion	del/N542-E543	5	Heterozygous
12	Deletion	del/E543-D544	3	Heterozygous
12	Indels	del/F537-K539 ins/K	1	Heterozygous
12	Indels	del/F537-K539 ins/L	2	Heterozygous
12	Indels	del/H538-K539 ins/L	4	Heterozygous
12	Indels	del/R541-E543 ins/K	1	Heterozygous
12	Indels	del/I540-D544 ins/MK	1	Heterozygous

		del/N542-D544		
12	Indels	ins/N	1	Heterozygous
12	Missense	T514M	2	Heterozygous
12	Missense	N533Y	1	Heterozygous
12	Missense	K539L	2	Heterozygous
12	Missense	H538Q K539L	1	Heterozygous
12	Missense	K539L L545V	1	Heterozygous
12	Missense	F547L	1	Heterozygous
13	Silent	G562	2	Heterozygous
13	Silent	Y570	4	Heterozygous
13	Silent	F556	1	Heterozygous
13	Missense	R564L	3	Heterozygous
13	Missense	R564Q	2	Heterozygous
13	Missense	V567A	1	Heterozygous
13	Missense	G571S	3	Heterozygous
13	Missense	G571R	1	Heterozygous
13	Missense	L579F	1	Heterozygous
13	Missense	H587N	1	Heterozygous
13	Missense	S591L	1	Heterozygous
14	Deletion	S593-N622	2	Heterozygous
14	Missense	H606Q	1	Heterozygous
14	Missense	V617F	>2000	Hetero/Homo
14	Missense	V617I	1	Heterozygous
14	Missense	V617F C618R	2	Hetero/Homo
14	Missense	C618R	1	Heterozygous
15	Missense	L624P	1	Heterozygous
15	Missense	I645V	1	Heterozygous

**Exon 12 (residues 511-547); Exon13 (residues 548-592); Exon14 (residues 593-622).*

[0101] EXAMPLE 2: Additional JAK2 Mutations

[0102] Table 2 presents additional specific examples of novel JAK2 mutations identified by sequencing, along with their deduced amino acid substitutions.

Table 2: Exons 12, 13, 14, and 15 Mutations

Exon 12	
JAK2 Mutation Nucleic Acid; (Codon Change)	JAK2 Mutation Protein; (Amino Acid Change)
Missense Mutations	
c2035t; (acg>atg)	T514M; (Thr → Met)
a2091t ; (aac>tac)	N533Y (Asn → Tyr)
t2127c; (ttg>gtg)	L545V; (Leu → Val)
t2133c; (ttt>ctt)	F547L; (Phe → Leu)
del: deletion; ins: insertion	
Exon 13	
JAK2 Mutation Nucleic Acid; (Codon Change)	JAK2 Mutation Protein; (Amino Acid Change)
Missense Mutations	
t2160g ttt>gtt	F556V (Phe → Val)
c2180t; (ggc>ggg)	G562 silent; (Gly)
g2185t; (cga>cta)	R564L; (Arg → Leu)
g2185a; (cga>caa)	R564Q; (Arg → Gln)
g2193t; (gta>tta)	V567L; (Val → Leu)
t2194c; (gta>gca)	V567A; (Val → Ala)
c2204t; (tac>tat)	Y570 Silent; (Tyr)
g2205a; (ggg>agt)	G571S; (Gly → Ser)
g2205c; (ggg>cgt)	G571R; (Gly → Arg)
c2229t; (ctt>ttt)	L579F; (Leu → Phe)
c2253a; (cac>aac)	H587N; (His → Asn)
c2266t; (tca>tta)	S591L; (Ser → Leu)
Exon 14	
JAK2 Mutation Nucleic Acid; (Codon Change)	JAK2 Mutation Protein; (Amino Acid Change)
Exon 14 Missense and Deletion Mutations	
c2312a; (cac>caa)	H606Q; (His → Gln)
2271-2358 (exon 14 deletion)	S593-N622
Exon 15	

Exon 15 Missense Mutations	
t2365c; (ctg>ccg)	L624P; (Leu → Pro)
a2427g; (ata>gta)	I645V; (Ile → Val)

[0103] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

[0104] The inventions illustratively described herein may suitably be practiced in the absence of any element or elements, limitation or limitations, not specifically disclosed herein. Thus, for example, the terms “comprising,” “including,” “containing,” etc. shall be read expansively and without limitation. Additionally, the terms and expressions employed herein have been used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

[0105] Thus, it should be understood that although the invention has been specifically disclosed by preferred embodiments and optional features, modification, improvement and variation of the inventions embodied therein herein disclosed may be resorted to by those skilled in the art, and that such modifications, improvements and variations are considered to be within the scope of this invention. The materials, methods, and examples provided here are representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention.

[0106] The invention has been described broadly and generically herein. Each of the narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein.

[0107] In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group.

[0108] All publications, patent applications, patents, and other references mentioned herein are expressly incorporated by reference in their entirety, to the same extent as if each were incorporated by reference individually. In case of conflict, the present specification, including definitions, will control.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising at least 17 contiguous nucleotides corresponding to SEQ ID NO: 1, wherein said nucleic acid comprises a mutation selected from the group consisting of the mutations shown in Table 2, and wherein said nucleic acid is less than 5000 nucleotides in length.
2. The isolated nucleic acid of claim 1, wherein said nucleic acid further comprises at least one additional mutation shown in Table 2.
3. The isolated nucleic acid of any one of claims 1-2, wherein said nucleic acid is labeled with a detectable label.
4. A polypeptide comprising at least 10 contiguous amino acids corresponding to SEQ ID NO: 2, wherein said polypeptide comprises a mutation selected from the group consisting of the mutations shown in Table 2, and wherein said polypeptide is less than 1100 amino acids.
5. The polypeptide of claim 4, wherein said polypeptide further comprises at least one additional mutation shown in Table 2.
6. The polypeptide of any one of claims 4-5, wherein said polypeptide is labeled with a detectable label.
7. A method for diagnosing a hematopoietic disease in an individual comprising:
 - a) providing sample from said individual, wherein said sample comprises JAK2 nucleic acid;
 - b) evaluating a sample containing nucleic acids from the individual for the presence or absence of one or more mutations in JAK2 nucleic acid, wherein said one or more mutations is selected from the group consisting of the mutations of Table 2; and
 - c) identifying said individual as having a hematopoietic disease when said JAK2 nucleic acid comprises at least one of said mutations.
8. The method of claim 7, wherein the JAK2 nucleic acid is RNA.

9. The method of any one of claims 7-8, wherein said sample is selected from the group consisting of blood, serum, and plasma.
10. The method of any one of claims 7-9, wherein said JAK2 nucleic acid further comprises at least one additional mutation shown in Table 2.
11. The method of any one of claims 7-10, wherein said hematopoietic disease is a myeloproliferative disease.
12. The method of claim 11, wherein said myeloproliferative disease is selected from the group consisting of polycythemia vera, essential thrombocythemia, idiopathic myelofibrosis, and unclassified myeloproliferative disease.
13. The method of any one of claims 7-12, wherein said evaluating step comprises amplifying JAK2 nucleic acid and hybridizing the amplified nucleic acid with a detection oligonucleotide that is capable of specifically detecting JAK2 nucleic acid under hybridization conditions.
14. The method of any one of claims 7-13, wherein said evaluating step comprises amplifying JAK2 nucleic acid and performing direct sequencing analysis of the amplified nucleic acid.
15. A method of determining a prognosis of an individual diagnosed with a hematopoietic disease, said method comprising:
 - (a) determining the presence or absence of one or more mutations in a JAK2 nucleic acid sample,

wherein said one or more mutations is selected from the group consisting of the mutations of Table 2; and
 - (b) identifying said individual as having poor prognosis when one or more mutations are present in a JAK2 nucleic acid sample.

16. A method for diagnosing a hematopoietic disease in an individual comprising:

- a) evaluating a sample from the individual for the presence or absence of one or more mutations in JAK2 polypeptide, wherein said one or more mutations is selected from the group consisting of the mutations of Table 2, and
- b) identifying said individual as having hematopoietic disease when at least one of said mutation in JAK2 polypeptide is present.

17. The method of any one of claims 15-16, wherein said sample is selected from the group consisting of blood, serum, and plasma.

18. The method of any one of claims 15-17, wherein said JAK2 polypeptide further comprises at least one additional mutation shown in Table 2.

19. The method of any one of claims 15-18, wherein said hematopoietic disease is a myeloproliferative disease.

20. The method of claim 19, wherein said myeloproliferative disease is selected from the group consisting of polycythemia vera, essential thrombocythemia, idiopathic myelofibrosis, and unclassified myeloproliferative disease.

21. The method of any one of claims 15-20, wherein said evaluating step comprises using an antibody that specifically binds to the mutated JAK2 polypeptide.

22. A method for determining a prognosis of an individual diagnosed with a hematopoietic disease, said method comprising:

- (a) determining the presence or absence of one or more mutations in a JAK2 polypeptide sample,

wherein said one or more mutations is selected from the group consisting of the mutations of Table 2; and

- (b) identifying said individual as having poor prognosis when one or more mutations in a JAK2 polypeptide is present.

Series of Representative Sequencing Chromatograms

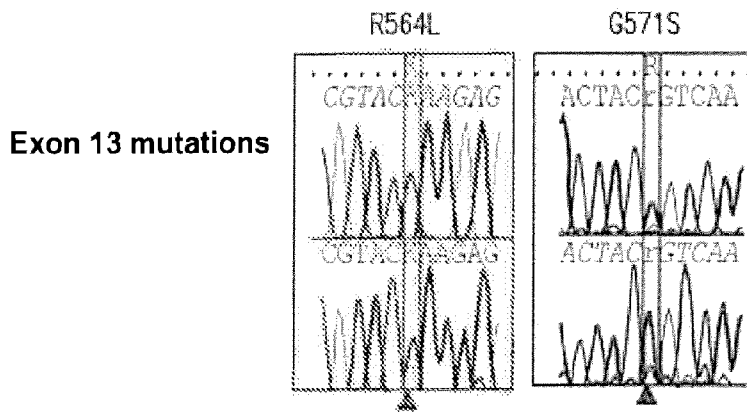


FIG. 1(A)

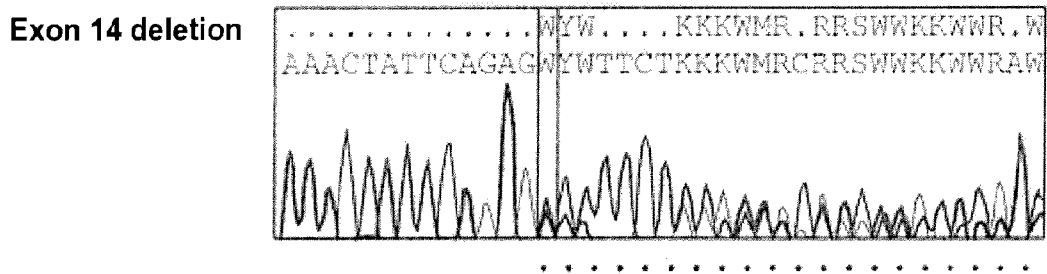


FIG. 1(B)

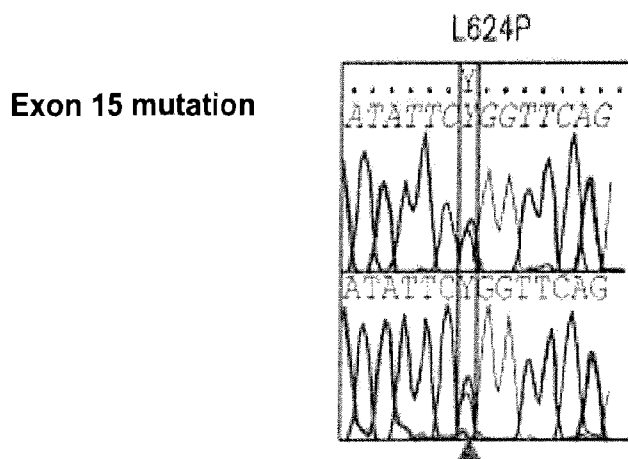


FIG. 1(C)

Diagram of JAK2 Gene Structure and Mutations

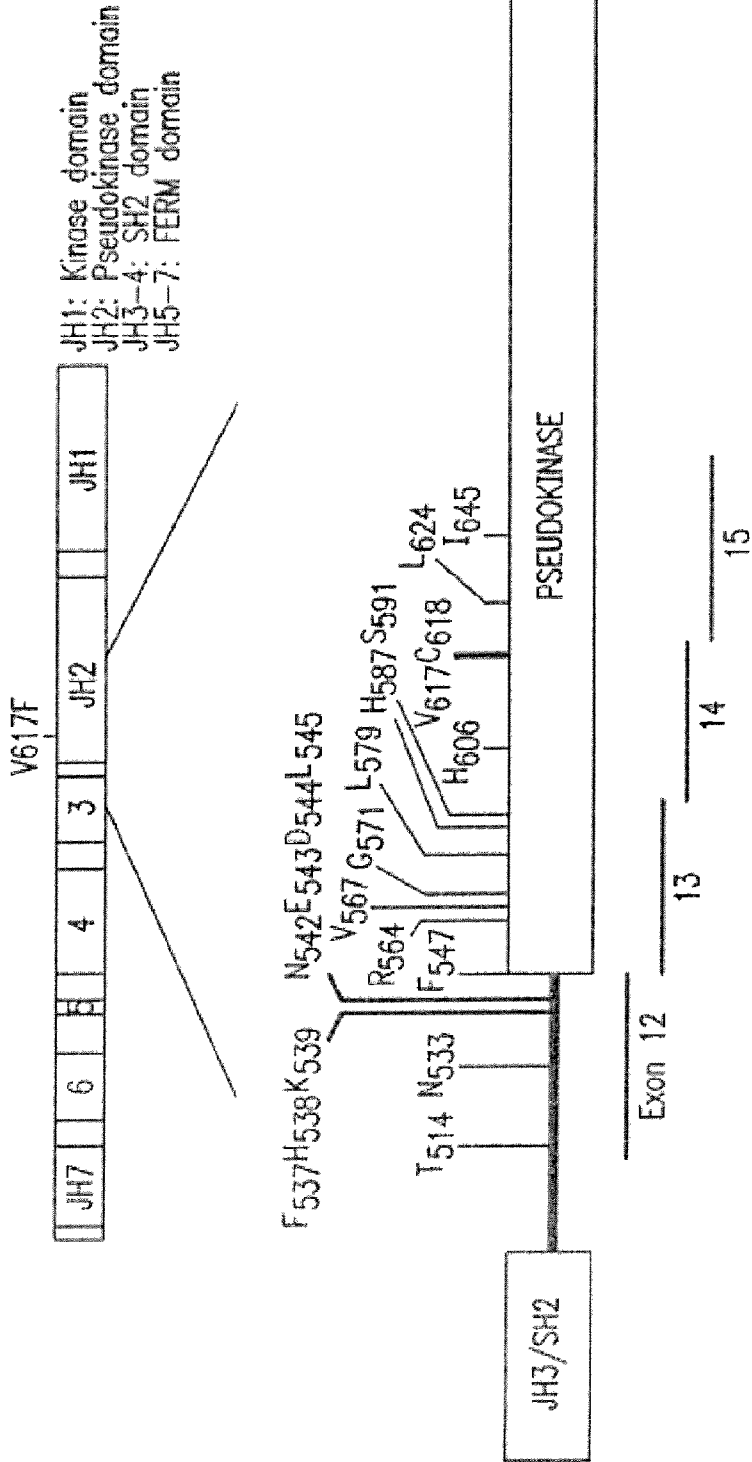


FIG. 2

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 09/61691

A. CLASSIFICATION OF SUBJECT MATTER
 IPC(8) - C12Q 1/68, G01N 33/53 (2009.01)
 USPC - 435/6, 435/7.2
 According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED
 Minimum documentation searched (classification system followed by classification symbols)
 IPC(8) - C12Q 1/68, G01N 33/53 (2009.01)
 USPC - 435/6, 435/7.2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 PubWEST - DB=PGPB,USPT,USOC,EPAB,JPAB; PLUR=YES; OP=ADJ; Google Scholar
 Search terms: JAK-2, JAK2, JAK 2, janus kinase, tyrosine kinase, PTK, mutat\$, variant, SNP, polymorph\$, PTK, tyrosine kinase, fragment, diagnos\$, prognos\$, hematopoietic, myeloprolif\$, t514m, n533y, l545v, f547l, f556v, g562, r564l, v567l, y570

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ---- Y	US 2007/0082332 A1 (MENDRICK et al.) 12 April 2007 (12.04.2007) para [0069]; [0070]; [0083]; [0084]; [0099]; [0100]; [0117]; Table 3; SEQ ID NO: 2276.	1-6 ----- 7-9, 15-17, 22
Y	US 2007/0248961 A1 (ALBITAR et al.) 25 October 2007 (25.10.2007) para [0006]-[0009]; [0011]; [0012]; [0014]; [0017]; [0029]; [0041]; [0049]; [0051]; [0062]; [0067]; [0073]; [0074]; Fig. 2.	7-9, 15-17, 22

Further documents are listed in the continuation of Box C.

* Special categories of cited documents:

“A” document defining the general state of the art which is not considered to be of particular relevance	“T” later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
“E” earlier application or patent but published on or after the international filing date	“X” document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
“L” document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	“Y” document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
“O” document referring to an oral disclosure, use, exhibition or other means	“&” document member of the same patent family
“P” document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 18 December 2009 (18.12.2009)	Date of mailing of the international search report 12 JAN 2010
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Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-3201	Authorized officer: Lee W. Young PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 09/61691

Box No. 1 Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:

a. (means)

on paper

in electronic form

b. (time)

in the international application as filed

together with the international application in electronic form

subsequently to this Authority for the purposes of search

2. In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 09/61691

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.: 10-14, 18-21
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- No protest accompanied the payment of additional search fees.

专利名称(译)	用于检测jak2核酸突变的组合物和方法		
公开(公告)号	EP2340315A1	公开(公告)日	2011-07-06
申请号	EP2009824031	申请日	2009-10-22
[标]申请(专利权)人(译)	奎斯特诊断投资公司		
申请(专利权)人(译)	Quest Diagnostics公司投资INCORPORATED		
当前申请(专利权)人(译)	Quest Diagnostics公司投资INCORPORATED		
[标]发明人	ALBITAR MAHER MA WANLONG		
发明人	ALBITAR, MAHER MA, WANLONG		
IPC分类号	C12Q1/68 G01N33/53		
CPC分类号	C12N9/1205 C12Q1/6883 C12Q2600/118 C12Q2600/156 C12Y207/10001 G01N33/573 G01N2333 /91205 G01N2800/22 G01N2800/56		
优先权	61/110501 2008-10-31 US 12/503318 2009-07-15 US		
其他公开文献	EP2340315A4 EP2340315B1		
外部链接	Espacenet		

摘要(译)

本文公开的发明基于JAK2基因和JAK2蛋白中的新突变的鉴定。本发明提供了用于诊断造血疾病的组合物和方法，包括例如骨髓增生性疾病。本发明还提供了用于确定被诊断患有造血疾病的个体的预后的组合物和方法。