

Natural-Killer/T-Cell Lymphoma (NKTCL) susceptibility prediction, diagnosis and therapy

FIELD OF THE INVENTION

5 The present invention relates to cancer therapy and/or diagnosis. In particular, it relates to Natural-Killer/T-Cell Lymphoma (NKTCL) therapy and/or diagnosis.

BACKGROUND OF THE INVENTION

10 Natural killer (NK)-cell lymphoma is a type of non-Hodgkin lymphoma (NHL). Most NHLs (90%) are of B-cell origin. NK-cell lymphomas do not arise from B-cells. However, controversy still exists over the normal cell from which NK-cell lymphomas arise. In particular, whether NK-cell lymphoma represents the presence of a true NK cell or merely the presence of a T cell with abnormal cell markers is under debate. In the absence of unequivocal proof of the exact lineage of NK-cell lymphoma, many investigators prefer to use the term NK/T-cell lymphoma (NKTCL) when classifying this condition.

15 Natural-killer T-cell lymphoma (NKTCL) is particularly prevalent in Asian countries and some parts of Latin America. It accounts for up to half of all mature T cell lymphoma cases in Asia (1). However, compared to the more common B cell lymphomas, very little is known about its molecular characteristics and pathogenesis. There has been little progress in basic science and clinical research in this subtype of lymphoma, which
20 continues to constitute a major challenge in managing these patients as there is currently no accepted standard first-line treatment for NKTCL. Despite multi-agent chemotherapy and involved-field radiotherapy, the 5-year overall survival is approximately 9% for non-nasal NKTCL and 42% for nasal NKTCL (2, 3).

25 Compared to B cell lymphomas which are relatively more common, very little is known about the molecular characteristics and pathogenesis of NKTCLs. This may be in part due to relative rarity in the West and difficulty in obtaining adequate biopsy. Treatment of NKTCLs with conventional chemotherapy has thus far yielded poor results and the outcome is almost always fatal for patients with stage III or IV disease.

30 It is desirable to identify novel genetic aberrations and potential treatment targets in NKTCL, as well as potential therapeutic agents for NKTCL.

SUMMARY OF THE INVENTION

The present invention relates to cancer therapy and/or diagnosis, in particular Natural-Killer/T-Cell Lymphoma (NKTCL) therapy and/or diagnosis.

According to a first aspect, the present invention relates to a method for predicting
 5 Natural Killer T-Cell Lymphoma (NKTCL) susceptibility and/or diagnosing NKTCL in a subject, comprising testing for the genotype of said subject for at least one *JAK* gene, wherein the presence of a mutant *JAK* gene indicates that a subject is at risk of developing and/or has NKTCL.

The invention also relates to a method for predicting Natural Killer T-Cell Lymphoma
 10 (NKTCL) susceptibility and/or diagnosing NKTCL in a subject, comprising testing for whether said subject expresses a wildtype or mutant *JAK* protein, wherein expression of a mutant *JAK* protein indicates that the subject is at risk of developing and/or has NKTCL.

According to a second aspect, the invention relates to a method for screening for an
 15 agent capable of treating NKTCL, comprising:

- (i) providing a NKTCL cell line comprising at least one mutant *JAK* gene;
- (ii) contacting the NKTCL cell line with the agent; and
- (iii) determining the effect of the agent on the mammalian NKTCL cell line;

wherein the ability of the agent to reduce the viability, growth and/or multiplication
 20 and/or increase apoptosis of the NKTCL cell line is indicative of the ability of the agent to treat NKTCL.

According to a third aspect, the invention relates to a method for screening for an agent capable of reducing the activity of at least one of *JAK* protein, comprising:

- (i) providing a NKTCL cell line carrying a mutant *JAK* gene;
- 25 (ii) contacting the NKTCL cell line with the agent; and
- (iii) determining the effect of the agent on the NKTCL cell line;

wherein the ability of the agent to reduce the viability, growth and/or multiplication and/or increase apoptosis of is indicative of the ability of the candidate agent to reduce the activity of at least one JAK protein.

According to a fourth aspect, there is provided an NKTCL animal model comprising at least one mutant *JAK* gene.

According to a fifth aspect, the invention relates to a method of treating Natural Killer T-Cell Lymphoma (NKTCL) comprising administering a JAK inhibitor to a subject.

The invention also includes use of a JAK inhibitor in the preparation of a medicament for the treatment of Natural Killer T-Cell Lymphoma (NKTCL).

The invention further includes a JAK inhibitor for use in treating Natural Killer T-Cell Lymphoma (NKTCL).

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows High-resolution melt (HRM) and Sanger sequencing data leading to the identification of JAK3 A572V and A573V mutations in NKTCL samples. Figure 1. (a) shows the location of the A572V and A573V mutation on the JH2 pseudokinase domain of the JAK3 gene. High-resolution melt (HRM) and Sanger sequencing data used to validate JAK3 mutations are shown in Figure 1(b) through (h). In particular: Figure 1(b) shows the percentage of the JAK3 A572V and A573V mutations in the pie chart (n=65). Figure 1(c) shows HRM difference plots (in replicates) normalized to the wild-type sample for three genotypes: wild-type JAK3, heterozygous JAK3 (c.1715C>T, p.Ala572Val) and homozygous JAK3 (c.1715C>T, p.Ala572Val). Figure 1(d) shows representative HRM difference curves of an Formalin-Fixed Paraffin-Embedded (FFPE) NKTCL sample which was sequenced and confirmed as heterozygous JAK3 (c.1718C>T, p.Ala573Val) mutation. Notably, HRM difference plots for sample with either JAK3 A572V or A573V mutation were similar due to the same C>T conversion. Representative sequencing chromatograms are also shown in Figure1 (e) for the JAK3 wild-type allele, Figure 1(f) for the A572V heterozygous mutant, Figure 1(g) for the A573V heterozygous mutant, and Figure 1(h) for the A572V homozygous mutant.

Figure 2 shows data demonstrating the effect of IL-2 on JAK3 and STAT5 phosphorylation and CP-690,550 treatment on NKTCL cell lines. Figure 2 (a) shows immunoblotting results for NK-S1 (JAK-mutant) and KHYG-1 (wild-type) cells which were cultured with or without recombinant human IL-2 (200 IU/ml), harvested at 48 h, and assayed for JAK3 and STAT5 phosphorylation by immunoblotting. NK-S1, KHYG-1 and K562 (control) cell lines were treated with the pan-JAK inhibitor CP-690,550 and the results of evaluation are shown in Figure 2(b) through 2(d). Figure 2(b) shows STAT5 phosphorylation in the samples evaluated by immunoblotting at 48 h. Figure 2(c) shows cell viability analyzed by MTS assay at 72 h. Figure 2(d) shows drug-induced apoptosis at 72 h evaluated by Annexin V-FITC staining and analyzed by flow cytometry. Experiments were repeated at least three times. Results in c and d represent the average of triplicates $\pm$ s.e.m. * Indicates $p < 0.05$ by paired Student's t-test.

Figure 3 provides data showing Cytokine independent growth of the mutant NKTCL cell line, NK-S1. In particular, NK-S1 (JAK3 mutant) and KHYG-1 (JAK3 wild-type) were cultured with or without recombinant human IL-2 (0 to 200 IU/ml). Cell viability data is shown in Figure 3(a) for NK-S1 and in Figure 3(b) for KHYG-1. Cell viability was monitored daily with MTS assay for seven days and cell growth was expressed as absorbance at 490 nm minus the reference at 650 nm. Results in a and b represent the average of triplicates $\pm$ s.d.

Figure 4 shows data demonstrating that JAK3 A572V mutation causes constitutive JAK3 activity and IL-2 independent proliferation of NKTCL cells. Figure 4A shows data for NK-S1 cells which were treated with 100 nM JAK3 siRNA (si-JAK3) or control siRNA (si-Ctrl) for 24 h prior and subjected to proliferation assays up to 72 h (Right panel). In parallel, these cells were harvested and protein extracts were subjected to Western blotting with antibodies against phosphorylated JAK3 (pJAK3), phosphorylated STAT5 (pSTAT5), JAK3, STAT5, or β -actin as a normalization control. Figure 4B shows data for KHYG-1 cells which were transiently transfected with wild-type JAK3 (JAK3 WT) or mutated JAK3 expression vectors (i.e. JAK3 A572V). The relative pJAK3, pSTAT5, JAK3 and STAT5 levels in these cells were detected by Western blotting (upper panel), and proliferation assays using these cells were performed for 48 h with or without IL-2 (lower panel). All results are expressed as mean SEM of three independent experiments. *, $p < 0.05$ compared with Vehicle control (Vehicle).

DEFINITIONS

As used in the present specification, the term "inhibitor" refers to any substance which is able to reduce the activity of a protein, for example a JAK inhibitor is able to reduce the activity of a JAK protein. In particular, a JAK3 inhibitor is able to reduce the activity of a JAK3 protein. Reducing the activity of a protein may be direct or indirect - for example, by interfering with the expression of the protein or the mechanism by which the protein functions in a biological context. For example, the JAK3 kinase may require binding of a molecule of ATP to an ATP-binding site, so by specifically binding to and blocking the ATP-binding site, the activity of the JAK3 kinase is reduced. The activity of the JAK protein may also require the activity of another protein, such as a cytokine receptor, so interference with the activity of this protein may also reduce the activity of the JAK protein. Alternatively, fewer JAK3 kinase proteins may be expressed by interfering with gene expression at the relevant nucleic acid domain, such as the translation of the corresponding mRNA.

NKTCL refers to NK/T cell lymphoma in accordance with WHO classification (6). The terms "Natural Killer T-Cell Lymphoma," NKTCL and "NK/T-cell lymphoma" are used interchangeably to refer to a type of non-Hodgkin lymphoma (NHL) that is not of B-cell origin. NKTCL has the classic morphology of tumor necrosis, angiocentricity as well as the appropriate immunophenotype, in particular, presence of CD56, cytoplasmic CD3 as well as near universal presence of EBER. NK/T cell lymphoma differs from Adult T cell Leukemia/Lymphoma, which is a disease of the T cell lineage and associated with HTLV-I infection.

The term "treating" includes alleviating, preventing and/or eliminating one or more symptoms associated with a disease, for example Natural killer/T-cell Lymphoma (NKTCL)

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to cancer therapy and/or diagnosis, in particular Natural-Killer/T-Cell Lymphoma (NKTCL) therapy and/or diagnosis.

According to a first aspect, there is provided a method for predicting Natural Killer T-Cell Lymphoma (NKTCL) susceptibility and/or diagnosing NKTCL in a subject, comprising testing for the genotype of said subject for at least one *JAK* gene wherein the presence of a mutant *JAK* gene indicates that a subject is at risk of developing and/or has NKTCL. The presence of either a heterozygous or homozygous mutant *JAK* gene indicates that the subject is at risk of developing and/or has NKTCL.

Any one or a combination of any of the *JAK* genes may be tested. The *JAK* gene tested may be selected from the group consisting of *JAK1*, *JAK2*, *JAK3* and *TYK2*. For example, the *JAK3* and/or *JAK1* genes may be tested. In general, SEQ ID NO: 1 indicates a wildtype *JAK3* gene. In one example, the presence of a mutant *JAK3* gene comprising a substitution of C with T at nucleotide 15792 and/or a substitution of C with T at nucleotide 15795 of SEQ ID NO: 1 indicates that a subject is at risk of developing and/or has NKTCL.

In general, SEQ ID NO: 3 indicates a wildtype *JAK1* gene. In another example, the presence of a mutant *JAK1* gene comprises a substitution of T with G at nucleotide 124823 of SEQ ID NO: 3 indicates that a subject is susceptible and/or has NKTCL. The presence of both mutant *JAK1* and *JAK3* genes also indicate that a subject is at risk of developing and/or has NKTCL.

The method may be performed on an isolated cell sample from the subject. The isolated cell sample may be from a blood and/or tumour sample. Accordingly, the method may further comprise providing an isolated cell sample from the subject for testing. The method may further comprise isolating nucleic acid molecules from the subject, blood sample and/or isolated cell sample for said testing. The isolated nucleic acid molecules may comprise genomic DNA or mRNA. In particular, the testing may be performed on genomic DNA, mRNA and/or cDNA.

Any suitable technique may be employed for testing. For example, testing may be by sequence analysis, restriction fragment length polymorphism analysis, hybridization, polymerase chain reaction (PCR) and/or reverse transcription PCR. In particular,

techniques such as Sanger sequencing and High resolution melt may be used for testing.

In another aspect of the invention, there is provided a method for predicting Natural Killer T-Cell Lymphoma (NKTCL) susceptibility and/or diagnosing NKTCL in a subject, comprising testing for whether said subject expresses a wildtype or mutant JAK protein, wherein expression of a mutant JAK protein indicates that the subject is at risk of developing and/or has NKTCL.

Any one or a combination of any of the JAK proteins may be tested. The JAK protein tested may be selected from the group consisting of JAK1, JAK2, JAK3 and TYK2. For example, the JAK3 and/or JAK1 proteins may be tested. In general, SEQ ID NO: 2 indicates a wildtype JAK3 protein. In one example, the presence of a mutant JAK3 gene comprising a substitution of A with V at amino acid 572 and/or a substitution of A with V at amino acid 573 of SEQ ID NO: 2 indicates that a subject is at risk of developing and/or has NKTCL.

In general, SEQ ID NO: 4 indicates a wildtype JAK1 protein. In another example, the presence of a mutant JAK1 protein comprising a substitution of Y with D at amino acid 652 of SEQ ID NO: 4 indicates a subject at risk of developing and/or has NKTCL. The presence of both mutant JAK3 and JAK1 proteins also indicate a subject at risk of developing and/or has NKTCL.

The method may be performed on an isolated blood and/or cell sample from the subject. The isolated cell sample may be from a tumour. Accordingly, the method may further comprise providing an isolated blood and/or cell sample from the subject for testing. The method may further comprise isolating proteins molecules from the subject, blood sample and/or isolated cell sample for said testing.

Any suitable method may be used to detect whether the relevant wildtype and/or mutant JAK protein is expressed. For example, testing may be by protein sequencing and/or antibody detection. In particular, Enzyme-linked immunosorbent assay (ELISA) using at least one antibody with specificity for the relevant wildtype and/or mutant JAK protein may be used.

In a second aspect of the invention, there is provided a method for screening for an agent capable of treating NKTCL, comprising:

- (a) providing a NKTCL cell line comprising at least one mutant JAK gene;
- (b) contacting the NKTCL cell line with the agent; and
- 5 (c) determining the effect of the agent on the NKTCL cell line;

wherein the ability of the agent to reduce the viability, growth and/or multiplication and/or increase apoptosis of the NKTCL cell line may be indicative of the ability of the agent to treat NKTCL.

10 In a third aspect of the invention, there is provided a method for screening for an agent capable of reducing the activity of at least one JAK protein, comprising:

- (i) providing a NKTCL cell line carrying at least one mutant *JAK* gene
- (ii) contacting the NKTCL cell line with the agent; and
- (iii) determining the effect of the agent on the NKTCL cell line;

15 wherein the ability of the agent to reduce the viability, growth and/or multiplication and/or increase apoptosis of cell line is indicative of the ability of the candidate agent to reduce the activity of at least one JAK protein.

The NKTCL cell line may carry any one or a combination of any of mutant *JAK1*, *JAK2*, *JAK3* or *TYK2* genes. For example, the NKTCL cell line may carry a mutant *JAK3* gene and/or a mutant *JAK1* gene. In particular, the mammalian NKTCL cell line may carry at
20 least one of the following mutations:

- (i) a substitution of C with T at nucleotide 15792 of SEQ ID NO:1 (in the *JAK3* gene);
- (ii) a substitution of C with T at nucleotide 15795 of SEQ ID NO:1 (in the *JAK3* gene); and
- 25 (iii) a substitution of T with G at nucleotide 124823 of SEQ ID NO:3 (in the *JAK1* gene).

According to a fourth aspect, the invention also relates to an NKTCL animal model comprising at least one mutant *JAK* gene. For example, the NKTCL animal model may comprise at least one mutation selected from the group consisting of mutant *JAK1*, *JAK2*, *JAK3* and *TYK2* genes. In particular, the NKTCL animal model comprises a mutant *JAK3* gene and/or a mutant *JAK1* gene. More in particular, the NKTCL animal model comprises at least one of the following mutations:

- (i) a substitution of C with T at nucleotide 15792 of SEQ ID NO: 1;
- (ii) a substitution of C with T at nucleotide 15795 of SEQ ID NO: 1; or
- (iii) a substitution of T with G at nucleotide 124823 of SEQ ID NO: 3.

The NKTCL animal model may also be useful for screening candidate agents capable of treating NKTCL.

According to a fifth aspect, there is provided a method of treating Natural Killer T-Cell Lymphoma (NKTCL) comprising administering at least one JAK inhibitor to a subject. Any suitable JAK inhibitor may be used. In another aspect of the invention, there is provided a use of at least one JAK inhibitor for the preparation of a medicament for the treatment of Natural Killer T-Cell Lymphoma (NKTCL). In another aspect of the invention, there is provided a JAK inhibitor for use in treating Natural Killer T-Cell Lymphoma (NKTCL). The JAK inhibitor may be able to reduce the activity of JAK3 protein.

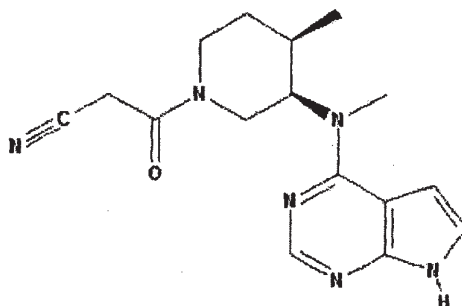
For example, the JAK inhibitor may inhibit at least one of *JAK1*, *JAK2*, *JAK3* and/or *TYK2*. Accordingly, the inhibitor may be a pan-JAK inhibitor. In one particular example, the JAK inhibitor may inhibit *JAK3* and/or *JAK1*. More in particular, the JAK inhibitor may inhibit *JAK3* or the JAK inhibitor may also inhibit *JAK1*.

In a first particular example, the JAK inhibitor may comprise 3-[(3R,4R)-4-methyl-3-[methyl(7H-pyrrolo[2,3-d]pyrimidin-4-yl)amino]piperidin-1-yl]-3-oxopropanenitrile (also known as CP-690,550). In a second particular example, may comprise (E)-2-cyano-3-(4-nitrophenyl)-N-((R)-1-phenylethyl)acrylamide (also known as WP-1034).

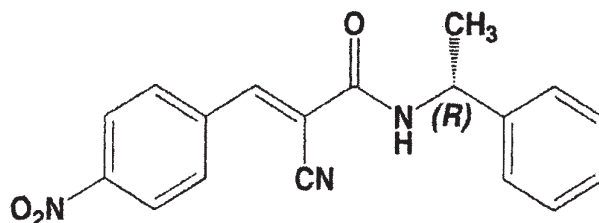
The subject to whom the JAK inhibitor is administered may comprise a mammal. The subject may comprise a human. The subject may carry a homozygous or heterozygous mutation in at least one of the *JAK* genes/*JAK* proteins. For example, the subject may carry a homozygous or heterozygous mutation in *JAK1/JAK1*, *JAK2/JAK2*, *JAK3/JAK3*

and/or *TYK2*/*TYK2*. In particular, the subject may carry a homozygous or heterozygous mutation in *JAK1*/*JAK1* and/or *JAK3*/*JAK3*. More in particular, the subject may have at least one mutation selected from the group consisting of *JAK3*-A572V, *JAK3*-A573V and *JAK1*-Y652D. However, the subject may also comprise a homozygous wildtype phenotype. The subject may have increased expression of any one of the *JAK* genes, its transcriptional and/or translational products (proteins), whether it carries a homozygous wildtype, heterozygous or homozygous mutant gene.

CP-690,550 is a JAK inhibitor. It is known as Tofacitinib, Tasocitinib, or by the trade name XELJANZ. Its chemical name is 3-[(3R,4R)-4-methyl-3-[methyl(7H-pyrrolo[2,3-d]pyrimidin-4-yl)amino]piperidin-1-yl]-3-oxopropanenitrile and its structural formula is:



WP-1034 has been described as having proapoptotic and antileukemic activity in Acute Myeloid Leukemia (Faderl et al., *Anticancer Research* 25: 1841-1850 (2005)) (8). It is a member of the tyrphostin family of tyrosine kinase inhibitors, which has been predominantly studied as an inhibitor of the Jak-Stat pathway. Its chemical structure and name are as follows:



WP1034 - (E)-2-cyano-3-(4-nitrophenyl)-N-((R)-1-phenylethyl)acrylamide

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention.

EXAMPLES

- 5 The molecular pathogenesis of Natural-killer/T-cell lymphoma (NKTCL) is not well understood. Gene mutations causing NK/T-cell lymphoma have not been fully identified. In this study, Janus kinase 3 (JAK3) somatic activating mutations (A572V and A573V) were identified through whole-exome sequencing in two out of four NKTCL patients. Further validation of the prevalence of JAK3 mutations was determined by
- 10 Sanger sequencing and High Resolution Melt (HRM) analysis in an additional 61 cases. In total, 23 of 65 (35.4%) cases harbored JAK3 mutations. Mutant NKTCL cell line harbouring JAK3 A572V mutation showed IL-2 independent growth and constitutive JAK3 and STAT5 phosphorylation suggesting its oncogenic role. Functional characterization of the JAK3 mutations support its involvement in cytokine-
- 15 independent JAK/STAT constitutive activation leading to increased cell growth. These mutations may play a significant role in the pathogenesis of NKTCL. Moreover, treatment of both JAK3-mutant and wild-type NKTCL cell lines with a novel pan-JAK inhibitor, CP-690,550, resulted in dose dependent reduction of phosphorylated STAT5, reduced cell viability and increased apoptosis. CP-690,550 is a pan-JAK inhibitor,
- 20 having an inhibitory effect on not just JAK3 but also JAK1. This may be important because in their function within the JAK-STAT signalling pathway system, JAK1 and JAK3 cross-talk and there may be some compensatory upregulation of one in response to inhibition of the other. For example, if JAK3 is inhibited, JAK1 may be upregulated so as to compensate for the reduced activity of JAK3, and this may preserve JAK-STAT
- 25 signalling. The reverse may also apply. To take the example further, treatment of NKTCL using a pan-JAK inhibitor that is able to reduce the activity of not just JAK1 but JAK3 as well may be especially effective at inhibiting JAK-STAT signalling.

Hence, targeting the deregulated JAK/STAT pathway could be a promising therapy for NKTCL patients. These findings have important implications for the management of

30 NKTCL patients.

Materials and Methods

Tissue samples

Matched fresh-frozen tissue and peripheral blood samples were obtained from four consented patients with NKTCL. The inventors further identified paraffin-embedded tissue blocks from 61 patients with NKTCL for validation. The diagnosis of NKTCL was made according to the 2008 World Health Organization (WHO) classification of tumors of the hematopoietic and lymphoid tissues (6). All samples were centrally reviewed by Singhealth hematopathologists. This study was approved by the SingHealth Centralized Institutional Review Board, Singapore.

DNA isolation

DNA of frozen tissue and paired blood samples was isolated using a DNeasy Blood and Tissue Mini Kit (Qiagen) and a QIAmp DNA Blood Midi Kit (Qiagen), respectively, according to manufacturer's instruction. For Formalin-Fixed Paraffin-Embedded (FFPE) samples, genomic DNA was extracted from one or two 10- μ M slices from each sample, paraffin was removed by xylene, tissues were washed twice with 100% ethanol, followed by overnight proteinase K digestion. DNA was then extracted using a DNeasy Blood and Tissue Mini Kit (Qiagen).

Detection of somatic mutations in Janus kinases

Genomic DNA of extracted from each sample was whole genome amplified with REPLI-g WGA Midi Kit (Qiagen). The coding exonic sequences of *JAK1*, *JAK2*, *JAK3* and *Tyk2* were sequenced by Sanger sequencing to detect mutations. Somatic origin of the mutations were confirmed when the mutations were only detected in the tumor but not in the paired blood sample.

The mutation sequence information is provided below in Table 1 and in the accompanying genomic DNA, protein and cDNA sequence listings (SEQ ID No.:1 to SEQ ID No.: 6), with the following sequence identifiers:

SEQ ID NO: 1 – JAK3 Wildtype genomic DNA

SEQ ID NO: 2 – JAK3 Wildtype amino acid sequence

SEQ ID NO: 3 – JAK1 Wildtype genomic DNA

SEQ ID NO: 4 – JAK3 Wildtype amino acid sequence

SEQ ID NO: 5 – JAK3 Wildtype cDNA

SEQ ID NO: 6 – JAK1 Wildtype cDNA

Table 1: JAK1 and JAK3 Mutation Information

	Protein	ORF ¹	cDNA	Gene
JAK1	Y652D ⁶	T1954G	T2203G ²	T124823G ⁴
JAK3	A572V ⁷	C1715T	C1815T ³	C15792T ⁵
JAK3	A573V ⁷	C1718T	C1818T ³	C15795T ⁵

Notes on Table 1:

- 5 ¹ORF: Open reading frame, coding region, starts from ATG
²NCBI Reference Sequence: NM_002227.2 (SEQ ID NO: 6)
³NCBI Reference Sequence: NM_000215.3 (SEQ ID NO: 5)
⁴NCBI Reference Sequence: NG_023402.1 (SEQ ID NO: 3)
⁵NCBI Reference Sequence: NG_007273.1 (SEQ ID NO: 1)
10 ⁶NCBI Reference Sequence: NP_002218.2 (SEQ ID NO: 4)
⁷GenBank: AAC50950.1 (SEQ ID NO: 2)

Mutation validation using high-resolution melt (HRM) and bi-directional Sanger sequence analysis

- 15 High-resolution melt (HRM) and Sanger sequencing were used to confirm the *JAK1* and *JAK3* mutations and validate their prevalence in the NKTCL patient population. Combining both methods will greatly improve the precision of mutation detection in FFPE samples. The JAK2 V617F mutation was also sequenced with both methods. The sequences of primer sets used for validation are listed in Table 2 (see below) and
20 included in the accompanying sequence listings under the corresponding identifiers.

Table 2: Validation Primer Sets Used for Sanger Sequencing and HRM Analyses

Primer Name	Primer Sequence (5' to 3')	Detection Method / Product Size	Sequence Identifier
JAK1_Seq_Exon14F	CTGGCCTGAGACATTCCTATG	Sanger Sequencing / 144 bp	SEQ ID NO.: 7
JAK1_Seq_Exon14R	TGAAAGAGAACACACTTACTC TCCAC		SEQ ID NO.: 8
JAK1_HRM_Exon14F	GCATGATGAGACAGGTCTCCC AC	HRM / 83 bp	SEQ ID NO.: 9

JAK1_HRM_Exon14R	GAGAACACACTTACTCTCCAC GTC		SEQ ID NO.: 10
JAK2_Seq_Exon12F	CAGCAAGTATGATGAGCAAGC	Sanger Sequencing / 121 bp	SEQ ID NO.: 11
JAK2_Seq_Exon12R	ACAGATGCTCTGAGAAAGGC		SEQ ID NO.: 12
JAK2_HRM_Exon12F	GCTTTCTCACAAGCATTTGG	HRM / 85 bp	SEQ ID NO.: 13
JAK2_HRM_Exon12R	GGCATTAGAAAGCCTGTAGT		SEQ ID NO.: 14
JAK3_Seq_Exon12F	GCAGGTCTGTGAGCACAAAAT	Sanger Sequencing / 167 bp	SEQ ID NO.: 15
JAK3_Seq_Exon12R	ACTGTCTCCAGCCATGCAC		SEQ ID NO.: 16
JAK3_HRM_Exon12F	CCACCTTCCCCAGTCATTC	HRM / 64 bp	SEQ ID NO.: 17
JAK3_HRM_Exon12R	GAGATGCCGGTACGACACTTG		SEQ ID NO.: 18

HRM Curve Analysis was used to discern the presence of the point mutations. SsoFast[™]EvaGreen Supermix® (Bio Rad, Cat. No. 172-5200) was used for amplification of target DNA fragments encompassing the relevant mutations from genomic DNA samples. HRM primers were used at a final concentration of 600 nM and reactions were performed with BioRad CFX96 Real time PCR Detection System in replicates. The cycling and melting conditions were as follows: one cycle of 98 °C for 2 min; 39 cycles of 98 °C for 5 sec, 58 °C for 10 sec; one cycle of 95°C for 30 min and a melt from 72 °C to 95 °C rising at 0.2 °C/sec. The HRM curves were analyzed with the Biorad Precision Melt Analysis[™] software. HRM difference curves deviating from the wild-type curve were considered to be harbouring a mutation.

For Sanger sequencing, PCR was performed with Invitrogen Platinum *Taq* Polymerase (Cat. No. 10966-083) and cycled at 95°C for 10 min; 39 cycles of 95 °C for 30 sec; 60 °C for 30 sec, 72 °C for 1 minute and a final extension of 72 °C for 10 min. Sequencing PCR was performed with ABI BigDye Terminator v3.1 (Cat. No. 4337457) and cycled at 96 °C for 1 min; 29 cycles of 96 °C for 10 sec; 50 °C for 5 sec & 60 °C for 4 min. The resulting products were run on ABI 3730 DNA Analyzer.

Cell lines, cell viability and apoptosis assays

NK-S1 is a cell line established from a previously described NKTCL xenograft(7). The xenograft was derived from metastatic tumor of the testis from the same patient found to have both JAK1 (Y652D) and JAK3 (A572V) mutations. NK-S1 was cultured for more than 60 passages in DMEM medium supplemented with antibiotics, heat-inactivated FBS (10%) and equine serum (ES) (10%). Phenotypic analysis showed

- surface CD3⁺CD56⁺, and Granzyme B⁺ by intracellular staining. NK-S1 NKTCL cell line was sequenced and confirmed to carry homozygous mutation for JAK3 A572V, as well as a mutation on *JAK1* codon 652. KHYG-1 is an IL-2 dependent aggressive NK leukemia cell line obtained from the Japanese Collection of Research Bioresources, and it was cultured in RPMI medium supplemented with antibiotics, heat-inactivated FBS (10%), ES (10%) and 200 IU/ml of recombinant human IL-2 (Proleukin, Novartis)⁷. KHYG-1 was sequenced and found to be wild-type for *JAK3* codon 572 and 573, and *JAK1* codon 652 and 658. K562 (CCL-234, ATCC) is a chronic myeloid leukemia (CML) cell line positive for the BCR-ABL fusion gene.
- To study the sensitivity of NKTCL cell lines to CP-690,550 (Selleck Chemical, Cat. No. S5001), a pan-JAK inhibitor, cells were seeded at 2×10^4 cells/100 μ L/well in 96-well plates and treated with CP-690,550 at various concentrations or with vehicle control. The viability was evaluated by MTS assay using a CellTiter 96® AQueous Non-Radioactive Cell Proliferation Assay Kit (Promega), absorbance was read at both 490 nm and 650 nm (as reference). The extent of drug-induced apoptosis was evaluated by Annexin V-FITC (BD Biosciences) staining. Acquisition of the data was performed on a FACSCalibur flow cytometer (BD Biosciences).

Immunoblotting

- Cells were harvested at indicated time intervals after incubation with or without recombinant human IL-2 (Proleukin, Novartis), or in the presence or absence of CP-690,550. Cells were washed with ice-cold phosphate buffer saline (PBS) and lysed in 50 μ L of ice-cold RIPA buffer [25 mM Tris-HCL, pH 7.6, 150 mM NaCl, 1% Nonidet P-40, 1% sodium deoxycholate, 0.1% SDS, 1X Phosphatase Inhibitor (Cat. No. 78420, Thermo Fisher Scientific), 1X Protease Inhibitor (Cat. No. 12978000, Roche Diagnostics) and 1 mM Sodium Orthovanadate]. Thereafter, cell lysates were sonicated twice on ice for 10 seconds, 20 Amp and agitated on ice for another 15 minutes. After centrifugation at 14,000 g for 15 minutes at 4°C, supernatants were removed and protein concentration was determined using Bio-Rad Protein assay (Cat. No. 500-0006, Bio-Rad Laboratories). Protein samples were separated on a 5% stacking and 8% resolving SDS-polyacrylamide gel using Mini-PROTEAN Tetra Electrophoresis System (Cat. No. 165-8006, Bio-Rad Laboratories) and transferred onto 0.45 μ M nitrocellulose membrane (Cat No. 162-0115, Bio-Rad Laboratories) using Mini Trans-blot Electrophoretic Transfer Cell (Cat. No. 170-3930EDU, Bio-Rad

Laboratories) at 100V for 120 minutes. Membranes were blocked with 5% Milk in PBST, followed by overnight incubation of rabbit anti-phospho-jak1 (Tyr 1022/1023) (Cat. No. 3331, Cell Signaling), rabbit anti-phospho-JAK3 (Tyr 980/981) (D44E3) (Cat. No. 5031, Cell Signaling), mouse anti-Phospho-Stat5 (Tyr 694) (Cat. No. 9356, Cell Signaling) and rabbit anti-phospho-stat3 (Tyr 705) (D3A7) (Cat. No. 9145, Cell Signaling) in 5% BSA and 5mM sodium orthovanadate in PBST. were visualized using enhanced chemiluminescence (ECL) (Cat. No. 3407, Thermo Fisher Scientific, and Cat. No. RPN 2132, Amersham). Antibody for Jak1 (6G4) (Cat. No. 3344, Cell Signaling), Jak3 (Cat. No. 3775, Cell Signaling), Stat5 (Cat. No. 9363, Cell Signaling) and β -actin (Cat. No. A1978, Sigma) were used to detect unphosphorylated proteins or as a loading control. All antibodies were used at the recommended dilutions.

Results

Sanger sequencing was used to sequence the exonic regions of *JAK1*, *JAK2*, *JAK3* and *Tyk2* in fresh frozen tumor and blood specimens from four patients with Extra nodal NKTCL. Two *JAK3* mutations, A572V (p.Ala572Val, c.1715C>T) and A573V (p.Ala573Val, c.1718C>T), and a novel *JAK1* mutation, Y652D (p.Tyr652Asp, c.1954T>G) were identified. Interestingly, *JAK3* A572V and *JAK1* Y652D mutations were found on the same sample. Both *JAK3* mutations are both located at exon 12 on the JH2 pseudokinase domain (Fig. 1a), which is known to have an auto-inhibitory effect on the JH1 kinase domain. All three missense mutations identified in *JAK1* and *JAK3* were confirmed to be somatic in origin and predicted by Polyphen to be probably damaging.

Mutations identified were validated in FFPE samples of additional 61 patients with ENKTCL to confirm their prevalence. From this validation study, another 21 patients with *JAK3* mutations were identified by Sanger sequencing. In total, out of 65 NKTCL patients 23 patients (35.4%) were found with *JAK3* mutations (Fig. 1b). High Resolution Melt (HRM) analysis was performed on 40 FFPE samples and 14 *JAK3* mutants were detected (35%). Amongst the 23 patients with *JAK3* mutations, there were 17 heterozygous A572V, two homozygous A572V, two heterozygous A573V mutants, one homozygous A573V mutant and one patient had both an A572V and A573V heterozygous mutations (Fig. 1c-h). No additional *JAK1* Y652D mutant was found. In addition, no patients were found with the *JAK2* V617F (p.Val617Phe or c.1849G>T) mutation, which is recently found to be present in a large proportion of patients with

classic BCR/ABL-negative chronic myeloproliferative disorders and several patients with other clonal hematological cancers such as myelodysplastic syndrome and acute myeloid leukemia.

Discussion

5 *JAK3*^{A572V} Activating Mutations Confer Cytokine Independent Growth

IL-2 is an essential cytokine required for the proliferation and activation of NK cells (4). JAK1 and JAK3 mediate IL-2 receptor signaling through phosphorylation of STAT transcription factors (5). In line with the functional importance of the activating *JAK3* mutations identified, we tested if *JAK3* mutations could confer IL-2 independent growth to the NKTCL cell line (NK-S1) that harbors a homozygous *JAK3*^{A572V} mutation. *JAK*-mutant (NK-S1) cells showed IL-2 independent growth (Fig. 3) and constitutive phosphorylation of both JAK3 and STAT5 (Fig. 2a). In contrast, *JAK3*-wild type KHYG-1 cells were clearly IL-2 dependent (Fig. 3 and 2a). Importantly, NK-S1 cells treated with *JAK3* siRNAs exhibited a significant reduction in cell proliferation and also decreased autophosphorylation of JAK3 and STAT5, compared with cells treated with control siRNAs (Fig. 4A). Reciprocally, KHYG-1 cells transiently over-expressing a mutated *JAK3* (*JAK3*^{A572V}) cDNA demonstrated IL-2 independent proliferation and autophosphorylation of JAK3 and STAT5 (Fig. 4B). These results indicate that the *JAK3* activating mutations are gain of function alleles and contribute to the constitutive activity of the JAK/STAT pathway in an IL-2 independent manner.

This study demonstrated that JAK mutations confers cytokine independent growth in a NKTCL cell line established from xenograft derived from patient sample harboring both *JAK3* A572V and *JAK1* Y652D mutation. NK-S1 showed IL-2 independent growth (Fig. 3), constitutive JAK3 and STAT5 phosphorylation (Fig. 2a) in contrast to the wild-type KHYG-1, which was tested not to carry *JAK1* and *JAK3* mutations identified (Fig. 2a).

Effects of CP-690,550 on NKTCL Cell Lines

The ability of CP-690,550, a pan-JAK inhibitor, to suppress the JAK-STAT pathway, was evaluated. Because activated JAK proteins directly phosphorylate STAT proteins, the *JAK*-mutated cell line (NK-S1) and the wild-type NKTCL cell line (KHYG-1) were treated with increasing concentrations of CP-690,550 and analyzed the pSTAT5 by immunoblotting (Figure 2b). Both the NK-S1 and KHYG-1 cell lines showed a dose-

dependent reduction of pSTAT5 (Fig. 2a) and reduced cell viability (Fig. 2b) upon treatment with the inhibitor. CP-690,550 did not inhibit pSTAT5 in the control K562 cell lines since its STAT5 phosphorylation is independent of activated JAK3 (Fig. 2b). The reduced viability of NK-S1 correlated with increased apoptosis as shown by Annexin V staining (Fig. 2c).

In summary, through exonic sequencing of Janus kinases (JAK) of Natural-killer/T-cell lymphoma (NKTCL) JAK3 A572 and A573V and JAK1 Y652D mutations have been identified in NKTCL patients, and the prevalence of JAK3 mutations was validated to be 35.4%. A mutant NKTCL cell line harboring JAK3 A572V mutation showed IL-2 independent growth and constitutive JAK3 and STAT5 phosphorylation suggesting an oncogenic role for mutations in the corresponding nucleic acid domain. In vitro study suggests that pan-Jak inhibitor could be a new therapeutic agent for NKTCL patients. CP-690,550, a pan-JAK-inhibitor, was shown to reduce cell viability and cause apoptosis in both JAK3 wild-type (KHYG-1) and mutant (NK-S1) cell lines. KHYG-1 is an IL-2 dependent NKTCL cell line, thus its sensitivity to pan-JAK inhibitor.

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CLAIMS

1. A method for predicting Natural Killer T-Cell Lymphoma (NKTCL) susceptibility and/or diagnosing NKTCL in a subject, comprising analysing an isolated blood and/or cell sample from the subject by (i) testing for the genotype of said subject
5 for the *JAK1* and/or *JAK3* gene or (ii) testing for whether said subject expresses a wildtype or mutant *JAK1* and/or *JAK3* protein, wherein the presence of a mutant *JAK1* and/or *JAK3* gene or a mutant *JAK1* and/or *JAK3* protein indicates that the subject is at risk of developing and/or has NKTCL.
2. The method according to claim 1, wherein:
10 a wildtype *JAK3* gene comprises a sequence with NCBI reference NG_007273.1 and the mutant *JAK3* gene comprises a substitution of C with T at nucleotide 15792 and/or a substitution of C with T at nucleotide 15795 of said sequence with NCBI reference NG_007273.1; and/or
a wildtype *JAK1* gene comprises a sequence with NCBI reference NG_023402.1
15 and the mutant gene comprises a substitution of T with G at nucleotide 124823 of said sequence with NCBI reference NG_023402.1.
3. The method according to claim 1 or 2, wherein:
the wildtype *JAK3* protein comprises a sequence with GenBank reference AAC50950.1 and the mutant *JAK3* protein comprises a substitution of A with V at
20 amino acid 572 and/or a substitution of A with V at amino acid 573 of said sequence with GenBank reference AAC50950.1; and/or
the wildtype *JAK1* protein comprises a sequence with NCBI reference NP_002218.2 and the mutant *JAK1* protein comprises a substitution of Y with D at amino acid 652 of said sequence with NCBI reference NP_002218.2.
- 25 4. The method according to any one of the preceding claims, wherein when the method comprises testing for the genotype of said subject, the method comprises isolating nucleic acid molecules from an isolated blood and/or cell sample from the subject for said testing.

5. The method according to any claim 4, wherein said testing is performed on genomic DNA, mRNA and/or cDNA;
6. The method according to claim 4 or 5, wherein the testing comprises sequence analysis, restriction fragment length polymorphism analysis, hybridization, polymerase chain reaction (PCR) and/or reverse transcription PCR.
7. The method according to any one of the preceding claims, wherein when the method comprises testing for whether said subject expresses a wildtype or mutant JAK1 and/or JAK3 protein, the method comprises isolating at least one protein from an isolated blood and/or cell sample from the subject for said testing.
8. The method according to claim 7; wherein the testing comprises protein sequencing and/or antibody detection methods.
9. A method for screening for an agent capable of treating NKTCL or for an agent capable of reducing the activity of at least one JAK protein, the method comprising:
 - (i) providing a NKTCL cell line comprising a mutant *JAK1* and/or *JAK3* gene;
 - (ii) contacting the NKTCL cell line with the agent; and
 - (iii) determining the effect of the agent on the mammalian NKTCL cell line;
 wherein the ability of the agent to reduce the viability, growth and/or multiplication and/or increase apoptosis of the NKTCL cell line is indicative of the ability of the agent to treat NKTCL or to reduce the activity of a JAK1 and/or JAK3 protein.
10. The method according to claim 9, wherein the NKTCL cell line comprises at least one of the following mutations:
 - (i) a substitution of C with T at nucleotide 15792 of a sequence with NCBI reference NG_007273.1;
 - (ii) a substitution of C with T at nucleotide 15795 of a sequence with NCBI reference NG_007273.1; or

- (iii) a substitution of T with G at nucleotide 124823 of a sequence with NCBI reference NG_023402.1.

11. A non-human NKTCL animal model comprising at least one of the following mutations:

- 5 (i) a substitution of C with T at nucleotide 15795 of a sequence with NCBI reference NG_007273.1; or
- (ii) a substitution of T with G at nucleotide 124823 of a sequence with NCBI reference NG_023402.1.