

Chapter 11

FLT3 in AML

Naval Daver and Farhad Ravandi

Abstract FMS-like tyrosine kinase 3 (FLT3) receptor and its ligand play a significant role in human hematopoiesis and the proliferation and malignant transformation of primitive hematopoietic cells. *FLT3* mutations are observed in approximately 30% of adult AML, 1–3% of adult B-ALL and 2–5% of MDS patients. Binding of *FLT3* ligand to *FLT3* receptor results in autophosphorylation and activation of downstream pathways that promote cell proliferation including the MAPK/ERK, Pi3K/AKT, signal transducer activator of transcription (STAT5), and BCL2-associated X protein (BAX) pathways. There are two major types of *FLT3* mutations: The *FLT3* internal tandem duplication (ITD) results from duplication and insertion of a fragment of the juxtamembrane domain coding sequence, whereas the less common tyrosine kinase domain (TKD) results from a missense point mutation within the activation loop of the second TKD. Studies suggest that patients with *FLT3*-ITD have significantly elevated peripheral blood white cell counts and increased bone marrow blasts at diagnosis. Furthermore, they have a significantly higher induction death rate, increased relapse risk, inferior event-free survival, and decreased overall survival. Recent studies have further indicated that *FLT3*-ITD mutations may be a significant prognostic indicator in patients with AML and diploid karyotype, but not in those with core-binding factor AML or AML with unfavorable cytogenetics. Also, presence of *FLT3*-ITD mutation may be a negative prognostic marker, not only at diagnosis but also at first relapse. Several small-molecule FLT3 inhibitors are currently in clinical trials and may improve responses for patients with *FLT3*-mutated AML.

Keywords FLT3 mutation · AML · FLT3 inhibitors · FLT3 ligand · FLT3 receptor

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11.1 Introduction

Leukemogenesis results from dysregulation of pathways that regulate proliferation, differentiation, and cell death of hematopoietic cells (Stirewalt and Radich 2003). The *FMS-like Tyrosine Kinase 3* (FLT3) receptor and its ligand have been shown to play a significant role in human hematopoiesis and the survival, proliferation, and malignant transformation of primitive hematopoietic cells (Lyman et al. 1993a; Zeigler et al. 1994; Hirayama et al. 1995; Hudak et al. 1995; Piacibello et al. 1995). In normal human cells, *FLT3* is predominantly expressed on early myeloid and B-lymphoid progenitors. *FLT3* expression on leukemic cells reflects this expression. Subsequently, high levels of FLT3 receptor expression are seen in 70–100% of cases of AML (Nakao et al. 1996), a vast majority of the cases of progenitor B cell acute lymphoblastic leukemia (B-ALL), some cases of T-ALL, and chronic myeloid leukemia (CML) in lymphoid blast phase (Carow et al. 1996; Rosnet et al. 1996; Drexler 1996). Additionally, activating mutations in *FLT3* are observed in approximately 30% of adult AML patients (Odenike et al. 2011), 1–3% of adult B-ALL patients, (Xu et al. 1999) and 2–5% of myelodysplastic syndrome (MDS) patients (Horiike et al. 1997; Yokota et al. 1997).

11.2 Class II Receptor Tyrosine Kinases

The *W* (dominant White spotting) locus resulting in white spots on the bellies of afflicted mice was first described in the early 1900s (Russell 1979). Subsequently, the *W* locus was isolated to chromosome 5, and numerous allelic variants involving multiple organ systems were identified. The *W* locus was found to encode a tyrosine kinase receptor known as *c-kit* (Geissler et al. 1988; Chabot et al. 1988). This discovery led to the identification of a new group of receptors for signaling molecules called the receptor tyrosine kinase (RTK) family of proteins. RTKs and their signaling ligands play a central role in hematopoiesis (Ullrich and Schlessinger 1990). FLT3 is a member of the class III RTK family (Rosnet et al. 1993a; Small et al. 1994). Other members of this family include receptors for colony-stimulating factor 1 (CSF-1) (Coussens et al. 1986; Rothwell and Rohrschneider 1987; Woolford et al. 1988; Sherr 1990) and steel factor (Williams et al. 1992), respectively, encoded by the *FMS* and *KIT* (Wagner and Alexander 1991) proto-oncogenes and the two receptors for platelet-derived growth factor receptors (PDGFR α and β) (Yarden et al. 1986; Matsui et al. 1989). The RTKs have significant sequence homology. Each of these receptors is approximately 1000 amino acids in length, has five immunoglobulin-like extracellular domains, a transmembrane (TM) domain, a juxtamembrane (JM) domain, and a split intracellular catalytic domain that phosphorylates tyrosine residues in specific target proteins after activation of the receptor by the ligand (Lyman and Jacobsen 1998).

11.2.1 *FLT3 Gene*

FLT3, also known as FLK-2 (fetal liver kinase-2) and STK-1 (human stem cell kinase-1) was first cloned by Mathews et al. in enriched mouse fetal liver cells in 1991 (Mathews et al. 1991). They described *FLT3* as a novel RTK related to the *W* locus gene product *C-KIT*. They found the *FLT3* RTK to be specifically expressed in stem cells and early uncommitted hematopoietic progenitor cells, with no expression in more mature cells. Almost simultaneously, Rosnet et al. also isolated and characterized murine *FLT3*. They found the gene to be expressed in placenta, in various adult tissues including gonads and brain, and in hematopoietic cells in mice (Rosnet et al. 1991). This was followed closely by the cloning and description of human *FLT3* gene in 1993 (Rosnet et al. 1993a). The human *FLT3* gene located on chromosome 13q12 has 85 % amino acid sequence homology with mouse *FLT3* (Rosnet et al. 1993b). The *FLT3* gene is expressed in precursors of both myeloid and B-lymphoid lineage (Rosnet et al. 1996; Brasel et al. 1995; Turner et al. 1996). Expression is usually restricted to early precursors, including CD34⁺ cells with high levels of CD117 (*C-KIT*) expression (Rosnet et al. 1996; Rasko et al. 1995). Cells of erythroid and megakaryocytic series do not express *FLT3* gene (Gabbianelli et al. 1995; Ratajczak et al. 1996). The *FLT3* gene is also expressed by placenta, liver, spleen, thymus, and gonads (deLapeyriere et al. 1995; Maroc et al. 1993).

11.2.2 *FLT3 Ligand*

The *FLT3* ligand (*FLT3L*) was cloned by Lyman et al. in 1993. (Lyman et al. 1993a) The *FLT3L* is a type 1 TM protein, which contains an amino-terminal signaling peptide, four extracellular helical domains, spacer and tether regions, a TM domain, and a small cytoplasmic domain. (Lyman and Jacobsen 1998; Lyman et al. 1994b) Ligand activity resides in the extracellular domain with the intracytoplasmic domain playing minimal to no role in *FLT3* activation and function. (Lyman et al. 1993b) The ligand can also be released as a soluble homodimeric protein. Both the soluble form and the TM form are capable of activating the *FLT3* receptor (Hannum et al. 1994; Lyman et al. 1995). The *FLT3L* is expressed by hematopoietic cells (spleen, thymus, and bone marrow), placenta, lung, colon, kidney, prostate, ovary, testis, and heart. Of note, the brain does not seem to express *FLT3L*. In the bone marrow microenvironment, *FLT3L* is expressed predominantly by myeloid cells, B and T lymphoid cells, (Brasel et al. 1995) and bone marrow fibroblasts (Lisovsky et al. 1996a). *FLT3L* on its own is not efficient at inducing hematopoietic progenitor cell proliferation (Lyman 1995; Lyman et al. 1994a; Ebihara et al. 1997; Ray et al. 1996). However, in synergy with other growth factors, it can act as a potent stimulus for CD34⁺ progenitor proliferation in vitro and in vivo (Rasko et al. 1995; Rusten et al. 1996; McKenna et al. 1995; McKenna 2001; Maraskovsky et al. 2000; Broxmeyer et al. 1995; Hunte et al. 1996).

11.2.3 *FLT3 Receptor*

Unlike the c-kit receptor which is ubiquitously distributed and found in high concentration on cells of both normal and malignant tissue, the FLT3 receptor has a more restricted distribution and expression pattern. (Matthews et al. 1991; Rosnet et al. 1991; Hannum et al. 1994; Birg et al. 1992; DaSilva et al. 1994) *FLT3* messenger RNA (mRNA) is found in early hematopoietic cells and in human myeloid leukemia blasts. Turner et al. first characterized FLT3 receptors on normal and leukemic human marrow cells in terms of receptor density, binding affinity, dimerization, and ligand internalization (Turner et al. 1996). In comparison to c-kit, the cells that expressed FLT3 receptors expressed relatively lower number of receptors on the cell surface. The highest expression was found in human myeloid cell lines. This is consistent with prior studies that demonstrated expression of FLT3 receptor mRNA predominantly on cells of myeloid/monocytic and pre-B cell lineage (Brasel et al. 1995; Meierhoff et al. 1995). Human erythroleukemia cells, mast cells, and megakaryocytes which strongly express c-kit receptors (Turner et al. 1995) have little to no FLT3 receptor surface expression (Ratajczak et al. 1996; Lyman et al. 1994a).

FLT3 receptors are usually found as monomers on the plasma membrane in an inactive state. Like other members of the class of proteins (Li and Stanley 1991; Blume-Jensen et al. 1991), ligand binding results in dimerization of the membrane-bound FLT3 and exposure of the TKD phosphoryl acceptor sites (Turner et al. 1996). Dimerization further stabilizes the conformational change of membrane-bound FLT3, resulting in enhanced activation of the receptor (Weiss and Schlessinger 1998). After dimerization, FLT3 dimer-phosphate complex is internalized and either degraded or recycled, whereas the FLT3L is usually degraded. Internalization usually begins at 5 min and reaches a peak at 15 min. Degradation products can be detected as early as 20 min post stimulation (Turner et al. 1996). Thus, similar to other RTKs, the entire process of activation, internalization, and degradation of FLT3 occurs within a matter of minutes.

11.3 *FLT3 Signal Transduction*

Binding of FLT3L to FLT3 receptor results in autophosphorylation of the receptor and sets off a chain of events resulting in downstream signaling of pathways that promote cell proliferation and inhibit apoptosis. These include the mitogen-activated protein kinase/extracellular signal-related kinase (MAPK/ERK), Pi3K/AKT, signal transducer activator of transcription (STAT5), and BCL2-associated X protein (BAX) (Srinivasa and Doshi 2002; Zhang and Broxmeyer 1999,2000; Zhang et al. 1999, 2000; Lisovsky et al. 1996b). Initial studies on FLT3 signal transduction were done prior to cloning of the FLT3L. These studies used a chimeric receptor containing the extracellular binding domains of human FLT3 with the intracellular catalytic domains of murine FLT3 (Dosil et al. 1993; Rottapel et al.

1994). The chimeric receptor was able to undergo independent activation in the absence of other growth factors. This activation resulted in direct association of the chimeric receptor with Src-homology 2 (SH2) domain of the p85 subunit of phosphatidylinositol 3-kinase (Pi3K), growth factor receptor-bound protein 2 (Grb2), and SH2-domain-containing inositol phosphatase (SHIP) (Marchetto et al. 1999). These associations led to phosphorylation of downstream effectors involved in the Ras-Raf-Mek-Erk pathway (Zhang et al. 1999) and other modulators of hematopoiesis such as Vav (Bustelo et al. 1992).

Cloning of the murine and human FLT3L has greatly enhanced our understanding of the signal transduction process (Lyman et al. 1993a, 1994b). Unlike chimeric FLT3 receptors, the wild-type (WT) human FLT3 did not directly associate with the p85 subunit of PI3K (Zhang and Broxmeyer 1999). Instead, it associates with numerous proteins including GRB2, GAB2, SHIP, SHP2, CBL, and CBLB (CBL-related protein) that subsequently bind to and activate p85 (Zhang and Broxmeyer 1999; Zhang et al. 1999). These proteins in association with FLT3 can stimulate the Ras-Raf-Mek-Erk pathway. Further research supports the hypothesis that the association between FLT3 and RAS pathways may play a crucial role in leukemogenesis (Lisovsky et al. 1996b; Nakagawa et al. 1992). The activated FLT3L-receptor complex can also activate STAT 5a, but not STAT 1 through 4 or STAT 5B. FLT3-mediated STAT activation occurs independent of Jannus Kinase (JAK) (Zhang et al. 2000). Thus, FLT3 plays a crucial role in differentiation, proliferation, and apoptosis of hematopoietic cells.

11.3.1 FLT3 in Immune Function

FLT3 seems to play an important role in immune regulation. Disruption of FLT3 gene in mice results in significant reduction in the number of dendritic cells, natural killer (NK) cells, and myeloid and B-lymphoid progenitors with resultant impairment of the immune system (McKenna et al. 2000). Conversely, FLT3L stimulation promotes dendritic-cell development resulting in the clonal expansion of dendritic cells in the bone marrow, lymph nodes, and peripheral blood (Morse et al. 2000; Manfra et al. 2003). FLT3 in synergy with granulocyte-macrophage colony-stimulating factor (GM-CSF) and interleukin-4 (IL-4) can induce dendritic cell differentiation. Similarly, FLT3 can stimulate IL-2 resulting in proliferation of an early CD34⁺ NK-cell progenitor (Maraskovsky et al. 1996; Yu et al. 1998). Attempts to harness the dendritic and NK cell proliferative activity of FLT3L for antineoplastic approach have met with mixed success. In murine models, FLT3L has been used successfully to induce tumor shrinkage in murine fibrosarcoma, lymphoma, melanoma, and breast cancer models (Lynch et al. 1997; Esche et al. 1998; Chen et al. 1997). Human studies have yielded mixed results. In a phase 1 human study, 11 patients with cancer (10 breast and 1 ovarian) were vaccinated with HER2/NEU peptide followed by infusion of FLT3L alone or FLT3L in combination with GM-CSF. No significant antitumor effect was noted; however, some patients developed autoimmune

manifestations possibly due to FLT3L-mediated expansion of interferon- γ T-cells (Disis et al. 2002).

11.3.2 FLT3 in Normal Hematopoiesis

Activated FLT3, both independently and in concert with other growth factors, plays a significant role in the proliferation and differentiation of primitive hematopoietic cells (Ray et al. 1996; Rusten et al. 1996; Veiby et al. 1996). Surprisingly, targeted disruption of FLT3 in mice resulted in healthy adult mice with relatively normal appearing hematopoietic populations (Mackarechtschian et al. 1995). However, further investigations confirmed deficiencies in pro-B cell and pre-B cell compartments. Also, transplantation experiments have shown that FLT3 nonfunctioning stem cells are unable to reconstitute myeloid and T-lymphoid cell lineages (Mackarechtschian et al. 1995). Similarly, mice with both FLT3 and C-KIT knocked out develop severe hematopoietic deficiencies (Mackarechtschian et al. 1995).

In normal human bone marrow, FLT3 is expressed predominantly on early myeloid and B-lymphoid precursors and fibroblasts (Brasel et al. 1995; Turner et al. 1996). Expression is restricted to early precursors, especially those with high CD34 expression (Rosnet et al. 1996; Rasko et al. 1995). FLT3 can promote differentiation of early hematopoietic precursors in the absence of other growth factors as shown by Gabbiani et al. (Gabbianelli et al. 1995; Rusten et al. 1996). In their experiments, FLT3 stimulation led to monocytic differentiation of hematopoietic receptors with muted proliferative response. However, FLT3-induced differentiation and proliferation of granulocyte-monocyte lineage is greatly enhanced in the presence of co-stimulatory growth factors such as IL-3, KIT-ligand, GM-CSF, G-CSF, and erythropoietin (EPO) (Gabbianelli et al. 1995; Rusten et al. 1996; Shah et al. 1996). Similarly, activated FLT3 in combination with IL-7 stimulates stromal-cell-independent expansion of human fetal pro-B cells and promotes differentiation of pro-B cells to pre-B cells (Namikawa et al. 1996). Furthermore, activated FLT3 in the presence of IL-3, IL-6, and IL-7 stimulates the growth and differentiation of early thymic progenitors of the T-cell lineage (Moore and Zlotnik 1997). As mentioned previously, FLT3 receptors are poorly expressed on erythroid and megakaryocytic precursors and FLT3 stimulation does not play a significant role in the proliferation or differentiation of these lineages (Gabbianelli et al. 1995).

11.3.3 FLT3 in Human Leukemia

Murine *FLT3* was cloned by Matthew et al. in 1991 (Matthews et al. 1991). This was followed closely by analysis and description of FLT3 expression in human leukemias by Berg et al. in 1992 (Birg et al. 1992). They performed northern blot analysis on RNA obtained from patients with AML, ALL, biphenotypic leukemia, and CML. Forty-four AML samples were analyzed to determine *FLT3* expression.

FLT3 gene was expressed in 41 of 44 samples (93%). This included eight of eight French–American–British (FAB) M1 cases, five of seven M2 cases, four of four M3 cases, nine of nine M4 cases, nine of ten M5 cases, four, two of two of the M7 subtype, and four of four of M0 (undifferentiated forms of AML of M1 subtype). Eight of eight B-ALL and four of six T-ALL samples also expressed *FLT3*. *FLT3* was also expressed in all of eight biphenotypic (hybrid) leukemia samples. Interestingly, *FLT3* transcript was detected in 0 of 11 chronic phase CML samples. In contrast, two of seven accelerated CML and twelve of sixteen blast-phase CML expressed *FLT3* transcript (Birg et al. 1992).

Further studies have confirmed that *FLT3* is expressed in 70–100% of cases of AML and B-ALL (Rosnet et al. 1996; Carow et al. 1996; Meierhoff et al. 1995; Birg et al. 1994; Stacchini et al. 1996). CLL cells and a majority of chronic phase CML phase cells do not express *FLT3*. Similarly, *FLT3* expression is uncommon in T-ALL (Uckun et al. 1997).

11.3.4 *FLT3* Mutations in Acute Myeloid Leukemia

As previously mentioned, high levels of *FLT3* receptor expression are seen in 70–100% of cases of AML (Nakao et al. 1996). Nakao et al. first described *FLT3*-ITD in AML in 1996. (Nakao et al. 1996) They observed *FLT3* expression in 22 of 30 (73%) AML and 39 of 50 (78%) ALL samples. Five patients with AML showed unexpectedly longer transcripts on primer amplification of the TM through JM domain. On genomic amplification, these patients with abnormal *FLT3* transcripts also expressed abnormal longer polymerase chain reaction (PCR) products. Sequence analysis of these abnormal reverse transcriptase-polymerase chain reaction (RT-PCR) products revealed tandem duplication of partial sequences. They concluded that ITD of the *FLT3* gene is a somatic change detected preferentially in AML and may play a significant role in the pathology of AML. Subsequently, other groups of investigators have confirmed these findings (Xu et al. 1999; Horiike et al. 1997; Yokota et al. 1997; Kiyoi et al. 1997; Stirewalt et al. 2001; Meshinchi et al. 2001; Schnittger et al. 2002; Thiede et al. 2002; Iwai et al. 1997, 1999).

FLT3-ITD mutations are found in 15–35% of patients with AML (Xu et al. 1999; Horiike et al. 1997; Yokota et al. 1997; Kiyoi et al. 1997; Stirewalt et al. 2001; Meshinchi et al. 2001; Schnittger et al. 2002; Thiede et al. 2002; Iwai et al. 1997, 1999; Kottaridis et al. 2001). Pooled data from >5000 newly diagnosed AML patients show an overall *FLT3*-ITD incidence of 23% (Levis and Small 2003). *FLT3*-ITD mutations have been identified in MDS and ALL, albeit at a much lower frequency (Xu et al. 1999; Horiike et al. 1997; Yokota et al. 1997; Fenaux 2001). *FLT3*-ITD mutations most frequently occur in exons 14 and 15 (previously known as exons 11 and 12). The *FLT3*-ITD results from duplication of a fragment of the JM domain coding sequence and its insertion in a direct head-to-tail orientation. The length of the ITD can vary from 3 to >400 base pairs, but the reading frame is always preserved (Schnittger et al. 2002).

The second most common type of *FLT3* mutation is the TKD mutation, seen in 7–10% of patients with AML (Thiede et al. 2002). This results from a missense point mutation in exon 20 (previously known as exon 17) of the TKD (Thiede et al. 2002; Spiekermann et al. 2002). These include single base substitutions, small deletions, or insertions within the activation loop of the second TKD (Thiede et al. 2002; Yamamoto et al. 2001; Abu-Duhier et al. 2001). These mutations are also called “activation loop mutations” as they cause the tyrosine kinase loop to adopt an activated configuration allowing access to the kinase. Activating mutations have been identified at amino acid position Asp816 of KIT and were subsequently identified at corresponding locations in other RTKs, including RET and MET. In *FLT3*, the corresponding aspartate residue is located at position 835. The most common nucleotide substitution involves substitution of aspartic acid 835 with tyrosine (D835Y). Other less frequent substitutions included Asp835Val, Asp835His, Asp835Glu, and Asp835Asn (Yamamoto et al. 2001). *FLT3*-TKD mutations have been identified in MDS (3%) and ALL (3%) (Yamamoto et al. 2001; Griffin 2001). Usually, the *FLT3*-ITD and *FLT3*-TKD mutations occur independently, although combined expression has been identified on rare occasions (Thiede et al. 2002; Meshinchi et al. 2003).

More recently, an additional class of *FLT3* mutations has been identified in AML patients in which isoleucine 836 is either deleted (*FLT3*-Ile836del) or substituted with methionine and arginine (*FLT3*-Ile836Met + Arg) (Thiede et al. 2002).

Thus, approximately 25–40% of the patients with AML will harbor *FLT3* mutations (ITD or TKD), making *FLT3* mutation one of the most frequent recurring molecular aberrations in this disease.

11.4 Incidence and Demographics of *FLT3*-ITD Mutations

FLT3-ITD mutations are clinically relevant in AML. The frequency of *FLT3* mutations in pediatric AML is 10–15% (Xu et al. 1999; Meshinchi et al. 2001; Iwai et al. 1999; Kondo et al. 1999), suggesting that these mutations occur more frequently in adults. The frequency seems to increase with age with a higher incidence of *FLT3*-ITD mutations noted in elderly populations (Stirewalt et al. 2001). *FLT3* mutations are found in all FAB subtypes; however, they are found with increased frequency in FAB M5a and M5b and are relatively uncommon in M2 and M6 subtypes (Thiede et al. 2002). *FLT3*-ITD mutations are more frequent in patients with normal cytogenetics, and those with t(15:17) and t(6:9) (Thiede et al. 2002; Slovak et al. 2000). Thiede et al. reported that *FLT3* mutations were three times more frequent in patients with normal karyotype. They noted that *FLT3*-ITD mutations were significantly more frequent in patients with t(15:17) and occurred in nearly 30% of the patients harboring this translocation (Thiede et al. 2002). Similarly, other investigators have reported *FLT3*-ITD incidences of 20.3, 28.6, and 36% in patients with t(15:17) (Kiyoi et al. 1997; Kottaridis et al. 2001; Schnittger et al. 2000). However,

patients with core-binding factor leukemias (i.e., t(8:21) and inv(16) mutations) have a low incidence of *FLT3*-ITD mutations (Kottaridis et al. 2001). As mentioned previously, *FLT3* mutations are occasionally identified in MDS and ALL (Xu et al. 1999; Horiike et al. 1997; Yokota et al. 1997; Fenaux 2001). As regards other hematopoietic malignancies, *FLT3* mutations have been detected in a very small number of cases of CML, adult T-cell ALL, CLL, lymphoma, and multiple myeloma (Xu et al. 1999; Horiike et al. 1997; Iwai et al. 1997). *FLT3* mutations have not been identified in solid tumors (Baldwin et al. 2001) or in normal hematopoietic cells (Ishii et al. 1999).

11.5 Biological Activity of *FLT3*-ITD Mutations in AML

FLT3-ITD mutations result in ligand-independent dimerization and autophosphorylation resulting in constitutive tyrosine kinase activation and activation of signaling pathways downstream of *FLT3* (Hayakawa et al. 2000; Mizuki et al. 2000; Kiyoi et al. 2002). Although the length of the duplicated sequence may vary in humans, it is always in frame and results in elongation of the JM domain. Investigators have shown that *FLT3*-ITD-transfected murine IL-3-dependent cell lines, such as Ba/F3 and 32D, are able to proliferate independent of IL-3 when inoculated in syngeneic mice (Hayakawa et al. 2000; Zhao et al. 2002).

The exact mechanisms by which *FLT3*-ITD mutations promote constitutive activation remain unknown. It is known that binding of *FLT3*-ligand to extracellular domain of *FLT3* results in receptor dimerization and juxtaposition of intracellular cytoplasmic domains. This results in phosphorylation of tyrosine kinase residues on the JM domain and activation of downstream signal-transduction molecules such as SHC, MAP kinase, and STAT5a. In the absence of *FLT3*-ligand, the kinase activity is suppressed by tyrosine phosphatases that maintain the tyrosine residues in a dephosphorylated state. Investigators have recently elucidated the crystal structure of the auto-inhibited, dephosphorylated form of *FLT3* (Griffith et al. 2004) and shown that, in normal resting state, the JM domain inhibits the autophosphorylation of WT *FLT3* in absence of *FLT3*-ligand. However, in *FLT3*-ITD-mutated samples, dimerization can occur without the addition of ligand and can activate WT *FLT3* (Kiyoi et al. 2002). Additional experiments support this hypothesis by showing that tyrosine residues within the JM domain were not essential for the signal transduction in the length-mutated *FLT3* (Kiyoi et al. 2002).

FLT3-TKD mutations also result in constitutive activation of the *FLT3* receptor through stabilization of the activation loop in its open binding configuration. Interestingly, in mouse transplant models, *FLT3*-ITD or *FLT3*-TKD mutations alone are not sufficient to cause overt AML. In fact, *FLT3*-ITD mutations alone induce a myeloproliferative (Kelly et al. 2002) state and *FLT3*-TKD mutations alone induce an oligoclonal lymphoproliferative state (Grundler et al. 2005). Thus, the exact mechanism by which loss of repression and constitutive activation of the *FLT3* tyrosine kinase domains ultimately result in leukemogenesis remains poorly understood.

11.6 Clinical Relevance and Prognostic and Predictive Implications of FLT3-ITD Mutations in AML

Initial studies reported conflicting data regarding the prognostic and predictive values of *FLT3*-ITD mutations in AML. An initial study from Japan suggested that *FLT3* mutations did not influence the complete remission (CR) rate, but adversely predicted for overall survival (OS) (Kiyoi et al. 1999). A Dutch study found that *FLT3* mutations were associated with both lower CR rate and increased relapse rate (Rombouts et al. 2000). Subsequently, two large studies examined the clinical impact of *FLT3*-ITD mutations in a well-defined population. The first of these, by Kottaridis et al., included 854 patients, mostly 60 years of age or younger, treated in the United Kingdom Medical Research Council (UKMRC) in 10 and 12 trials (Kottaridis et al. 2001). Patients with *FLT3*-ITD had significantly elevated peripheral blood white cell counts and increased bone marrow blasts at diagnosis. Furthermore, they had a significantly higher induction death rate, increased relapse risk, inferior event-free survival (EFS), and decreased OS. There was a borderline association with a lower complete remission rate ($P=0.05$). Thiede et al. analyzed the clinical and prognostic significance of *FLT3*-ITD and *FLT3*-TKD mutations in 979 patients treated according to the AML-96 multicenter protocol of the German Suddeutsche Hamoblastose group (SHG) (Thiede et al. 2002). Again, both ITD and TKD mutations were associated with elevated leukocyte count and bone marrow blasts. Presence of *FLT3* mutations had no association with remission rates. Both ITD and TKD mutations were associated with significantly increased risk for relapse. *FLT3*-ITD mutations had significant association for disease-free survival (DFS) but not for OS, whereas the converse was true for TKD mutations. They also analyzed the effect of *FLT3* mutant to WT ratio on outcome. Patients below the age of 60 years with diploid cytogenetics had significantly shorter OS and DFS if their *FLT3* ratios were above the preselected threshold median value of 0.78. They had a relative risk of relapse of 1.6. On further sub-classifying patients on the basis of mutant to WT ratio, it was noted that patients with the highest ratio had the worst outcome with a highly significant shorter DFS and OS. Thus, in addition to the analysis for presence or absence of mutation, quantification of the mutant to WT *FLT3* alleles may provide additional prognostic information. Whitman et al. noted that patients with *FLT3*-ITD mutation with concomitant *FLT3* allelic loss had a worse prognosis than patients with WT *FLT3* or *FLT3* mutation without allelic loss (Whitman et al. 2001). In addition to quantification of mutant to WT burden, the presence of single versus multiple *FLT3*-ITD mutation variants may be of prognostic importance. Borthakur et al. noted that among patients with AML with diploid karyotype, CR duration was significantly longer in patients who had multiple *FLT3*-ITD mutations ($P=0.03$; Borthakur et al. 2012). However, OS and EFS did not seem to be affected by the number of *FLT3*-ITD mutation variants.

Although *FLT3*-ITD mutations are associated with worse outcomes in AML in general, the precise prognostic impact of these mutations in different cytogenetic subclasses of AML remains poorly understood. In a study by Santos et al., 481 AML

patients were divided into three cytogenetic subgroups: good risk/core-binding factor AML, normal karyotype AML and poor risk/unfavorable cytogenetics (Santos et al. 2011). The presence of *FLT3*-ITD mutation did not affect the EFS in patients with core-binding factor AML or poor risk cytogenetics. However, EFS was significantly worse for patients with normal karyotype AML who had the *FLT3*-ITD mutation ($P < 0.001$). Thus, the presence of *FLT3*-ITD mutations is a significant prognostic indicator in patients with AML and diploid karyotype, but not in those with core-binding factor AML or AML with unfavorable cytogenetics.

Recent data suggest that the presence of *FLT3*-ITD mutation may be associated with negative outcomes, not only at diagnosis but also at first relapse. Patients with *FLT3*-ITD mutations at relapse have a reduced likelihood of achieving second CR and a shortened survival (Ravandi et al. 2010). The feasibility of *FLT3*-ITD mutations at CR as a marker for minimal residual disease (MRD) has also been investigated. Nazha et al. noted that *FLT3*-ITD mutations were unstable and lacked consistency at follow-up (Nazha et al. 2012). Furthermore, *FLT3* mutations could occur for the first time at relapse. They concluded that *FLT3*-ITD is not a reliable marker for MRD monitoring in AML. Prognostic impact of *FLT3* mutations in the presence of other concomitant mutations also remains poorly understood. Among these, the best studied is the concurrent occurrence of *FLT3*-ITD and *NPM1* mutations. Presence of *FLT3*-ITD in patients with *NPM1* mutations abrogates the positive effects on CR rate and OS associated with mutated *NPM1* (Schnittger et al. 2005; Gale et al. 2008).

FLT3-ITD occurs more frequently in older patients with AML but does not adversely affect outcomes. In a large study by Stirewelt et al. *FLT3* mutations were identified in 34% of evaluable elderly patients with AML (Stirewelt et al. 2001). The *FLT3*-ITD mutation was associated with higher absolute white cell counts, higher peripheral blast percentages, normal cytogenetics, and less disease resistance. *FLT3* mutations were not associated with inferior clinical outcomes. It is possible that *FLT3* mutations may not be as significant a prognostic marker in the elderly AML population as in the younger patients due to the already poor outcome of the former.

The high frequency and negative impact of *FLT3* mutations, particularly the *FLT3*-ITD mutation, make it an ideal candidate for targeted therapy in AML patients. Several small molecule inhibitors have been developed and are currently in clinical trials. A full discussion of the mechanism of actions, efficacy, and side effects of a number of these drugs are included elsewhere in this publication. There is hope that such targeted therapies will improve responses without increasing toxicity in the treatment of patients with *FLT3*-mutated AML.

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