The myeloma-associated oncogene fibroblast growth factor receptor 3 is transforming in hematopoietic cells

Zhihua Li, Yuan Xiao Zhu, Elizabeth E. Plowright, P. Leif Bergsagel, Marta Chesi, Bruce Patterson, Teresa S. Hawley, Robert G. Hawley, and A. Keith Stewart

Translocations involving fibroblast growth factor receptor 3 (fgfr3) have been identified in about 25% of patients with myeloma. To directly examine the oncogenic potential of fgfr3, murine bone marrow (BM) cells were transduced with retroviral vectors containing either wild-type fgfr3 or an activated mutant form of the receptor, fgfr3-TD. Mice transplanted with FGFR3-TD–expressing BM developed a marked leukocytosis and lethal hematopoietic cell infiltration of multiple tissues within 6 weeks of transplantation. Secondary and tertiary recipients of spleen or BM from primary fgfr3-TD mice also developed tumors within 6 to 8 weeks. Analysis of the circulating tumor cells revealed a pre-B-cell phenotype in most mice, although immature T-lymphoid or mature myeloid populations also predominated in some animals. Enhanced lymphoid but not myeloid colony formation was observed in the early posttransplantation period and only interleukin 7 and FGFR3-responsive pre-B-cell lines could be established from tumors. Cell expansions in primary recipients appeared polyclonal, whereas tumors in later passages exhibited either clonal B- or T-cell receptor gene rearrangements. Mice transplanted with wild-type FGFR3-expressing BM developed delayed pro-B-cell lymphoma/leukemias approximately 1 year after transplantation. These studies confirm that FGFR3 is transforming and can produce lymphoid malignancies in mice. (Blood. 2001;97: 2413-2419)

© 2001 by The American Society of Hematology
Materials and methods

Construction of FGFR3 retroviruses

Two pcDNA3 plasmids containing full-length human complementary DNAs (cDNAs) of the wild-type or TDII mutant form of fgfr3 were obtained from Daniel J. Donoghue (San Diego, CA). The fgfr3 was released by restriction cutting with HindIII and SpeI, which also removed the 3’ untranslated region. The recessed 3’ termini of the cDNA fragments were filled and the fragments ligated into a HpaI/SnaBI-digested MINV retrovirus, containing the neomycin resistance gene as the selectable marker. The resulting vectors were termed MFINV-WT (wild-type fgfr3) and MFINV-TD (TDII K650 mutant fgfr3). The parental MINV vector (neo’ only) was used as a negative vector control.

Retroviral packaging lines

Twenty micrograms of the constructed retroviral vectors and the parental MINV vector were electroporated into 1.5 × 10^6 PA317 amphotropic packaging cells. After 48 hours the supernatant was collected, passed through a 0.45 mm filter, and overlaid on subconfluent monolayers of GP+ E 86 ecotropic packaging cells in the presence of 8 μg/mL polybrene (Sigma, St Louis, MO). On days 3 and 4 of culture this process was repeated. Transfected GP+ E 86 cells were selected in 1.2 mg/mL G418 (Sigma, St Louis, MO). On days 3 and 4 of culture this process was repeated. Transfected GP+ E 86 cells were selected in 1.2 mg/mL G418 (Sigma, St Louis, MO). On days 3 and 4 of culture this process was repeated.

Transduction of BM precursors and transplantation

Eight- to 10-week-old female BALB/c mice (Charles River Canada, Montreal, QB) were used as BM donors or transplant recipients. The transplantation of BM cells was performed as previously described. In brief, BM was flushed from the hind limbs of donor mice that had been injected 4 days previously with 150 mg/kg 5-flurorouracil (Roche, Laval, QC) in phosphate-buffered saline (PBS). Following erythrocyte lysis, nucleated cells were cultured in 100-mm dishes at a density of 5 × 10^6 cells/mL in prestimulation medium in the presence or absence of 2 mM EDTA, 1% penicillin/streptomycin (Life Technologies), 2 mM glutamine (IMDM; Life Technologies), 10% fetal calf serum (FCS; Life Technologies), 1% penicillin/streptomycin (Life Technologies), 2 mM glutamine (Life Technologies), 50 μM 2-mercaptoethanol (2-ME) supplemented with 10% conditioned medium from X630-rIL3 cells, 21 10% conditioned medium from GP+ E 86/WT (wild-type FGFR3), and GP+ E 86/TD (TDII mutant FGFR3).

Colony assay and cell line establishment

Pre-B-cell and myeloid colony-forming unit assays were performed on both in vitro cultured, retrovirus-engineered BM cells and on BM cells harvested from transplant recipient mice. Pre-B and myeloid colonies were cultured in Methocult M3630 or Methocult M3434 methylcellulose medium, respectively (Stemcell Technologies, Vancouver, BC) at 1 × 10^4 cells/mL per dish. In attempts to establish cell lines, retroviral-transduced BM cells or tumor-derived cells from mice were also cultured in IMDM, 10% FCS, 50 μM 2-ME, 2 mM l-glutamine, and 1% penicillin/streptomycin plus 10 ng/mL murine stem cell factor (mSCF), 10% mIL-3–conditioned medium, 2% mIL-6–conditioned medium, 2% murine granulocyte-macrophage colony-stimulating factor (mGM-CSF)–conditioned medium with or without 2 ng/mL recombinant mIL-7 (Pharmingen, Mississauga, ON). Cytokines were individually withdrawn to determine the dependence of cultured cells on growth factors.

Western blot analysis

Tissue samples were minced and incubated in RIPA buffer (50 mM Hepes pH 7.23, 150 mM NaCl, 50 μM ZnCl2, 50 μM NaF, 50 mM orthophosphate, 2 mM EDTA, 1% Nonidet P40, 0.1% sodium deoxycholate, 0.1% sodium dodecyl sulfate (SDS)) containing 2 μg/mL phenylmethylsulfonyl fluoride and 2 μg/mL orthovannadate while being pressed through a 70-μm nylon kines were individually withdrawn to determine the dependence of cultured cells on growth factors.

Flow cytometric analysis

Reagents used included antimouse B220–PE, CD43–FITC, CD3e–FITC, CD4–biotin, CD4–FITC, CD8a–PE, CD11b–FITC, CD16/CD32 (FcγIII/II receptor, Fc blocker) (all the preceding from Pharmingen); antimouse CD117–FITC (c-kit), CD25–biotin, streptavidin–PE–Cy5 (all 3 from Cedarlane, Hornby, ON); and antimouse IgM–FITC (Southern Biotechnology Associates, Birmingham, AL). Single-cell suspensions from tissues were prepared, washed in a solution of PBS, 0.1% NaF, 11.8% FCS and resuspended. Cells were analyzed by flow cytometry on a FACScan (Becton Dickinson) using CellQuest software.

Nucleic acid analysis

Southern blot analysis was carried out according to standard procedures. Probes included: a 1.4-kb BamHI–NcoI fragment of the neo gene (MINV); a 0.5-kb EcoRI–XhoI fragment of a murine T-cell receptor (TCR) (chain gene cDNA (pCOWβ,B) containing Cα2 constant region sequences; a 2.0-kb BamHI–EcoRI fragment of the murine IgH chain locus (pSV2-gpt-vBa-c) containing the Jα1 and Jα3 joining gene segments (provided by Dr Tak Mak, Amgen Institute, Toronto, ON). VIDJH rearrangements were assessed by using Vα and Vβ degenerate Vα and Vβ-specific primer and the 3’ Jα4 primer. Polymerase chain reaction (PCR) products were separated by gel electrophoresis, transferred to HydroB nylon membrane (Amersham), and hybridized with a Jα4 internal probe. Mutation analysis of FGFR3 was conducted using single-strand conformation polymorphism (SSCP) analysis as previously described.2

Results

Lethal hematopoietic tumors develop in mice transplanted with FGFR3-expressing BM

The BM from donor mice was transduced with either MFINV-WT (wild-type fgfr3), MFINV-TD (TDII K650 mutant fgfr3), or...
parental MINV (neo only) retroviruses to assess the potential effect of ectopic FGFR3 expression on hematopoiesis. The transduced BM cells from donor mice were injected intravenously into lethally irradiated recipient BALB/c mice. Compared to control mice, mice receiving BM expressing wild-type FGFR3 displayed only a transient leukocytosis. However, those mice receiving FGFR3-TD–expressing BM developed a leukemic blood picture with marked leukocytosis, polychromasia, and thrombocytopenia within 3 to 4 weeks after transplantation (Figure 1A). High white blood cell (WBC) counts of FGFR3-TD mice coincided with systemic illness and organ infiltration with immature hematopoietic cells. The morphology of the blood cells of FGFR3-TD mice suggested that there was an increase in the number of immature lymphoid cells (Figure 2).

Among 9 primary recipients of FGFR3-TD–expressing BM, 4 mice died between weeks 4.5 and 6 and the remaining 5 mice had to be killed at 6 weeks after transplantation due to morbidity. Postmortem analysis of FGFR3-TD mice revealed splenomegaly. Most of the FGFR3-TD mice also had enlarged thymuses and lymph nodes and exhibited fragile bones. Tumors arising in FGFR3-TD mice were then serially passaged by transferring either spleen or BM cells from the primary tumor-bearing mice to a second and subsequently third or fourth generation sublethally irradiated recipient mouse. All mice receiving serial transplants also became moribund within 6 to 8 weeks of transplantation. Necropsy of these mice revealed hematopoietic tumors infiltrating major organs.

In contrast, mice overexpressing FGFR3-WT were initially well but began to develop profound leukocytosis and became moribund around 1 year of age (Figure 1B). Of 4 FGFR3-WT mice alive at late reconstitution times, 2 looked in poor health and died spontaneously at 9 and 12 months, respectively. The remaining 2 animals became sick at about 12 months and were killed. PB films demonstrated very elevated WBC counts with a morphology resembling that of acute lymphoblastic leukemia in humans. Histologic examination of major organs at autopsy demonstrated infiltration of tissue with lymphoid cells. Three control mice transplanted with BM cells expressing parental MINV and left to live did not develop neoplasms up to 18 months after transplantation.

FGFR3-induced tumors are multilineage in nature but pre-B-cell leukemia/lymphomas predominate

Flow cytometry on the autopsied spleens of primary FGFR3-TD mice 6 weeks after transplantation revealed a marked increase in overall numbers of both B220+IgM+ pre-B cells and CD11b+ myeloid cells (Figure 3). Analysis of tumors arising in secondary and tertiary FGFR3-TD recipients demonstrated a predominant pre-B (B220+IgM+/CD43+/CD25+/c-kit−) cell population (Figure 4). In total, 9 of 13 secondary recipients of tumor cells from FGFR3-TD mice had a distinguishable pre-B cell population that infiltrated the BM, spleen, and thymus; in some cases, the malignant pre-B cells also invaded liver, kidney, and lung. In contrast, 3 of the secondary recipient mice displayed predominantly T-cell abnormalities (CD4+, CD8+, CD3−) (Figure 5) and one secondary recipient mouse had more than 90% B220+CD11b+ mature-appearing neutrophils within the PB and BM (not shown). One of the secondary recipients of FGFR3-TD–expressing cells displayed abnormalities in all 3 cell lineages: B cells, T cells, and myeloid cells (not shown). In wild-type FGFR3 mice, tumors
FGFR3 expression promotes pre-B-cell expansion

To further investigate the progenitor cell type targeted by the transforming capacity of FGFR3-TD, primary murine BM cells were transduced and divided for use in either transplantation models or for long-term in vitro suspension culture. In long-term culture, pre-B-cell colony frequency was increased after 4 weeks in comparison to controls and a predominant B220+ cell phenotype was evident by FACS analysis at week 7 (Figure 6A, B). In contrast no increase in myeloid colony formation was observed (not shown). A c-kit+B220− colony arising from FGFR3-TD–expressing cells was plucked and recultured in suspension. After 3 months in culture, a predominant B220+ B-cell population was again evident (Figure 6C). Finally, in mice receiving transplants, serial analysis of PB demonstrated the emergence of a pre-B-cell population only 2 weeks after transplantation (Figure 6D). The frequency of pre-B-cell colonies in the BM of FGFR3-TD–transplanted mice was increased at all tested time points above control levels (not shown).

The ability to establish permanent cell lines from the FGFR3-TD tumors was then investigated. Single-cell suspensions of tumor-infiltrated spleen or BM were cultured in varying combinations of cytokines in attempts to generate cell lines of multiple lineage. This method enabled the consistent establishment of only B220+/IgM+ /c-kit−IL−7– and FGF-responsive cell lines. Thus the available evidence suggests that FGFR3 predominantly targets an early B-cell progenitor population.

Signaling pathways in FGFR3-induced tumors

The FGFR3 protein was overexpressed in the tumor samples from FGFR3-TD and wild-type FGFR3 mice when compared to controls (Figure 7). Because transformation in FGFR3-WT–expressing mice was delayed, this suggested that cooperating oncogenes were involved or alternatively that the FGFR3-WT transgene had undergone activating mutation(s). Analysis of FGFR3-WT by SSCP failed to demonstrate any acquired mutations. As expected from previous studies, both STAT3 phosphorylation and bcl-xL expression were increased in FGFR3-expressing tumors (Figure 7). Of interest, global tyrosine phosphorylation patterns also varied between controls, wild-type FGFR3, and FGFR3-TD–induced tumors (Figure 8).

FGFR3-induced tumors can be serially passaged and exhibit clonal DNA rearrangements

Malignant cells of both T- and B-cell phenotype from the BM or spleen of secondary FGFR3-TD recipient mice could be passaged through third or fourth generation sublethally irradiated syngeneic recipients with hematopoietic tumors consistently developing. Primary tumors arising in wild-type FGFR3 mice could also be serially passaged.

To examine clonality of the tumors, the status of the IgH and TCRβ loci were investigated by Southern blots using IgH and TCR Cβ constant region probes, respectively. Southern blot analysis demonstrated rearranged IgH bands only in late generation B-cell tumors, whereas primary and secondary recipients only showed a germline configuration. JH was also rearranged in B220+ cell lines derived from both secondary and later recipient mice (Figure 9A). PCR analysis using degenerate primers for the IgH locus and subsequent Southern blotting with a JH probe
demonstrated that some FGFR3-TD secondary recipient mice had more intense IgH bands than primary recipients suggesting progressive clonal expansion of B-cell populations (data not shown). Taken together, these data demonstrated that initial cell expansions were polyclonal with clonal cell populations gradually emerging. Hybridization of the TCR Cβ probe indicated the presence of uniquely rearranged TCRβ bands only in mice that showed abnormal T-lineage cells by flow cytometry, whereas germline TCR configuration was detected in mice with B-cell tumors (Figure 9A). All tumors arising in wild-type mice receiving FGFR3 transplants exhibited germline JH configuration (Figure 9B).

Genomic DNA digested with EcoRI (cuts MFINV-WT once) and hybridized with a neo probe was used to enumerate the proviral copy number and further examine the clonality of the tumors. This analysis revealed that initial FGFR3-TD recipients had a single predominant population of retrovirus-transduced cells within a more diffuse polyclonal background. With serial transplantation, further clonal bands appeared, confirming the emergence of an oligoclonal population of retrovirus-engineered cells (Figure 9A). The presence of multiple clones was confirmed by the observation that a TCR gene rearrangement was present in TD5.1 but not TD5.2 mice. Both mice received an infusion of the same tumor cells from the TD5 mouse. In FGFR3-WT recipient mice, no emerging clonality was observed (Figure 9B).

Discussion

It has been reported that translocations into the IgH switch region on chromosome 14 are ubiquitous in MM.1-3 Fgr3 is one of the more
activating mutations. We have previously demonstrated that ectopic in vivo expression of activated mutant FGFR3 is capable of rapidly transforming hematopoietic cells, resulting in tumors in lethally irradiated recipient mice. To examine this issue we transplanted FGFR3-expressing BM cells into recipient mice. We therefore postulated that the ectopic overexpression of FGFR3 in primary hematopoietic cells correlates closely with the level of activation of FGFR3. We therefore correlated the level of activation of FGFR3 with the rate of transformation.

It has previously been shown that wild-type FGFR3 is generally not capable of transforming cells in short-term assays. For example, Li and colleagues demonstrated that the transmembrane region of wild-type FGFR3 is incapable of transforming NIH3T3 cells. Furthermore, expression of the cytoplasmic domain of wild-type FGFR3 as a chimeric receptor did not result in cellular transformation of NIH3T3 cells. The inability of wild-type FGFR3 to transform cells in such transient assays may reflect the weaker kinase activity of FGFR3 in comparison to other FGFRs and to mutant FGFR3. However, in vivo data demonstrate that wild-type FGFR3 is capable of transforming hematopoietic cells but only after a period of prolonged latency. Thus other events may be required to complement transformation, for example, acquisition of activating mutations of the gene as identified in myeloma patients. Nevertheless, no activating mutations of FGFR3 in late-onset tumors were evident in the mice analyzed here.

Previous studies of activated mutant FGFR3-TD have produced conflicting reports concerning its transforming potential. It has been suggested that full-length activated mutant FGFR3-TD is not capable of transforming cells. However, even in the absence of ligand, NIH3T3 cells expressing activated mutant FGFR3 have a greater transformation potential than controls. It has also been shown that only the intracellular portion of FGFR3-TD, expressed as a chimeric receptor, is capable of transforming NIH3T3 cells, suggesting that the extracellular and transmembrane portions of FGFR3 may act as negative regulators of the kinase domain. Our in vivo model demonstrates unequivocally that activated mutant FGFR3 is indeed capable of transforming cells. In our BMT model, activated mutant FGFR3 expression in hematopoietic cells led to polyclonal cell expansion and outgrowth of clonal leukemia/lymphoma cells predominantly of pre-B-cell lineage.

The ability of activated mutant FGFR3 to transform cells in comparison to the latent transformation potential of wild-type FGFR3 likely relates to the activation state of the receptor. The TDIIII mutant form of FGFR3 has been shown to have higher intrinsic kinase activity than wild-type FGFR3. The activating mutation K650E (FGFR3-TD) results in the receptor being capable of autophosphorylation at a level 100-fold higher than wild-type FGFR3. Similarly, the severity of the hereditary chondrodysplasia phenotypes resulting from FGFR3 mutations correlates with the activation state of the receptor. This suggests that the enhanced activation state (or the increased degree of kinase activity) of the FGFR3-TD receptor is responsible for the accelerated rate of transformation.

Of interest, accumulating evidence suggests that various FGFs or FGF receptors may play a role in human cancer formation or progression. Many cancer cells overexpress FGFs; for example, FGF8 has been found to be overexpressed in breast cancer samples, whereas bFGF expression in pancreatic cancers relates to shorter postoperative survival. In addition to FGF overexpression in primary tumors, it has been found that FGFRs are overexpressed in several tumor cell lines, including some breast cancer and pancreatic cancer lines. Moreover, expression of a dominant negative FGFR1 in pancreatic tumor cells decreases the ability of these cells to form tumors in nude mice. One study examining FGF2 and FGFR expression in 9 tumor types...
demonstrated that at least one FGFR was expressed in 90% of the tumors analyzed.\textsuperscript{37} FGFR3 messenger RNA (mRNA) has previously been found to be expressed mainly in ovarian, non–small-cell lung carcinomas, colon, and breast cancers.\textsuperscript{37} In a study on human thyroid carcinoma it was determined that 6 of 7 papillary carcinomas expressed FGFR3.\textsuperscript{38} In vitro it was shown that overexpression of FGFR3 in a human papillary thyroid carcinoma cell line led to overgrowth of the cells, suggesting that FGFR3 may modulate cell contact recognition in these cells.\textsuperscript{38} Of particular interest, activating mutations of the gene have been found not only in MM\textsuperscript{2} but also in bladder and cervical carcinomas.\textsuperscript{38} The overexpression of FGFRs and FGFRs in several types of cancers thus suggests that these molecules play a central role in the in vivo formation of many different tumors.

Our previous work on FGFR3 overexpression in MM suggests an important contribution of the receptor to the development of this disease.\textsuperscript{14} When activated mutant FGFR3 was expressed in B9 cells, an IL-6–dependent myeloma line, the cells became capable of proliferating in the absence of IL-6. Furthermore, a marked reduction in cellular death in the absence of IL-6 was evident and was associated with phosphorylation of STAT3 and up-regulation of bcl-x\textsubscript{L}, indicating that the receptor might be involved in both mitogenic and antiapoptotic signaling cascades. Thus, overexpression of FGFR3 in MM is likely a significant event in the formation of this malignancy, enabling the affected B cells to expand and survive independently of growth factor stimulation.

In summary, the transformation of primary B and T cells by ectopic FGFR3 expression reported here provides compelling evidence in support of the notion that translocation of fgfr3 into the IgH switch region in MM is likely to be pivotal in tumor development. Nonetheless, wild-type FGFR3 is not dominantly transforming, requiring additional cooperating oncogenic events. In particular, mutation of fgfr3, subsequent to translocation into the IgH locus, would appear to have devastating consequences because all mice expressing FGFR3-TD rapidly developed tumors.

\textbf{References}


The myeloma-associated oncogene fibroblast growth factor receptor 3 is transforming in hematopoietic cells

Zhihua Li, Yuan Xiao Zhu, Elizabeth E. Plowright, P. Leif Bergsagel, Marta Chesi, Bruce Patterson, Teresa S. Hawley, Robert G. Hawley and A. Keith Stewart