Ewing’s sarcoma is a highly malignant bone tumor found in children and adolescents, and the origin of this malignancy is not well understood. Here, we introduced a Ewing’s sarcoma–associated genetic fusion of the genes encoding the RNA-binding protein EWS and the transcription factor ETS (EWS-ETS) into a fraction of cells enriched for osteochondrogenic progenitors derived from the embryonic superficial zone (eSZ) of long bones collected from late gestational murine embryos. EWS-ETS fusions efficiently induced Ewing’s sarcoma–like small round cell sarcoma formation by these cells. Analysis of the eSZ revealed a fraction of a precursor cells that express growth/differentiation factor 5 (Gdf5), the transcription factor Erg, and parathyroid hormone-like hormone (Pthlh), and selection of the Pthlh-positive fraction alone further enhanced EWS-ETS–dependent tumor induction. Genes downstream of the EWS-ETS fusion protein were quite transcriptionally active in eSZ cells, especially in regions in which the chromatin structure of the ETS-responsive locus was open. Inhibition of β-catenin, poly (ADP-ribose) polymerase 1 (PARP1), or enhancer of zeste homolog 2 (EZH2) suppressed cell growth in a murine model of Ewing’s sarcoma, suggesting the utility of the current system as a preclinical model. These results indicate that eSZ cells are highly enriched in precursors to Ewing’s sarcoma and provide clues to the histogenesis of Ewing’s sarcoma in bone.

Introduction

Ewing’s sarcoma is a highly malignant bone tumor in children and adolescents. It frequently develops as a small round cell sarcoma. It is frequently observed in the metaphysis of long bones (1). The origin of Ewing’s sarcoma has been a enigma since the first case was reported in 1921 (2). Primitive neural crest cells, hematopoietic cells, and muscle cells as well as mesenchymal stem cells (MSCs) have been considered possible cells of origin (3, 4). Chromosomal translocation–related genetic fusions between EWSR1 on chromosome 22 and genes encoding ETS family transcription factors, such as FLI1 and ERG, were then identified. The EWS and the transcription factor ETS (EWS-ETS) fusion is now considered a genetic hallmark of human Ewing’s sarcoma (5–7). However, it has been difficult to establish an appropriate animal model by introduction of EWS-ETS chimeras (8), suggesting that introduction of EWS-ETS is not sufficient to define the origin of the tumors. A few groups have reported successful development of Ewing’s sarcoma–like tumors by introduction of EWS-FLI1 into murine mesenchymal cells (9, 10). However, it is unclear whether there is a special subfraction that includes the cell of origin of Ewing’s sarcoma. The difficulty of inducing Ewing’s sarcoma suggests that the target cells of EWS-ETS might be the cells of a narrow lineage and/or of a limited differentiation stage.

Unlike osteosarcoma, which generally involves the metaphyses of long tubular bones, Ewing’s sarcoma occurs at almost equal frequencies in flat bones and the diaphysis of tubular bones (11). This fact suggests that mutations related to the proliferation of bony tissue might not contribute to the genesis of Ewing’s sarcoma. Moreover, it suggests that the primary genetic event, the EWS-ETS fusion, might occur at an earlier stage of bone development.

Members of the ETS family of genes that are involved in EWS fusions are important for transcriptional regulation in mouse embryonic and perinatal limb skeletogenesis (12). Accumulation of Erg progenitor cells occurs in the embryonic superficial zone (eSZ) of long bones from dpc 15.5 to P7, after which expression is downregulated rapidly (13, 14). These results suggest that temporospatial expression of Erg might be critical for induction of bipotential progenitors during osteochondrogenic differentiation and that dysregulated expression due to chromosomal translocation and fusion to EWSR1 might result in abnormal accumulation of progenitor cells that exhibit increased proliferative potency (10).

To clarify the possible cellular origin of Ewing’s sarcoma, we purified eSZ cells from murine embryonic long bones that expressed Erg and introduced EWS-FLI1 or EWS-ERG fusion genes. We found that EWS-ETS target cells were highly enriched in the eSZ fraction. Moreover, the epigenetic status of genes responsive to transcriptional regulation by EWS-ETS is important for Ewing’s sarcoma development and its phenotypic manifestation.

Results

Development of Ewing’s sarcoma–like small round cell tumors by EWS-ETS expression in the eSZ cells. Erg, one of the EWS fusion partners in Ewing’s sarcoma, is transiently expressed in the joint surface of embryonic and perinatal bones. Therefore, we predicted that the EWS-ETS fusion would affect differentiation and induce abnormal proliferation of Erg-expressing cells. To test this hypothesis, femoral and humeral bones of dpc 18.5 murine embryos were separated into the eSZ, embryonic growth plate (eGP), the embryonic shaft and synovial regions (eSYR) by microdissection (Figure 1A). Embryonic mesenchymal cells of the head and trunk were also prepared. Each cell fraction was mildly digested with type I collagenase. The cells were immediately subjected to retrovirus-mediated integration of the EWS-ETS transgene (Figure 1B). It was shown that eSZ cells were efficiently transduced by retrovirus, while the other fractions were barely infected (Figure 1C). Moreover, the eSZ cells were efficiently transduced with EWS-ETS within 24 hours after infection (Figure 1D).

Conflict of interest: The authors have declared that no conflict of interest exists.

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gene transfer of EWS-FLI1 to all cell types by spin infection. The transduction efficiency was examined by flow cytometric analyses (Supplemental Figure 1A; supplemental material available online with this article; doi:10.1172/JCI72399DS1), and the expression of EWS-FLI1 was confirmed by FACS and immunofluorescent staining using anti-FLAG (Supplemental Figure 1, B–D). One million transduced cells of each fraction were injected subcutaneously into nude mice. Recipients transplanted with eSZ cells transduced with EWS-FLI1 or EWS-ERG developed a subcutaneous mass at 100% penetrance, with a mean latency of 8 weeks (Figure 1, B–D). As few as $1 \times 10^4$ injected transduced eSZ cells could develop Ewing’s sarcomas. In contrast, $1 \times 10^6$ cells from EWS-FLI1-transduced eGP, embryonic shaft, or eSyR fractions were required for tumor development, clearly indicating that Ewing’s sarcoma precursors were highly enriched in the eSZ fraction (Table 1). When embryonic mesenchymal cells purified from the mouse
head or trunk were transduced with *EWS-FLI1*, the incidence of small round cell sarcomas was again lower, and fibrosarcoma-like tumors were also obtained (Figure 1B and Supplementary Figure 2A). In addition, no tumor was induced when *EWS-CHOP* or *SYT-SSX1*, which are found in myxoid liposarcoma or synovial sarcoma, respectively, were introduced into eSZ cells (Figure 1B). Development of nonneoplastic bone and cartilage was observed when we transplanted eSZ cells treated with an empty vector (Supplemental Figure 2B).

Histological analysis showed that tumors expressing *EWS-FLI1* or *EWS-ERG* were composed of aggressively growing, small round cells, a feature typical of Ewing’s sarcoma (Figure 1D). All the tumors examined (10 of 10) were capable of secondary transplantation (Supplemental Table 1 and Supplemental Figure 2C), and 3 of 9 tumors had metastatic potential by tail vein injection (Figure 1D, Supplemental Table 1, and Supplemental Figure 2D). EWS-ETS expression was confirmed by immunoblotting and immunostaining of FLAG-tagged proteins (Supplemental Figure 2E). MIC2 (also known as CD99), a surface marker for human Ewing’s sarcoma (15), was focally detected (Supplemental Figure 2F). CD99 gene sequences are only partially conserved between human and mouse (16), and therefore, CD99 was not useful as a specific marker for murine Ewing’s sarcoma.

**Table 1**

Summary of the incidences of tumors in limiting dilution experiments using eSyR, eSZ, eGP, shaft, trunk, or head cells

<table>
<thead>
<tr>
<th>Cells</th>
<th>Numbers of transplanted cells</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1 × 10^4</td>
</tr>
<tr>
<td>eSZ</td>
<td>25/25 (100%)</td>
</tr>
<tr>
<td>eGP</td>
<td>3/9 (33%)</td>
</tr>
<tr>
<td>eSyR</td>
<td>2/12 (17%)</td>
</tr>
<tr>
<td>Shaft</td>
<td>1/9 (11%)</td>
</tr>
<tr>
<td>Trunk</td>
<td>3/9 (33%)</td>
</tr>
<tr>
<td>Head</td>
<td>2/9 (22%)</td>
</tr>
</tbody>
</table>

ND, not done.

*Cre/loxP*-mediated genetic recombination and knockout of the *EWS-FLI1* transgene induced complete growth arrest of the tumor (Figure 1E), and senescence-like cellular phenotypes were observed in 91.4% of surviving cells (1.4% in non-Cre-treated cells) (Supplemental Figure 2). These results indicate that cellular targeting of eSZ cells using PTHLH (Supplemental Figure 1D), and senescence-like cellular phenotypes were observed adjacent to nonneoplastic cartilage (Figure 3). Small foci of EWS-FLI1–positive (FLAG-positive) cells were observed adjacent to nonneoplastic cartilage (Supplemental Figure 3A). Rapid cell cycle progression was confirmed in assess-
ments of BrdU incorporation (Figure 3B). The early neoplastic lesions did not express neural, myogenic, epithelial, vascular, or hematopoietic markers, including CD57, NGFR, S-100, myosin, desmin, von Willebrand factor, cytokeratin, or CD45 (data not shown). A few FLAG-positive cells expressed collagen type 2, a marker of immature chondrocytes (18, 24), and were observed in the peripheral areas around the early neoplastic foci (Figure 3C). Interestingly, these differentiating cells exhibited cytoplasmic staining for EWS-FLI1. Staining was essentially localized to the nucleus in the central part of the early neoplastic lesion (Figure 3B). Whereas nuclear localization of EWS-FLI1 fusion protein has been confirmed in most cell types (25), its cytoplasmic localization in differentiating cells suggests that cytoplasmic exclusion of EWS-FLI1 might represent an inhibitory mechanism in tumorigenesis of Ewing’s sarcoma. The existence of cytoplasmic exclusion suggests that EWS-FLI1 expression alone is insufficient to induce complete tumorigenesis. In addition, more differentiated chondrocytes, positive for S100 or collagen type 10, were observed.
in the surrounding area (Figure 3D and Supplemental Figure 5). EWS-FLI1 expression was hardly detected in S100-positive cells (Figure 3D). Microdissection and gene expression analyses of early EWS-FLI1 expression was hardly detected in S100-positive cells in the surrounding area (Figure 3D and Supplemental Figure 5). EWS-FLI1 expression was hardly detected in S100-positive cells (Figure 3D). Microdissection and gene expression analyses of early EWS-FLI1 expression was hardly detected in S100-positive cells in the surrounding area (Figure 3D and Supplemental Figure 5).

**Table 2**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Expression properties</th>
<th>Levels in eSZ</th>
<th>Other mesenchymes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Erg</td>
<td>High</td>
<td>S100 (E)</td>
<td></td>
</tr>
<tr>
<td>Gdf5</td>
<td>High</td>
<td>S100 (E)</td>
<td></td>
</tr>
<tr>
<td>Pithh</td>
<td>High</td>
<td>S100 (E, A)</td>
<td></td>
</tr>
<tr>
<td>Prg4</td>
<td>High</td>
<td>S100 (E, A)</td>
<td></td>
</tr>
<tr>
<td>Col2a1</td>
<td>Moderate</td>
<td>Proliferating chondrocytes (E, A)</td>
<td></td>
</tr>
<tr>
<td>Col10a1</td>
<td>None</td>
<td>Hypertrophic chondrocytes (E, A)</td>
<td></td>
</tr>
<tr>
<td>Nanog</td>
<td>Low</td>
<td>ES, EMPC</td>
<td></td>
</tr>
<tr>
<td>Sox2</td>
<td>low</td>
<td>ES, EMPC</td>
<td></td>
</tr>
<tr>
<td>Oct4</td>
<td>low</td>
<td>ES, EMPC</td>
<td></td>
</tr>
</tbody>
</table>

**Summary of eSZ cell profiles**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Expression properties</th>
<th>Levels in eSZ</th>
<th>Other mesenchymes</th>
</tr>
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<tbody>
<tr>
<td>Erg</td>
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<td>S100 (E)</td>
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<td></td>
</tr>
<tr>
<td>Pithh</td>
<td>High</td>
<td>S100 (E, A)</td>
<td></td>
</tr>
<tr>
<td>Prg4</td>
<td>High</td>
<td>S100 (E, A)</td>
<td></td>
</tr>
<tr>
<td>Col2a1</td>
<td>Moderate</td>
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<tr>
<td>Col10a1</td>
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<td></td>
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<tr>
<td>Nanog</td>
<td>Low</td>
<td>ES, EMPC</td>
<td></td>
</tr>
<tr>
<td>Sox2</td>
<td>low</td>
<td>ES, EMPC</td>
<td></td>
</tr>
<tr>
<td>Oct4</td>
<td>low</td>
<td>ES, EMPC</td>
<td></td>
</tr>
</tbody>
</table>

SZ, superficial zone or articular cartilage; ES, embryonic stem cell; EMPC, embryonic mesenchymal progenitor cell. Parenthetical E or A indicate embryo or adult, respectively.

Common upregulated genes in murine and human Ewing’s sarcoma are presented in Supplemental Excel File 3 and Supplemental Figure 6A. The analysis revealed that 336 genes were upregulated in both murine and human Ewing’s sarcomas, including known EWS-FLI1 targets such as Dkk2, Prkcb1, enhancer of zeste homolog 2 (Ezh2), Id2, Nkx2.2, Nr0b1, and Ptpn13 (26–32). Furthermore, 6,014 genes, including EWS-FLI1 targets such as Aurora, Gata4, Tert, Tnc, and Upp1, were upregulated in murine Ewing’s sarcoma (Figure 4C, Supplemental Excel File 3, and refs. 33–37). These 5 genes were identified by EWS-FLI1 overexpression or silencing studies or by an immunohistochemical analysis that might cause exclusion of them as upregulated genes in human Ewing’s sarcoma. Twenty-two out of thirty upregulated targets proposed by Ordonez et al. (8) were indeed upregulated in our model. In addition, 360 genes (including Tgfbr2) (38) were downregulated in both murine and human Ewing’s sarcoma (Supplemental Figure 6A and Supplemental Excel File 4). These genes were potentially EWS-FLI1–responsive genes and might be important in the early oncogenic process as well as in the progression toward more malignant phenotypes. These gene expression results support the authenticity of our murine model for human Ewing’s sarcoma.

The same analysis showed that 129 genes were upregulated in both murine and human Ewing’s sarcoma as well as human neuroblastoma. Upregulation of a series of neuronal differentiation-related genes (Gfra2, Ncan, Nrxn1, and Ntrk1) and synapse-related genes (Supplemental Figure 6B) in murine Ewing’s sarcoma was also observed in human neuroblastoma, indicating that the neuronal phenotype could be induced from osteochondrogenic progenitors, probably through transdifferentiation processes. The neuroectodermal-related signaling pathway, including NTRK1/NTRK3 and N-MYC, might play some role in neuronal phenotypes of Ewing’s sarcoma. Although the number of commonly upregulated genes in murine Ewing’s sarcoma and neuroblastoma was larger than that in murine and human Ewing’s sarcoma, most of the known target genes described above were included in the latter category, suggesting that the core mechanisms of EWS-FLI1 transcriptional regulation might be preserved in our model.

EWS-FLI1–responsive genes and chromatin modification in eSZ cells. The relationship between the cell of origin of Ewing’s sarcoma and EWS-ETS fusions is important, given the strict limitations on the origin of murine Ewing’s sarcoma. Gene expression profiles were therefore compared between eSZ and eGP cells in the presence or absence of EWS-FLI1 (Figure 5A and Supplemental Excel File 5) (data are available at NCBI Gene Expression Omnibus [GEO] with accession number GSE32618). Most of the known EWS-FLI1 target genes (8) were upregulated in eSZ cells following EWS-FLI1 introduction (Supplemental Excel File 5). EWS-FLI1 encodes an aberrant transcription factor (8, 30), and the response to it differed between eSZ and eGP cells (Figure 5B, Supplemental Figure 7, and Supplemental Excel File 6). The different gene responses in eSZ and eGP cell fractions were probably caused by differences in chromatin conditions at target loci. Histone modifications were therefore examined on representative genes, such as Dkk2, Prkcb1, and Ezh2. Histones H3K9/K14ac and H3K4me, which are activation marks for gene expression, were observed predominantly in eSZ cells as well as mouse Ewing’s sarcoma cells, whereas histone H3K9me3 and H3K27me3, which are repressive marks, were observed predominantly in eGP cells (Figure 5C). These results strongly suggest that transcriptional activation of EWS-ETS target genes occurred in eSZ cells at maximum efficiency and that
The histone status in eSZ cells was preserved after transformation, thereby providing the aggressive oncogenic function of EWS-ETS.

**Upregulation of the WNT/β-catenin pathway in eSZ cells and in Ewing’s sarcoma cells.** Gene set enrichment analyses (GSEA) using gene sets of EWS-FLI1–expressing eSZ and eGP cells 48 hours after gene introduction exhibited enrichment of genes within the WNT/β-catenin pathway as well as the EGF and RTK signaling pathways (Figure 6A and Supplemental Figure 7). In the

**Figure 3**
An early neoplastic lesion of murine Ewing’s sarcoma 3 weeks after transplantation. (A and B) Immunofluorescent assessment of FLAG. (A) High-power images of early neoplastic cells (see boxed region 1 shown at higher magnification) and nonneoplastic cartilage (see boxed region 2 shown at higher magnification) are shown. Scale bar: 100 μm. (B) The boxed region in A shown at higher magnification. Accumulation of BrdU-positive nuclei in the central early neoplastic lesions. Nuclear localization of EWS-FLI1 (FLAG) was observed in the central region, whereas cytoplasmic translocation of EWS-FLI1 is remarkable in the differentiating zone. Scale bar: 20 μm. (C) The differentiating zone with cytoplasmic EWS-FLI1 staining is characterized by collagen 2 expression. Scale bar: 20 μm. (D) Further differentiation toward the chondrogenic lineage in a more peripheral area is indicated by expression of S100 (top row), which is negative in the central early neoplastic lesion (bottom row). Scale bar: 100 μm. (E) Quantitative real-time PCR analysis for Erg, Gdf5, Pthlh, Prg4, and Col10a1 expression in early neoplastic cells and the differentiating zone. The mean ± SEM of 3 independent experiments are shown.
WNT/β-catenin pathway, the expression of Dkk2 and Wif1 was observed in eSZ cells expressing EWS-FLI1 (Figure 5B and Figure 6B). Dkk2 expression was comparable between parental eSZ and eGP cells, and EWS-FLI1, introduction induced upregulation of Dkk2 only in eSZ cells (Figure 5B and Figure 6B). In contrast, expression of Dkk1, which is antagonistic to DKK2, remained unaltered by EWS-FLI1 introduction in eSZ cells. Higher Wif1 expression was observed in eSZ cells but not in eGP cells, and the difference in expression between eSZ and eGP cells was preserved after EWS-FLI1 introduction. The WNT/β-catenin pathway was not enriched when gene sets of nontransduced eSZ and eGP cells were tested (data not shown). In addition, gene sets for the EGF pathway and receptor protein kinase activity were enriched (Figure 6B and Supplemental Figure 8). Prkcb1 is a gene downstream of EWS-FLI1 (39) and is inherently expressed at higher levels in eSZ cells than in eGP cells. Notably, its expression was increased to higher levels by introducing EWS-FLI1 into eSZ cells. Flt4 (also known as VEGFR3) and Mosk, which are important in signaling of vascular and neuromuscular systems, were also identified as EWS-FLI1–responsive genes (Figure 6B and Supplemental Figure 8). Furthermore, IGF1R and IGF2R, which are involved in IGF1 signaling and are attractive targets in Ewing's sarcoma therapy (40, 41), were also identified by GSEA (Supplemental Figure 8).

Dkk2 is a member of the dickkopf family of proteins. As modulators of the WNT/β-catenin pathway, this family plays important roles in the development and homeostasis of bone and cartilage (42). A previous study showed that DKK2 was downregulated upon EWS-FLI1 knockdown in Ewing's sarcoma cells, while the opposite response was observed in DKK1 (26). Although previous studies suggested that DKK1 and DKK2 might have functions independent of the canonical WNT/β-catenin pathway (43), possible roles of WNT activation in human Ewing's sarcoma were reported (44).

To confirm the involvement of the WNT/β-catenin pathway in tumorigenesis of Ewing's sarcoma, expression of β-catenin protein was evaluated. β-Catenin expression was increased by transient introduction of EWS-FLI1 into eSZ cells (Supplemental Figure 9A). As described above, murine Ewing's sarcoma was serially transplantable into syngeneic mice and showed high potency of proliferation (Supplemental Figure 2C). In the invasive area of the secondary tumor, increased expression of β-catenin was frequently observed (Supplemental Figure 9B). RNA interference–mediated EWS-FLI1 knockdown resulted in decreased transcriptional activities of β-catenin (Supplemental Figure 9C). Collectively, these data indicate strong association between the upregulation of WNT/β-catenin signaling and cell growth of Ewing's sarcoma.

Inhibition of tumor growth by suppression of critical signals. The result indicates that EWS-FLI1 and its downstream signals are effective targets for therapy. Indeed, gene knockdown experiments showed that tumor cell proliferation was significantly inhibited by siRNA treatments specific for Fli1, Dkk2, Catnb, Prkcb1, Ezb2, or Igf1 (Figure 6C). Knockdown of the same genes in the human Ewing's sarcoma cells showed similar suppression of cell proliferation (Supplemental Figure 10). Moreover, suppression of the EGF/RAS/MAPK pathway by a MEK1 inhibitor (U0126) showed inhibition of tumor growth in vitro in a dose-responsive manner (Figure 6D). These results demonstrated the importance of the signaling pathways activated by EWS-FLI1 in the progression of Ewing's sarcoma and its potential as a novel target for clinical treatment.

Use of the mouse model to test therapy targeted against Ewing's sarcoma. Animal models of human cancer provide platforms for evaluation of novel therapies. Ideally, the phenotypes and developmental mechanisms of the human and model systems should be similar. In this context, specific inhibitors of the WNT/β-catenin pathway, EZH2 and poly (ADP-ribose) polymerase 1 (PARP1), were tested using the current model both in vitro and in vivo. The β-catenin inhibitors, iCRT14 and PNU74654, showed marked growth suppression of both mouse and human Ewing's sarcoma, and an EZH2 inhibitor DZNeP showed modest but substantial growth suppression (Figure 7A and Table 3). Moreover, olaparib, a PARP1 inhibitor reported to exhibit Ewing's sarcoma–specific growth inhibition (45), also inhibited both mouse and human Ewing's sarcomas (Figure 7A and Table 3). Cell cycle analyses showed that iCRT14 and DZNeP induced cell cycle arrest, as indicated by increased G1 populations and decreased G2/M populations (Figure 7B). PNU74654 and olaparib also increased a sub-G1 population, indicating apoptosis induction (Figure 7B). These reagents also suppressed in vivo growth of Ewing's sarcoma, with the greatest effect observed with iCRT14, followed by olaparib, DZNeP, and PNU74654 (Figure 7C).

Thus, the current model provides an effective tool to explore and evaluate novel therapeutic drugs both in vitro and in vivo.

Discussion

Here, we demonstrate efficient and specific induction of a mouse equivalent of human Ewing's sarcoma. We showed that the origin of the tumor is closely related to embryonic osteochondrogenic progenitor cells. Selection of a PTHLH-expressing cellular fraction in eSZ enabled us to obtain substantially higher efficiency and greater specificity and consistency of tumor formation than previously reported investigations using bone marrow–derived mesenchymal stem/progenitor cells (9, 10). In addition, EWS-FLI1 expression induced apoptosis and growth arrest in several cell types, including embryonic fibroblasts (46, 47). These data indicate that induction of Ewing's sarcoma by EWS-ETS fusion genes is much more effective for progenitor cells of a certain cell lineage, including the osteochondrogenic axis, especially in developing bone. A previous study indicated that EWS-FLI1 induces cancer stem cell properties in pediatric MSCs but not in adult MSCs (48). The plasticity for cellular differentiation in embryonic and pediatric precursor cells might be important for Ewing's sarcoma development in younger patients. Moreover, EWS-ETS might induce the development of small round cells and neuroectoderm-like phenotypes.

Ewing's sarcoma is a rather rare neoplasm that affects children and adolescents with an incidence of 2.1 cases per million children (49). The low incidence of disease is also observed in other translocation-related sarcomas affecting young people, such as alveolar rhabdomyosarcoma, clear cell sarcoma, synovial sarcoma, or myxoid liposarcoma (50). This is in contrast to acute myeloid leukemia (AML), which is also characterized by gene fusion. It is likely that the difference in frequencies between sarcomas and AMLs is due to the rarity of progenitor cell populations in which chromatin conditions necessary for the oncogenic action of EWS-ETS are present. Such a narrow window of target cell emergence reflects the difficulty of inducing tumor in vivo models.

Once the EWS-FLI1 fusion occurs in an eSZ cell during the perinatal period or even in utero, the cell survives with acquired growth advantages. After a decade of incubation that allows additional genetic/epigenetic events in the mutated eSZ cell, Ewing's sarcoma eventually emerges in the bone as a highly aggressive tumor in human child-
Figure 4
Clustering analysis of murine and human sarcomas. (A) Supervised clustering of gene expression profiles of 10 samples of murine Ewing's sarcomas (mES), 32 cases of human Ewing's sarcomas (ES), 21 malignant fibrous histiocytomas (MFH), 20 myxoid liposarcomas (MLS), 16 synovial sarcomas (SS), 11 osteosarcomas (OS), 10 neuroblastomas (NB) and 7 chondrosarcomas (CS). (B) Gene expression profiles of mouse and human Ewing's sarcoma (hES) were compared with those of other small round cell tumors of the other species. The frequencies of matched genes in 2,000 gene sets are indicated. Expression profiles of 6 human poorly differentiated synovial sarcoma (hPDSS) cases, 14 cases of human malignant lymphoma, 5 samples of murine synovial sarcoma, 7 murine neuroblastomas, and 6 murine malignant lymphoma were examined. (C) Quantitative RT-PCR for upregulated genes common between eSZ cells with EWS-FLI1 (EF) and murine Ewing's sarcomas. The numbers listed above “mES” denote tumor IDs. The mean ± SEM of 3 independent experiments are shown. *P < 0.001 vs. hES; **P < 0.01 vs. mES.
hood. This scenario explains why the location of Ewing’s sarcoma is different from that of osteosarcoma, which is frequently observed in the metaphysis of long bones. There is a variant of human Ewing’s sarcoma that develops in the soft tissue and is also characterized by the invariable EWS-ETS fusion. As the origin of Ewing’s sarcoma in the soft tissue remains to be clarified, the relatively late onset of the tumor suggests that dysregulation of the differentiation program in the mesenchymal system might play some role in its tumorigenesis.

Upregulation of the WNT/β-catenin pathway is a direct effect of EWS-ETS expression in preneoplastic and sarcoma cells, at least in part. However, rather mild β-catenin induction by EWS-FLI1 in the eSZ (Supplemental Figure 9A) suggests that additional genetic events might be required for constitutive activation of the pathway. Pathways involving receptor tyrosine kinases are also important in Ewing’s sarcoma (40, 51), as was indicated in our model. Indeed, potential clinical benefits from the use of pazopanib, a multikinase inhibitor, for the treatment of childhood sarcoma, including Ewing’s sarcoma, have been reported recently (52).

Tumor formation in our mouse model of Ewing’s sarcoma was EWS-ETS dependent, as was clearly exhibited by Cre/loxP-mediated knockout experiments. This finding suggests that therapeutic

Figure 5
Differences in gene expression between eSZ and eGP cells. (A) Comparison of gene expression profiles between eSZ/EWS-FLI1 and eSZ and eSZ/EWS-FLI1 and eGP/EWS-FLI1 48 hours after introduction. Scatter plots of eSZ with (vertical axis) or without EWS-FLI1 (horizontal axis) and eSZ with EWS-FLI1 (vertical axis) or eGP with EWS-FLI1 (horizontal axis) are shown. Red dots indicate probes of present call, and green dots indicate those of absent call. The threshold lines above and below the diagonal indicate \( y = 2x \) (2-fold increase) and \( y = 0.5x \) (2-fold decrease), respectively. (B) Expression patterns of Dkk2, Prkcb1, and Ezh2 were validated by quantitative RT-PCR. The mean ± SEM of 3 independent experiments are shown. (C) ChIP-PCR for histone modification at Dkk2, Prkcb1, and Ezh2 promoter regions in eSZ, eGP, and murine Ewing’s sarcomas. Rpl30 and Foxa2 were used as controls for active and repressive histone marks, respectively. The mean ± SEM of 3 independent experiments are shown.
approaches should pursue the direct targeting of EWS-ETS as well as related pathways. Gene knockdown experiments and screening of inhibitory drugs in our model should prove valuable. Unlike the xenograft model of human cancer cells, the present mouse model excludes the unexpected bias caused by rather low penetrance of transplantation, an altered relationship between tumor cells and the microenvironment, and defects in certain signaling pathways due to differences in species-dependent binding affinities between ligands and receptors. Thus, our platform will allow us to explore and evaluate novel targeted therapies in combination with tests using human Ewing's sarcoma cell lines.

In summary, purification of the targets of primary oncogenic stimuli permitted us to establish a mouse model that closely recapitulates important characteristics of human Ewing's sarcoma. Taken together, the efficiency of tumor induction and the gene expression analyses of both the very limited cell population obtained by laser microdissection and the early neoplastic lesion strongly suggest that the cell of origin of Ewing's sarcoma is enriched in the eSZ cells. The present ex vivo method could be useful for generating other important animal models for human cancers, particularly when conventional transgenic models are driven by a gene expression-based method that is not always successful.

**Figure 6**

Modulation of gene expression and growth suppression of tumor cells by gene silencing. (A) GSEA of eSZ and eGP cells with EWS-FLI1 (left and central panels) and between eSZ/EWS-FLI1 and eGP, eSZ, and eGP/EWS-FLI1 (right) resulted in enrichment of the WNT/β-catenin pathway, the EGF pathway, and receptor tyrosine kinase activities. (B) Real-time quantitative RT-PCR for Dkk2, Dkk1, Wif1, Prkcb1, Flt4, and Musk in eSZ or eGP cells with/without EWS-FLI1 at 0 or 48 hours after introduction. The mean ± SEM of 3 independent experiments are shown. (C) Inhibition of cell proliferation by knockdown of EWS-FLI1 and genes of the pathways specified in A. Relative growth of tumor cells 48 hours after siRNA treatment was calculated by comparing each cell number to cells treated with control siRNA. The symbols of siRNA used are indicated. Dkk1 was tested as a negative control. Gene knockdown was confirmed by immunoblotting (Flt1, Catnb, Ezh2, and Prkcb1) or RT-PCR (Dkk2 and Igf1). The experiment was repeated 3 times, and representative results are shown. (D) Effect of MAPK pathway inhibition on tumor growth. Erk phosphorylation was inhibited by a MEK1/2 inhibitor U0126 (10 µM) (top), and tumor proliferation was inhibited in a dose-dependent manner 48 hours after treatment (bottom). The mean ± SEM of 3 independent experiments are shown. *P < 0.01; **P < 0.02.
targeting exact cell types. The plasticity of precursor cells as well as their oncogenic potency due to chimeric transcription factors can be evaluated by the present approach and constitutes a useful tool for clarifying oncogenic mechanisms of childhood cancer.

Methods

Purification of eSZ cells. Femoral and humeral bones of BALB/c mouse embryos were removed aseptically on 18.5 dpc, and they were microdissected into eSZ, eGP, and eSyR under a stereomicroscope (Zeiss Stermi 2000-C, Carl Zeiss MicroImaging). Embryonic mesenchymal cells of the head or trunk were also prepared from the same embryos during each experiment. Each region was minced and gently digested with 2 mg/ml collagenase (Wako Pure Chemical) at 37°C for 2 hours. They were cultured in growth medium composed of Iscove’s Modified Dulbecco’s Medium (Invitrogen) supplemented with 15% fetal bovine serum and subjected immediately to retroviral infection. Fractionation of PTHLH+ and PTHLH– eSZ populations was achieved using a rabbit anti-PTHLH (Abcam) and a CELLection Biotin Binder Kit (Dynal) according to the manufacturer’s protocol. The frequency of the PTHLH+ cells reached 8.3% of total eSZ cells (12-fold enrichment).

Retroviral infection and transplantation. N-terminal FLAG-tagged EWS-FLI1 and EWS-ERG were introduced into the pMYs-IRES-GFP or pMYs-IRES-Neo vectors. The full-length EWS-FLI1 cDNA was a gift from Susanne Baker (St. Jude Children’s Research Hospital, Memphis, Tennessee, USA), and EWS-ERG was cloned from a human Ewing’s sarcoma case. Retroviral infections of eSZ, eGP, or shaft cells were performed as described previously (53). Infection efficiency was examined using a FACSCalibur flow cytometer (Becton Dickinson). After 48 hours of spin infection, the cells were mixed with growth factor–reduced Matrigel (Becton Dickinson) and were transplanted subcutaneously to BALB/c nude mice. The mice were observed daily to check for tumor formation and general condition. Tumors were resected and subjected to further examination when subcutaneous masses reached 15 mm in diameter. Some tumors (1 \times 10^6 cells) were serially transplanted subcutaneously into nude mice, and tumor volume was measured every other day. Mean tumor volumes ± SD for 5 mice of each group are plotted. *P < 0.01; **P < 0.03.
Table 3

<table>
<thead>
<tr>
<th>Tumor cells</th>
<th>Inhibitors</th>
<th>IC50 values (μM)</th>
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<tr>
<td></td>
<td>iCRT14</td>
<td>PNU74654</td>
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<tr>
<td>hDS_U2OS</td>
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</table>

Probes, anti-mouse CD99 (a gift of Dietmar Vestweber, Max Planck Institute for Molecular Biomedicine, Muenster, Germany), anti-COL2A (Millipore), anti-S100 (Dako), anti-COL10 (SLS), anti-CD57 (Sigma-Aldrich), anti-β-catenin (Becton Dickinson), anti-nestin (Chemicon), and anti-myosin (Nichirei). Immunofluorescent images were photographed with a Zeiss LSM 710 laser scanning microscope with a ×40 objective (Zeiss) and LSM Software ZEN 2009 (Zeiss).

Western blotting. Western blot analysis was performed using lysates of whole tumor tissues as described previously (54).

RT-PCR and real-time quantitative RT-PCR. Total RNA extraction, reverse transcription, and RNA quantification were performed according to methods described previously (54). Conventional RT-PCR and real-time quantitative RT-PCR were performed by using a Gene Amp 9700 thermal cycler (Applied Biosystems) and a 7500 Fast Real-Time PCR System (Applied Biosystems), respectively. The sequences of the oligonucleotide primers are shown in Supplemental Excel File 6.

 Luciferase assay. A 1,340-bp genomic DNA fragment upstream from the murine Gdf5 exon 1 was amplified by PCR using the following primers: forward (5′-TTCTATATACTCTACCTGTA-3′) and reverse (5′-CTGAAAATAACCTCGTTCTTG-3′). The fragment was inserted into the pGL4.10 vector (Promega) and transfected into eSZ, eGP, eSyR, or trunk cells using Lipofectamine 2000 (Invitrogen). Luciferase assays were performed as described previously (54).

In vitro differentiation assay. Cells were plated at 2 × 10^5 cells per well in 6-well plates and cultured in growth medium. Adipogenic, chondrogenic, osteogenic, myogenic, and neurogenic differentiation assays were conducted according to the methods previously described (55–57).

Microarray analysis. GeneChip analysis was conducted to determine gene expression profiles. A per cell normalization method was applied to eSZ and eGP samples (58). Briefly, cellular lysates were prepared with RLT buffer (Qiagen). After RNA cocktails were added to the cell lysates according to the amount of DNA, total RNA was extracted using the RNeasy Mini Kit (Qiagen). The murine Genome 430 2.0 Array (Affymetrix) was hybridized with aRNA probes generated from eSZ and eGP cells and murine Ewing’s sarcoma tissue. After staining with streptavidin-phycocyanin conjugates, arrays were scanned using an Affymetrix GeneChip Scanner 3000 and analyzed using Affymetrix GeneChip Command Console Software (Affymetrix) and GeneSpring GX 11.0.2 (Agilent Technologies) as described previously (59). The expression data for eSZ and eGP cells were converted to mRNA copy numbers per cell by the Percolome method, quality controlled, and analyzed using Percolome software (58). GSEA was performed using GSEA-P-2.0 software (60).

Data comparisons and clustering between murine and human microarray data sets. The microarray data from 10 murine Ewing’s sarcoma samples were compared with human microarray data sets. Data from the ONCOMINE database (https://www.oncomine.org/) were accessed in June 2011. Five microarray studies containing 117 tumor samples that were analyzed using Human Genome U133A Array (Affymetrix) were queried for gene expression. CEL files from E-MEXP-353 (61), E-MEXP-1142 (62), GSE6481 (63), GSE7529 (64), GSE1122 (65), GSE6461 (66), GSE42548 (67), GSE23972 (68), GSE20196 (69), and GSE10172 (70) were downloaded. The probe sets of the human U133A array were translated into 23,860 murine 430 2.0 arrays by the translation function of GeneSpring using Entrez Gene ID to make a novel common platform. Hierarchical clustering was achieved using log-transformed data and the following procedure. For the initial statistical analysis, 13,026 genes that showed a “present” or “marginal” call in at least 24 of a total of 32 human Ewing’s sarcoma samples were selected. Then, 12,340 probes were selected by 1-way ANOVA (P < 0.05) analysis. Finally, 1,819 probes that showed >2-fold differences of expression in at least 3 tumor types were selected. With these 1,819 probes, hierarchical clustering was performed using the average linkage method and the Pearson’s centered measurements. In addition, a probe set consisting of the 2,000 sequences that were the most altered in expression in human and mouse round cell tumors (Ewing’s sarcoma, neuroblastoma, poorly differentiated synovial sarcoma, and malignant lymphoma) was used to distinguish each tumor from the other 3 using a fold-change analysis. Then, the frequencies of these 2,000 probes were compared between mouse Ewing’s sarcoma and 4 human tumor types and between Ewing’s sarcoma and 4 mouse tumor types to find the closest tumor type using similar entities from GeneSpring.

ChIP. A total of 5 × 10^5 cells per immunoprecipitation were cross-linked with 10% formaldehyde for 10 minutes at room temperature. Histone immunoprecipitation was performed with anti-histone antibodies targeted against H3K9/K14Ac, H3K4/me3, H3K27/me3, total H3 (Cell Signaling Technologies), or H3K9/me3 (Millipore) preconjugated to protein G magnetic beads. Immunoprecipitated DNA was amplified with primers specific for each region. Sequences are shown in Supplemental Excel File 6.

Cre/loxP-mediated gene silencing. eSZ cells were transduced with a floxed EWS-FLI1 retrovirus, and Ewing’s sarcoma cells were obtained from a subcutaneous tumor developed in a nude mouse. Tumor cells were transduced with pMSCV-Cre-puro retrovirus in vitro. Senescence-associated β-galactosidase expression was detected using a Senescence Detection Kit (Bovision) 4 days after transduction of the retrovirus.

siRNA interference studies. For knockdown of FLI1, Dkk2, Catnb, Prkcb1, Ezr2, Ifg1, Dkk1, and Erg, siRNAs were purchased from Qiagen. The list of siRNAs is shown in Supplemental Excel File 7. siRNAs were introduced into mouse Ewing’s sarcoma cells according to the manufacturer’s protocol. Knockdown efficiencies were confirmed by Western blotting using anti-FLAG (Sigma-Aldrich), anti-ERG and anti-PKC B1 (Santa Cruz Biotechnology), anti-β-catenin (Becton Dickinson), and anti-EZH2 (Cell Signaling Technologies) or RT-PCR.

Pharmacological experiments with specific inhibitors. Mouse Ewing’s sarcoma cells were treated with MEK1 inhibitor U0126 (Cell Signaling Technologies) in vitro. Both mouse and human Ewing’s sarcoma cell lines were treated with WNT/β-catenin inhibitors, iCRT14 and PNU74654 (Tocris Biosciences); an EZH2 inhibitor, DZNeP (Cayman Chemical); or a PARP1 inhibitor, olaparib (Selleckchem), both in vitro and in vivo. Inhibition of ERG phosphorylation was examined by Western blotting using anti-P-ERK1/2 and anti-ERK1/2 (Cell Signaling
Technologies). For in vivo experiments, 1 × 10^6 tumor cells were transplanted subcutaneously into nude mice, and the mice were treated with specific inhibitors when the tumor diameter reached 5 mm. All the inhibitors were dissolved in 0.2% DMSO, and they were administered by intraperitoneal injection 3 times per week.

**Cell cycle assay.** Single-cell suspensions were permeabilized with 0.1% Triton X-100 in PBS, and 50 mg/ml propidium iodide and 1 mg/ml RNase A were added. The cell suspensions were then analyzed by using a FACSCalibur flow cytometer and ModFit software (Becton Dickinson).

**Cloning retroviral integration sites.** Retroviral integration sites of individual mouse Ewing’s sarcoma were isolated by inverse PCR, sequenced, and mapped as described previously (71).

**Accession numbers.** The microarray data sets are accessible through the NCBI Gene Expression Omnibus (GEO) database (http://www.ncbi.nlm.nih.gov/geo), with accession numbers GSE32615 and GSE32618.

**Statistics.** Continuous distributions were compared with 2-tailed Student’s *t* test. Survival analysis was performed using the Kaplan-Meier life table method, and survival between groups was compared with the log-rank test. The 2-proportion *z* test was used to evaluate the significance of differences in the matched probe sets between 2 tumor types. All *P* values were 2 sided, and a *P* value of less than 0.05 was considered significant.

**Study approval.** Animals were handled in accordance with the guidelines of the animal care committee at the Japanese Foundation for Cancer Research, which gave ethical approval for these studies.

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6. Zucman J, et al. Combinatorial generation of retroviral integration sites of individual mouse Ewing’s sarcoma were isolated by inverse PCR, sequenced, and mapped as described previously (71).