EWS-WT1 Chimeric Protein in Desmoplastic Small Round Cell Tumor is a Potent Transactivator of FGFR4

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Abstract

Desmoplastic small round cell tumor (DSRCT) is a rare but highly aggressive malignant neoplasm that typically involves the abdominal or pelvic peritoneum in children and young adults. This tumor is characterized by the presence of a specific EWS-WT1 fusion gene, which is the result of recurrent chromosomal translocation, t(11;22)(p13;q12). EWS encodes a putative RNA binding protein of unknown function with an N-terminal domain that mediates potent transcriptional activation when fused to heterologous DNA binding domains. WT1 is a tumor suppressor gene initially identified based on its inactivation in Wilms tumor. The chimeric proteins resulting from these chromosomal translocations usually possess gain-of-function transcriptional activities and define histologically and biologically distinct tumor types. EWS-WT1 has two isoforms of EWS-WT1(-KTS) and EWS-WT1(+KTS). Previous studies have identified several EWS-WT1(-KTS) target genes, most of which are involved in growth factor signaling. In the current study, we identified a putative RNA binding protein of unknown function with an N-terminal domain that mediates potent transcriptional activation when fused to heterologous DNA binding domains. The Wilms tumor suppressor (WT1) was initially identified based on its inactivation in Wilms tumor [1]. The chimeric proteins resulting from these chromosomal translocations usually possess gain-of-function transcriptional activities and define histologically and biologically distinct tumor types. Alternative isoforms of either EWS-WT1(-KTS) or EWS-WT1(+KTS) have also been shown to differ in DNA binding affinity and specificity [6,7]. The molecular targets and associated mechanisms of these fusion proteins have not yet been fully characterized. The molecular targets of EWS-WT1(-KTS) chimeric proteins that have been reported include insulin-like growth factor-I receptor (IGF-IR) gene [8-10]; the beta-chain of the interleukin-2/15 receptor (IL-2/15Rβ) [11]; platelet-derived growth factor-A (PDGFA) [12]; BAI1-associated protein 3 (BAIAP3), which encodes a protein implicated in regulated exocytosis; a potential regulator of growth-factor release [13]; and T-cell acute lymphoblastic leukemia-associated antigen 1 (TALLA-1) [14]. In addition, expression of the transmembrane protein, leukemia-rich repeat containing 15 (LRRC15), was found to be induced by EWS-WT1(+KTS) [15]. Recently, equilibrative nucleoside transporter 4 (ENT4), which encodes a pH-dependent adenosine transporter has been identified as a potential EWS-WT1(+KTS) target that defines epithelial characteristics of DSRCT. Furthermore, up-regulation of CTNNB1 driven by EWS-WT1(-KTS) was found to be independent of FGFR4 regulation. Expressions of FGFR4 and CTNNB1 in DSRCT clinical samples were confirmed by immunohistochemistry. This study provides regulatory mechanisms of FGFR4 in DSRCT and also novel insights into the acquisition of epithelial characteristics in DSRCT.

Keywords: Desmoplastic small round cell tumor; EWS-WT1; Target gene; FGFR4; CTNNB1

Introduction

Desmoplastic small round cell tumor (DSRCT) is a rare but highly aggressive malignant tumor that typically involves the abdominal or pelvic peritoneum in children and young adults [1]. This tumor is characterized histologically by solid nests of small round-cell tumor cells expressing epithelial, muscular, and neural markers, surrounded by a dense reactive stroma. The chimeric proteins resulting from these chromosomal translocations usually possess gain-of-function transcriptional activities and define histologically and biologically distinct tumor types. Alternative isoforms of either EWS-WT1(-KTS) or EWS-WT1(+KTS) have also been shown to differ in DNA binding affinity and specificity [6,7]. The molecular targets and associated mechanisms of these fusion proteins have not yet been fully characterized. The molecular targets of EWS-WT1(-KTS) chimeric proteins that have been reported include insulin-like growth factor-I receptor (IGF-IR) gene [8-10]; the beta-chain of the interleukin-2/15 receptor (IL-2/15Rβ) [11]; platelet-derived growth factor-A (PDGFA) [12]; BAI1-associated protein 3 (BAIAP3), which encodes a protein implicated in regulated exocytosis; a potential regulator of growth-factor release [13]; and T-cell acute lymphoblastic leukemia-associated antigen 1 (TALLA-1) [14]. In addition, expression of the transmembrane protein, leukemia-rich repeat containing 15 (LRRC15), was found to be induced by EWS-WT1(+KTS) [15]. Recently, equilibrative nucleoside transporter 4 (ENT4), which encodes a pH-dependent adenosine transporter has been identified as a potential EWS-WT1(+KTS) target that defines epithelial characteristics of DSRCT. Furthermore, up-regulation of CTNNB1 driven by EWS-WT1(-KTS) was found to be independent of FGFR4 regulation. Expressions of FGFR4 and CTNNB1 in DSRCT clinical samples were confirmed by immunohistochemistry. This study provides regulatory mechanisms of FGFR4 in DSRCT and also novel insights into the acquisition of epithelial characteristics in DSRCT.

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Materials and Methods

Cell culture and preparation of cell blocks of JN-DSRCT

The JN-DSRCT cell line was kindly provided by Dr. Iwasaki, Fukuoka University, Japan [29], and grown in a 1:1 mixture of DMEM and Ham’s F-12 (Kyokuto Pharmacology, Tokyo, Japan), supplemented with 10% FCS and kanamycin sulfate (100 µg/ml). After 80% confluence, cells were treated with trypsin and harvested by centrifuge to make a cellblock of JN-DSRCT for immunocytochemical analysis. In addition, immnocytochemical analysis was performed using the JN-DSRCT cell block. For immunocytochemistry, SHBR3-a breast cancer cell line, was used as a positive control. The antibodies used for immunocytochemistry were as follows: rabbit polyclonal anti-c-erbB-2 antibody (DakoCytomation Envision, #A0485), rabbit polyclonal anti-ErbB-3antibody (Santa Cruz, C-17), and mouse monoclonal anti-α-tubulin antibody (Cell Signaling Technology, #9272), pAKT (Cell Signaling Technology, #9272), PAKT (Cell Signaling Technology, clone 587F11). Furthermore, mouse monoclonal anti-α-tubulin (Sigma, B-5-1-1) antibody and mouse monoclonal anti-GAPDH (Santa Cruz, 6C5) antibody were used as alternative internal controls.

Immunohistochemistry and immunocytochemistry

Two DSRCT clinical samples were prepared for immunohistochemistry. Immunohistochemical analysis was performed using the following antibodies: rabbit polyclonal anti-FGFR-4 IgG (Santa Cruz Biotechnology, clone sc-124) diluted at 1:200, mouse monoclonal antibody β-catenin (BD transduction lab, clone 14) diluted at 1:200, and mouse monoclonal antibody E-cadherin (BD transduction lab, clone 36/E-cadherin) diluted at 1:1000. In addition, immunocytochemical analysis was performed using the JN-DSRCT cell block. For immunocytochemistry, SHBR3-a breast cancer cell line, was used as a positive control. The antibodies used for immunocytochemistry were as follows: rabbit polyclonal anti-c-erbB-2 antibody (DakoCytomation Envision, #A0485), rabbit polyclonal anti-ErbB-3antibody (Santa Cruz, C-17), and mouse monoclonal anti-epidermal growth factor Receptor (EGFR) antibody (Zymed Laboratories, Clone 31G7).

Establishment of tetracycline-regulated EWS-WT1(-KTS) inducible cell line

T-Rex HeLa cells (Invitrogen, life technologies Japan) were cultured in 10 cm dishes with DMEM supplemented with 10% FBS (Tet system approved FBS; BD Bioscience, NJ). At 70% confluence, cells were transfected with 2 µg of DNA of pcDNA4-TO-EWS-WT1(-KTS), which is tagged with myc, by using Fugene6 (Roche) transfection reagent, as previously described [17]. At 48 h after transfection, drug selection was started in a fresh medium supplemented with 400 µg/ml Zeocin (Invitrogen) for 6 weeks, and drug-resistant colonies were isolated. Cells from isolated colonies were treated with 1 µg/ml tetracycline (Invitrogen) to induce EWS-WT1(-KTS)expression.

Immunofluorescence

HeLa cell lines were grown on several glass cover slips in DMEM with 10% FCS and transfected with pcDNA4-EWS-WT1(-KTS) for 48 h. Attached cells on the cover slips were fixed in 4% paraformaldehyde for 10 min and then treated with 0.1% Triton X-100 in PBS for 5 min. The fixed cells were incubated overnight at 4°C for double staining with rabbit polyclonal anti-FGFR-4 IgG (sc-124, carboxyl terminal human FGFR-4; Santa Cruz Biotechnology) and mouse monoclonal antibody β-catenin (BD transduction lab, clone 14), anti-β-catenin (anti-ABC), (Upstate, clone 8E7), anti-cytokeratin (Becton Dickenson, clone CAM5.2), rabbit monoclonal antibody to human cyclin D1 (DBS, clone SP4), MAPK (Cell Signaling Technology, clone L34F12), pMAPK (Cell Signaling Technology, clone 20G11), Akt (Cell Signaling Technology, #9272), PAKT (Cell Signaling Technology, clone 587F11). Furthermore, mouse monoclonal anti-α-tubulin (Sigma, B-5-1-1) antibody and mouse monoclonal anti-GAPDH (Santa Cruz, 6C5) antibody were used as alternative internal controls.

Knockdown of FGFR4 in the JN-DSRCT cell line

To see whether FGFR4 affects β-catenin expression level in a JN-DSRCT cell line, knockdown of FGFR4 was performed using siRNA according to the manufacturer’s protocol. Both FGFR4 and non-targeting siRNAs were purchased from Dharmacon (Thermo Fisher Scientific K.K.). JN-DSRCT cells were harvested to extract protein for homodimerization and autophosphorylation, and subsequent initiation of multiple signaling pathways [18]. Overexpression of FGFR has also been implicated in neoplastic transformation. For example, FGFR4 is overexpressed in several types of human tumors, including colon, liver, breast, neuroendocrine, pancreatic carcinomas, hepatocellular carcinoma, and pediatric rhabdomyosarcomas [19-26]. Furthermore, comparison of gene expression profiles of apoptosis-sensitive breast cancer cells and corresponding apoptosis-resistant clones led to the identification of FGFR4 as a gene with increased gene expression in response to treatment with doxorubicin or cyclophosphamide [27]. By cDNA microarray analysis, FGFR4 has been identified as one of the most highly expressed tyrosine kinase receptors in DSRCT [28], and this gene has also been described previously as a candidate target of EWS-WT1(-KTS), although this has not been validated [11]. In the present study, we confirmed that FGFR4 was highly expressed in DSRCT clinical samples and in a JN-DSRCT cell line, and that FGFR4 overexpression was primarily restricted to EWS-WT1(-KTS) transfected cells. Furthermore, the use of an exogenous EWS-WT1 induction system revealed that CTNNB1, a Wnt signaling component, which is also involved in FGF/FGFR signaling, might be a potential downstream target of EWS-WT1(-KTS).
western blotting 48 h after transfection. Furthermore, cell proliferation rates were counted at every 24 hrs after each siRNA transfection.

Results

FGFR4 is overexpressed in JN-DSRCT cell line and human DSRCT

Tyrosine kinase receptors were previously found to be highly expressed in DSRCT, based on cDNA microarray data from 139 sarcoma samples and 17 cell lines or xenografts representing 5 different sarcoma histologic subtypes (Supplementary Table 1) [28]. These expression microarray data are freely available at http://cbio.mskcc.org/Public/sarcoma_array_data/. In addition to ERBB2 (HER2) and FGFR4 listed in Supplementary Table 1, the expressions of ERBB3 (Her3) and EGFR were examined by immunocytochemistry in the JN-DSRCT cell line. Among them, FGFR4 was confirmed by immunocytochemistry to be the most highly expressed tyrosine-kinase receptor gene product in the JN-DSRCT cell line (Figure 1A-G). In addition, overexpression of FGFR4 was shown by immunohistochemistry in one of the 2DSRCT clinical samples (Figure 1H); weak FGFR4 expression was observed in the second clinical sample (data not shown). Using western blot, we revealed that FGFR4 was highly expressed at the protein level in the JN-DSRCT cell line compared to other cell lines (Figure 2A).

FGF19, the ligand for FGFR4, is expressed at lower levels in the JN-DSRCT cell line

We next examined the mRNA expression level of FGF19, the ligand for FGFR4, by semi-quantitative RT-PCR. Compared to the FGF19 expression level in other cell lines except SKBR-3 and AU565, the expression level of FGF19 in the JN-DSRCT cell line was relatively lower (Figure 2B).

Exogenous expression of EWS-WT1 in HeLa cells induced FGFR4 and β-catenin expression

First, to see whether FGFR4 is a potential target of EWS-WT1(-KTS), immunofluorescence was performed after transfection of EWS-WT1(-KTS) in HeLa cells. FGFR4 expression was restricted to the EWS-WT1(-KTS) transfected cells (Figure 3A), suggesting that FGF4 is a potential target of EWS-WT1(-KTS). This was also confirmed by the induction of EWS-WT1(-KTS) in HeLaTrex cells (Figure 4A). Next, because it has been shown that Wnt and FGF signaling cross-talk during a variety of cellular processes [30] and that DSRCT has epithelial characteristics, we evaluated the expression levels of β-catenin in EWS-WT1(-KTS)-induced cells after confirmation of β-catenin expression in DSRCT clinical samples. β-catenin expression in DSRCT was observed at membrane and cytoplasm, and E-cadherin membranous expression was also noted (Figure 3B). The total expression level of β-catenin was increased in EWS-WT1(-KTS)-induced HeLa cells (Figure 4A). Interestingly, β-catenin has also been shown to be one of the over expressed genes in DSRCT compared to other translocation-sarcomas (data not shown).

Induction of exogenous EWS-WT1 expression accompanied by an increase in pMAPK and pAkt

We further evaluated a possible change in the expression level of keratin as a marker for epithelial differentiation; however, no changes were observed (Figure 4A). This exogenous EWS-WT1 expression was accompanied by increased expression of the phosphorylated forms of MAPK and Akt, though total expression level of MAPK and Akt kept almost the same level (Figure 4A).

Knockdown of FGFR4 does not influence active β-catenin expression level in the JN-DSRCT cell line

Because, it has been demonstrated that the loss of FGFR4 leads to reduced β-catenin pathway signaling and decreased tumor growth in vivo and clonal growth in vitro [31], we next knocked down FGFR4 transiently by using siRNA in the JN-DSRCT cell line. However, we did not observe alterations in the expression level of cyclinD1 or β-catenin isoforms, including the active form of β-catenin (Figure 4B), suggesting that β-catenin overexpression driven by EWS-WT1(-KTS) was independent of FGFR4 overexpression. Furthermore, this transient knockdown of FGFR4 did not cause an obvious difference in the cell proliferation rate (Figure 4C).

Discussion

The immunohistochemical profile of DSRCT shows divergent differentiation characterized by the co expression of epithelial and mesenchymal markers with occasional expression of myogenic and
neurogenic markers. In immunohistochemical analyses, DSRCTs show keratin expression in 86% and epithelial membrane antigen in 93% [32] higher than that observed in synovial sarcoma, which is well-known to exhibit epithelial characteristics. In this study, we observed membranous expression of β-catenin in 2 DSRCT clinical samples. In addition, β-catenin expression was up regulated by the exogenous expression of EWS-WT1(-KTS) in HeLa cells, suggesting that CTNNB1 could be a potential target of EWS-WT1(-KTS). β-catenin is a multi-functional protein that plays an important role in maintaining cell-cell adhesion and acts as a downstream effector of the Wnt-signaling cascade. Thus, it is possible that EWS-WT1(-KTS) is involved in the acquisition of epithelial characteristics in DSRCT; however, we could not confirm an increase in the keratin expression in our exogenous EWS-WT1(-KTS) expression model by using the HeLa cell line in which transcription of the E-cadherin gene was constitutively and strongly repressed. Regarding this point, the authors have experienced that E-cadherin protein expression was not observed using the same tetracycline-regulated exogenous SYT-SSX expression system regardless of the increased E-cadherin mRNA expression [17].

A recent study has shown that co activation of FGF and Wnt signaling pathways in tumors leads to more malignant phenotypes [30]. Furthermore, it has also been demonstrated that FGFR4 knockdown resulted in reduced β-catenin pathway signaling and decreased tumor growth in vivo and clonal growth in vitro and that FGF19 increased GSK-3β phosphorylation and active β-catenin [31]. Therefore, we assessed the possible cross-talk between FGF19/FGFR4 signaling and Wnt signaling in a JN-DSRCT cell line. Regarding this point, we confirmed the presence of β-catenin cytoplasmic staining and membranous expression in both DSRCT clinical samples, as well as FGFR4 overexpression and lower mRNA expression of FGF19 in a JN-DSRCT cell line. However, a transient knockdown of FGFR4 in JN-DSRCT cell line did not alter the expression of β-catenin isoforms, including the active form. Furthermore, the expression of cyclinD1, one of the downstream targets of the Wnt signaling pathway [32,33], was not either altered by this treatment. By transient knockdown of FGFR4 using siRNA transfection in JN-DSRCT cell line, we confirmed that β-catenin overexpression and subsequent possible Wnt signaling activation in DSRCT is independent of FGFR4 expression. Thereby, in this experiment cyclin D1 expression which we selected as a marker of Wnt signaling activation, although this is not always the case in soft tissue sarcomas [34], was not altered after FGFR4 siRNA transfection. Taking into consideration that FGF19 was expressed at much lower levels in JN-DSRCT cell line, we further investigated the role of FGF19 in Wnt signaling activation in DSRCT.
overexpression of FGFR4 in DSRCT is partly derived from the data reported by Wong et al. [11], our findings suggest that expresses a variant form of EWS-WT1 [29]. Considered in conjunction in DSRCTs [7]. It has also been shown that the JN-DSRCT cell line with differing oncogenic properties were previously characterized 2DSRCT clinical samples used in this study, 2 isoforms of EWS-WT1 although we could not examine the types of EWS-WT1 isoforms in the [11]. In the present study, we also showed overexpression of FGFR4 in a JN-DSRCT cell line and in 1 of the 2 DSRCT clinical samples. [26], and that therapeutic inactivation of FGF19 could be beneficial for the treatment of colon and liver cancer [41]. Therefore, inhibition of the FGF19/FGFR4 signaling pathway was also expected to have antitumorigenic effects on DSRCT cells. However, lesser expression level ofFGF19 in JN-DSRCT cells suggests that the inactivation of FGF19 would be less effective for blocking the FGFR4 signaling pathway in DSRCT. Furthermore, the blocking of FGFR4 would be predicted to be so far less effective, given that we did not observe differences in the cell proliferation rates after treatment of a JN-DSRCT cell line with FGFR4 siRNA. However, further studies are necessary to evaluate the therapeutic effects of constitutive inhibition of FGFR4 signaling.

Conclusions

EWS-WT1(-KTS) chimeric protein is a potential transactivator of FGFR4. In addition, CTNNB1 could be a potential target of EWS-WT1, and this transactivation of CTNNB1 is likely to play an important role in defining epithelial characteristics in DSRCT.

Conf Interest Statement

All authors declare that we have no conflict of interest.

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