Expression of connective tissue growth factor (CCN2) in desmoplastic small round cell tumour

A W Rachfal, M H Luquette, D R Brigstock

Background: Desmoplastic small round cell tumour (DSRCT) is a rare and often fatal abdominal tumour that is distinguished by well defined islands of cells, surrounded by prominent desmoplastic stroma. DSRCT has a very poor prognosis and, despite surgery, radiotherapy, and chemotherapy, patients typically die within several months to a few years after diagnosis. DSRCT is associated with a recurrent chromosomal translocation, t(11;22)(p13;q12), which fuses the N-terminus of the Ewing sarcoma (EWS) gene to the C-terminus of the Wilms’s tumour protein (WT1) gene, and causes a loss of the typical repressive function of WT1 on gene transcription. The EWS–WT1 fusion encodes a novel transcription factor comprising a strong EWS transcriptional activation domain merged with a WT1 DNA binding domain. This fusion creates an oncogenic chimaera, which may lead to loss of the tumour suppressor effects of the WT1 gene, in addition to an increase in the EWS driven expression of growth factors usually repressed by WT1.

WT1 represses activators that stimulate initiation and/or elongation steps in RNA polymerase II transcription. In addition, through a cis acting epidermal growth factor receptor (EGFR) binding site in their promoters, the transcription of insulin-like growth factor II (IGF-II), platelet derived growth factor α chain (PDGF-α), and transforming growth factor β (TGFβ) are repressed by WT1. WT1 may also play an important role in regulating TGFβ expression and indirectly controlling extracellular matrix production. These same genes, in addition to the PDGF-α and IGF-1 receptors, are also targets for the EWS–WT1 fusion protein. Instead of being repressed by WT1, these genes are upregulated in DSRCT tumours.

Recently, WT1 was reported to regulate connective tissue growth factor (CCN2) expression via novel elements in the promoter region of CCN2. CCN2 is a TGFβ inducible matricellular protein, produced by diverse cell types, which regulates many diverse cellular functions. Although there has been considerable focus on the role of CCN2 in the fibrosis of vital organs, its production by desmoplastic tumours has received relatively little attention. Given its matrigenic properties and transcriptional regulation by WT1, we analysed CCN2 expression in DSRCT.

Aims: To assess the expression and localisation of connective tissue growth factor (CCN2) in DSRCT because this protein is transcriptionally repressed by WT1 and is associated with the production of abundant extracellular matrix.

Methods: CCN2 was assessed by in situ hybridisation and immunohistochemistry.

Results: CCN2 mRNA and protein were colocalised to the tumour cells themselves, in addition to stromal fibroblasts and vascular endothelial cells.

Conclusions: These data show that CCN2 is produced in high amounts by several cell types in DSRCT, and highlight a potential role for this factor in the autocrine and paracrine regulation of tumour cell growth, matrigenesis, and angiogenesis.

SHORT REPORT

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RESULTS

Based on diagnostic RT-PCR and sequencing, two of the three tumours were positive for the EWS–WT1 fusion. Table 1 summarises the presence of this translocation, together with the clinical features and CCN2 expression profile of each tumour. Interestingly, the EWS–WT1 negative tumour was also negative for CCN2 expression, whereas the two tumours that harboured the characteristic WT1 translocation were positive for CCN2 expression, as shown by hybridisation to the CCN2 antisense probe but not to the CCN2 sense probe (fig 1A, B). The pattern of CCN2 mRNA distribution was very similar to that of the CCN2 protein, which was readily detected by anti-CCN2 IgG but not by non-immune IgG (fig 1C, D). CCN2 mRNA and protein expression were localised to the tumour cells (fig 1B, D; fig 2A), fibroblasts within the stromal compartment (fig 1B, D; fig 2B, E), and endothelial cells of the capillaries and arterioles (fig 2C, D, F). Haematoxylin and eosin staining confirmed the presence of characteristic islands of rounded, undifferentiated tumour cells within a collagen rich stromal matrix (fig 1E).

DISCUSSION

Our study showed that DSRCT expresses CCN2 in both the tumour cells and supporting stromal fibroblasts and vascular endothelial cells, suggesting that CCN2 is involved in autocrine and paracrine pathways of action. Interestingly, the one DSRCT specimen that did not stain positively for CCN2 expression also did not have the typical EWS–WT1 translocation. Thus, our data suggest that CCN2 expression is associated with the EWS–WT1 fusion, which occurs in DSRCTs with a frequency of $95\%$.11 Alternatively, it is possible that the EWS–WT1 negative tumour was incorrectly identified as DSRCT, although this would be inconsistent with other pathological indicators at the time of initial diagnosis (for the archival tissue in question, RT-PCR was performed several years after and independently of diagnosis).

Studies of other tumour types have shown considerable variability in the cellular localisation of CCN2. For example, glioblastomas, infantile myofibromatosis, malignant fibrohistiocytic tumours, and malignant haemangiopericytomas have moderate to intense CCN2 staining in the tumour cells, with mild to moderate CCN2 expression in the surrounding vascular endothelial cells.12 13 In contrast, CCN2 is not expressed in the tumour cells of angiofibromas, squamous cell carcinomas associated with lung cancer, or mammary ductal carcinomas, yet it is present at high concentrations in the surrounding endothelial cells and stromal fibroblasts.12 14 15 In desmoplastic tumours of the oesophagus and pancreas, CCN2 is expressed more prominently by stromal fibroblasts than by the tumour cells themselves.16 17

"Our data suggest that, in desmoplastic small round cell tumour, the inhibitory control of CCN2 gene expression by WT1 may be overcome by the pathological fusion of EWS1 to WT1, leading to localised CCN2 overexpression and the concomitant formation of a desmoplastic stroma"
The production of CCN2 by several cell types in DSRCT is consistent with its participation in autocrine and paracrine pathways that are involved in processes such as tumour growth, angiogenesis, and desmoplasia. Although the matricigenic, fibrogenic, and angiogenic properties of CCN2 are well documented, its precise roles in tumour cell function have yet to be clarified. CCN2 overexpression is correlated with increased survival in oesophageal squamous cell carcinoma, oral squamous cell carcinoma, and chondrosarcoma, but negatively correlated with survival in oesophageal adenocarcinoma. In addition, increased expression of CCN2 was associated with a loss of tumorigenicity in human embryonal carcinoma cells, and CCN2 expression was decreased in Wilms's tumour. Increased concentrations of CCN2 are present in pancreatic tumours and are associated with tumorigenicity in astrocytomas, whereas the ability of breast cancer cells to metastasise is associated with the expression of both CCN2 and its close relative, CCN1.

WT1 plays important roles in development, tumorigenesis, RNA splicing, DNA replication, and apoptosis, but is best characterised as a tumour suppressing transcription factor. Novel binding sites in the CCN2 promoter are used by WT1 to suppress CCN2 expression, both in its endogenous location and in a reporter construct. The EWS–WT1 fusion is able to recognise and activate the same set of target genes that are usually negatively regulated by WT1. Taken together, our data suggest that, in DSRCT, the inhibitory control of CCN2 gene expression by WT1 may be overcome by the pathological fusion of EWS1 to WT1, leading to localised CCN2 overexpression and the concomitant formation of a desmoplastic stroma. Although this mechanism has yet to be confirmed, the related family member, CCN3, was identified as a potential target of WT1, and was highly expressed in a case of DSRCT. Thus, CCN2 or other CCN proteins may be useful targets for developing novel therapeutic approaches for combating DSRCT.
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