

Journal of Cancer Research and Practice

journal homepage: www.ejcrp.org



Case Report

Parapharyngeal Inflammatory Myofibroblastic Tumor Harboring Fibronectin 1-ROS Protooncogene 1 Fusion Responded to Crizotinib

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Abstract

Inflammatory myofibroblastic tumor (IMT) is a rare tumor type usually arising in the thoracic or abdominal cavity. Despite its rarity, IMT commonly harbors driver gene rearrangements involving anaplastic lymphoma kinase (*ALK*), ROS proto-oncogene 1 (*ROS1*), and neurotrophic tropomyosin-related kinase. We present a rare case of the parapharyngeal IMT with convoluted diagnostic test results in determining driver gene rearrangement. The immunohistochemical stains were *ALK*-negative and *ROS1* positive, but the result of *ROS1* fluorescence *in situ* hybridization was equivocal. Amplicon-based targeted next-generation sequencing (NGS) did not detect any *ROS1* rearrangement, but hybridization capture-based NGS revealed a rare fibronectin 1 (*FN1)-ROS1* fusion. Eventually, the patient started crizotinib and had a tumor response with tolerable toxicity. This case highlights the importance of appropriate molecular testing of IMTs to guide the proper targeted therapy.

Keywords: Case report, crizotinib, fibronectin 1-ROS protooncogene 1, inflammatory myofibroblastic tumor

INTRODUCTION

Inflammatory myofibroblastic tumor (IMT) is a rare mesenchymal tumor of borderline malignancy. Only 150–200 cases are diagnosed in the United States annually. IMT usually affects children and adolescents, and frequently involves sites, including the lung, abdomen, and retroperitoneal spaces.^[1] The head-and-neck IMTs only account for 15% of

 Submitted:
 30-Jul-2020
 Revised:
 28-Sep-2020

 Accepted:
 29-Sep-2020
 Published:
 01-Dec-2020

Supplementary material available online	
Access this article online	
Quick Response Code:	Website: www.ejcrp.org
	DOI: 10.4103/JCRP.JCRP_25_20

all IMTs and are more prevalent among adults. Symptoms of the head-and-neck IMTs are related to the primary site from which they arise. The larynx, pharynx, sinonasal area, skull base, salivary glands, trachea, and orbit have been reported to be primary sites of IMT.^[2]

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How to cite this article: Kuo YJ, Lee JC, Chen CN, Chen TW. Parapharyngeal inflammatory myofibroblastic tumor harboring fibronectin 1- ROS protooncogene 1 fusion responded to crizotinib. J Cancer Res Pract 2020;7:179-83.

More than half of IMTs harbor anaplastic lymphoma kinase (*ALK*) rearrangements and respond to *ALK* inhibitors such as crizotinib. For IMTs without *ALK* rearrangements, Lovly *et al.* first reported ROS proto-oncogene 1 (*ROS1*) as well as platelet-derived growth factor receptor B (*PDGFRB*) fusions in 2014.^[3] Other genetic alterations such as RET protooncogene (*RET*) and neurotrophic tropomyosin-related kinase (*NTRK*) have also subsequently been reported.^[4,5] *ROS1* fusions have been reported in 7%–13% of IMTs, and most of them were TRK-fused gene (*TFG*)-*ROS1* fusion.^[3-15] Here, we present a case of parapharyngeal IMT with a unique initial presentation and rare fibronectin 1 (*FN1*)-*ROS1* fusion.

CASE REPORT

A 26-year-old woman presented with a headache for 1 month. The headaches were located at the left temporal area with radiation to the ear, neck, and upper shoulder, and she also complained of phonophobia, photophobia, and left ear fullness. She went to a neurology clinic and was tentatively treated for migraine. Nonsteroid anti-inflammatory drugs, muscle relaxants, and even antidepressants were tried, but her symptoms did not resolve at all.

Her headaches persisted and got worse in the following 6 months, with newly developed diplopia, hoarseness, dysphagia, and weight loss of around 8 kg. Contrast-enhanced of the head-and-neck magnetic resonance imaging (MRI) revealed a 6.3 cm necrotic tumor at the left carotid space with invasion to left C1 and skull base. The left internal carotid artery and the left internal jugular vein were encased [Figure 1]. Fiberoptic nasopharyngoscopy showed bulging of the left nasopharynx and oropharynx. Left vocal cord palsy was also noted.

An echo-guided core needle biopsy was done, which showed a spindle cell tumor with scattered inflammatory cells and focal myxoid stroma [Figure 2]. Immunohistochemically, the spindle cells showed focal weak staining for smooth muscle actin (SMA). Murine double minute 2 showed scattered staining, and a desmin stain was negative. These findings suggested an atypical myofibroblastic tumor. CD34 (marker for solitary fibrous tumor and epithelioid sarcoma) and S100 (marker for nerve sheath tumor) were negative. An *ALK* (D5F3) stain was negative, wheres a *ROS1* stain was diffusely and strongly positive with cytoplasmic staining. The myofibroblast-like cytomorphology and striking *ROS1* immunostaining suggest the likelihood of a *ROS1*-rearranged IMT. However, an informal ROS1 fluorescence *in situ* hybridization (FISH) study revealed an equivocal result. Therefore, a formalin-fixed paraffin-embedded sample was sent for an amplicon-based targeted next-generation sequencing (NGS) focusing on 31 fusion genes and 182 transcripts [Supplement 1].

While waiting for the results, crizotinib 250 mg twice daily was started. Grade 1 blurred vision was noted; otherwise, she tolerated the treatment well, and her headaches gradually resolved. Follow-up examinations at the otolaryngologist clinic after 3 weeks showed less left parapharyngeal swelling. A contrast-enhanced neck MRI after taking crizotinib for 1 month confirmed partial response and significantly smaller tumor.

The NGS study did not report a *ROS1* fusion, which could not explain the response to crizotinib. Therefore, a computed tomography (CT)-guided biopsy was done, and the tumor tissue was sent for another targeted-NGS study using a hybrid-capture method (FoundationOne[®] Heme) [Supplement 2], which identified a rare *FN1-ROS1* fusion with *FN1* exon 23 (NM_002026) fused with *ROS1* exon 32 (NM_002944) [Figure 3]. Other alterations identified included Tet methylcytosine dioxygenase 2 (*TET2*) mutation (mutation allele frequency [MAF]: 25.7%), neurofibromin 2 mutation (MAF: 15.5%), and lysine methyltransferase 2D exon 6 rearrangements, all of which are tumor suppressor genes found in hematologic or solid organ malignancies.

The patient has been on crizotinib for 6 months with a partial response and ongoing necrosis within the tumor according to follow-up MRI images [Figure 1].

DISCUSSION

IMT is a mesenchymal myofibroblastic lesion of borderline malignancy, with frequent local recurrence but rare



Figure 1: Neck and brain magnetic resonance imaging with contrast enhancement: (T1, fat-saturated phase). A 6.3 cm necrotic tumor at the left carotid space, with invasion to the left C1, occipital condyle, clivus, left skull base, left hypoglossal canal, and medial part of the jugular foramen. The left internal carotid artery and left internal jugular vein were encased. The tumor responded to crizotinib treatment and was smaller on serial follow-up images

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Figure 2: A spindle cell tumor arranged in fascicles. There were focal hypercellular areas comprising plump spindle cells with up to moderate nuclear atypia, increased mitoses, and scattered lymphocyte and plasma cells. Focal myxoid stroma was noted (a-c). Immunohistochemically, the spindle cells showed focal weak staining for smooth muscle actin (d). ROS1 stain was diffusely and strongly positive (e). ROS1 fluorescence *in situ* hybridization was equivocal (<10% tumor cells harboring split signals) (f), while fibronectin 1 fluorescence *in situ* hybridization was positive (g)



Figure 3: Illustration of fibronectin 1-ROS1 fusion in this case

distant metastasis. The characteristic histology of IMT is plump or elongated myofibroblasts with inflammatory infiltration of lymphocytes, plasma cells, and eosinophils. Immunohistochemically, the majority of IMTs are positive for SMA. In addition, about 50% of IMTs are positive for *ALK* immunohistochemical (IHC) staining, which is correlated with *ALK* rearrangement and response to *ALK* inhibitors such as crizotinib. On the other hand, IMTs with negative *ALK* IHC stains have been reported to be more aggressive and to have a higher frequency of distant metastasis.^[16]

The application of NGS in oncology practice has led to the discovery of other druggable genetic alterations in patients with *ALK*-negative IMTs. Rearrangements of *ROS1*, *PDGFRB*, *NTRK*, and *RET* have all been reported in *ALK*-negative IMTs, of which *ROS1* fusion was the first reported and the most prevalent genetic alteration. In the reported case series, the *ROS1* fusion has been reported in 7%–13% of all IMT patients.^[3-15] A positive of *ROS1* IHC stain can predict *ROS1* rearrangement in IMT, and the staining pattern can be cytoplasmic staining, nuclear staining, or both.^[6] *ROS1* IHC has very high sensitivity (100%) but unsatisfactory specificity (84%) on detecting *ROS1* fusions in nonsmall-cell

lung cancer (NSCLC). Therefore, *ROS1* FISH, reverse transcription-polymerase chain reaction (RT-PCR), or NGS is needed as a confirmatory test.^[17] A total of 29 patients with *ROS1*-rearranged IMTs have been reported in the literature;^[3-15] however, only one case with negative *ROS1* stain has been reported to have a *TFG-ROS1* fusion by RT-PCR.^[11] Thus, *ROS1* IHC stain can be used as a screening tool, especially for *ALK*-negative IMTs.

FISH using the break-apart method is the gold standard for the detection of *ROS1* rearrangements in NSCLC.^[18] However, our patient's FISH result was equivocal. Reviewing the literature, two other IMTs with *ROS1* fusions also had false-negative FISH results, which eventually proved to harbor *TFG-ROS1* fusions by RT-PCR. The equivocal *ROS1* FISH results may be due to a more complex mechanism of rearrangement instead of simple, balanced translocation of the partner gene.^[5,10]

We performed two different NGS studies sequentially. The first used an amplicon-based library focusing on 31 fusion genes and 182 transcripts, and the result turned out to be a false negative. The other used hybrid-capture based library sequencing of both DNA (406 genes and selected introns of Kuo, et al.: Journal of Cancer Research and Practice (2020)

31 genes involving rearrangements) and RNA (265 genes commonly involved in fusions), and detected a rare *FN1-ROS1* fusion. Both amplicon-base and hybrid-capture-based NGS methods have their pros and cons. Amplicon-based NGS needs less genomic material and hence is very sensitive to detect hotspot single-nucleotide variations. However, the sensitivity to detect gene rearrangements, especially those with different partners with variable breakpoints, is limited by the number of primers (amplicons). In contrast, hybrid capture-based NGS has an advantage in the detection of gene rearrangements because of the direct hybridization of the sequence of interest without the necessity of PCR. However, the higher demand for genomic material and longer turn-around time for library preparation are disadvantages that should be taken into consideration.^[19]

To date, 29 *ROS1*-rearranged IMTs have been reported, of which 21 have been confirmed by RT-PCR or NGS, and *TFG-ROS1* was the most common fusion transcript (77%). ^[3-15] Our patient is the second reported case harboring an *FN1-ROS1* fusion in the medical literature. The other patient with an *FN1-ROS1* fusion IMT was reported by Lopez-Nunez *et al.* in 2020, but the *FN1* breakpoint was exon 41 (NM_212482) and the *ROS1* breakpoint was exon 32 (NM_002944).^[13] Other fusion genes, such as *YWHAE-ROS1* and *TIMP3-ROS1*, have also been reported.^[3,15] In terms of efficacy, the reported response rate of crizotinib was 100% (seven responders in seven cases) in IMT patients harboring *TFG-ROS1*.^[3-15] Ceritinib and entrectinib have been reported to be effective in treating *ROS1*-rearranged IMTs as well.^[8,12]

The *FN1-ROS1* fusion found in our patient demonstrated a similar fusion pattern to other oncogenic *ROS1* fusion proteins, with a retained *ROS1* kinase domain at the 3' end and the junction point on *ROS1* occurring at the 5' end of exon 32. Although the *FN1-ROS1* fusion protein is rare, *FN1* has been reported to fuse with *ALK* on IMTs.^[3] *In vitro* studies have demonstrated different oncogenic properties and different responses to tyrosine kinase inhibitors among different *ALK* fusion partners, and *FN1-ALK* fusion protein has been reported to have the greatest ability to form foci in agar compared to all other *ALK* fusions.^[20] Whether the *FN1-ROS1* fusion has different oncogenicity or different efficacy to tyrosine kinase inhibitors compared with other *ROS1* fusions remains unknown.

CONCLUSION

Our patient demonstrated that *ROS1* IHC still plays an important role in *ALK*-negative IMT patients, as it is a cheap and fast diagnostic tool to guide further treatment. As NGS has become a popular choice of confirmatory test, different library preparation methods might have different sensitivity, especially when targeting oncogenic fusions with a variety of partner genes. Crizotinib for IMT patients with *FN1-ROS1* fusion is effective and tolerable.

Ethical approval and declaration of patient consent

This study was approved by the NTUH research ethics committee (project number: 202007045W).

The authors certify that they have obtained all appropriate patient consent forms. In the forms, the patient has given her consent for her images and other clinical information to be reported in the journal. The patient understands that her name and initials will not be published, and due efforts will be made to conceal her identity, but that anonymity cannot be guaranteed.

Financial support and sponsorship Nil.

Conflicts of interest

There are no conflicts of interest.

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SUPPLEMENTARY MATERIAL AVAILABLE ONLINE

Supplement 1: List of selected fusion genes and transcripts included in the amplicon-based next-generation sequencing

Fusion genes:

ABL1, ALK, BCR, BRAF, CD74, ERG, ESR1, ETV1, ETV4, ETV5, ETV6, EZR, FGFR1, FGFR2, FGFR3, KMT2A, MET, NRG1, NTRK1, NTRK2, NTRK3, NUTM1, PDGFRA, PDGFRB, RARA, RET, ROS1, RSP02, SDC4, SLC34A2, TMPRSS2

Transcripts for ROS1:

CCDC6-ROS1, CD74-ROS1, CLIP1-ROS1, CLTC-ROS1, ERC1-ROS1, EZR-ROS1, GOPC-ROS1, MS-ROS1, MYO5A-ROS1, PPFIBP1-ROS1, SDC4-ROS1, SLC34A2-ROS1, TFG-ROS1, TMEM106B-ROS1, TPM3-ROS1

Supplement 2: List of selected genes for rearrangement included in the hybrid capture-based next-generation sequencing:

ALK, BCL2, BCL6, BCR, BRAF, CCND1, CRLF2, EGFR, EPOR, ETV1, ETV4, ETV5, ETV6, EWSR1, FGFR2, IGH, IGK, IGL, JAK1, JAK2, KMT2A (MLL), MYC, NTRK1, PDGFRA, PDGFRB, RAF1, RARA, RET, ROS1, TMPRSS2, TRG