



## Case Report

# Perinatal imaging findings and molecular genetic analysis of thanatophoric dysplasia type 1 in a fetus with a c.2419T>G (p.Ter807Gly) (X807G) mutation in *FGFR3*



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## ABSTRACT

**Objective:** We present perinatal imaging findings and molecular genetic analysis of thanatophoric dysplasia type I (TD1) in a fetus.

**Case Report:** A 28-year-old woman was referred for genetic counseling at 22 weeks of gestation because of abnormal prenatal ultrasound findings. Level II ultrasound examination revealed a narrow chest, shortened and curved long limbs, protrusion of the abdomen, and macrocephaly. A tentative diagnosis of TD1 was made. After genetic counseling, the pregnancy was terminated and a malformed fetus was delivered. Postnatal radiography findings were consistent with the diagnosis of TD1, with additional findings of short ribs, platyspondyly, and horizontal acetabular roofs. Molecular genetic analysis using umbilical cord tissue revealed a heterozygous mutation of c.2419T>G (p.Ter807Gly) (X807G) in the fibroblast growth factor receptor 3 gene (*FGFR3*).

**Conclusion:** A second-trimester fetus with a heterozygous c.2419T>G mutation in *FGFR3* may present characteristic ultrasound and X-ray findings of TD1.

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## Introduction

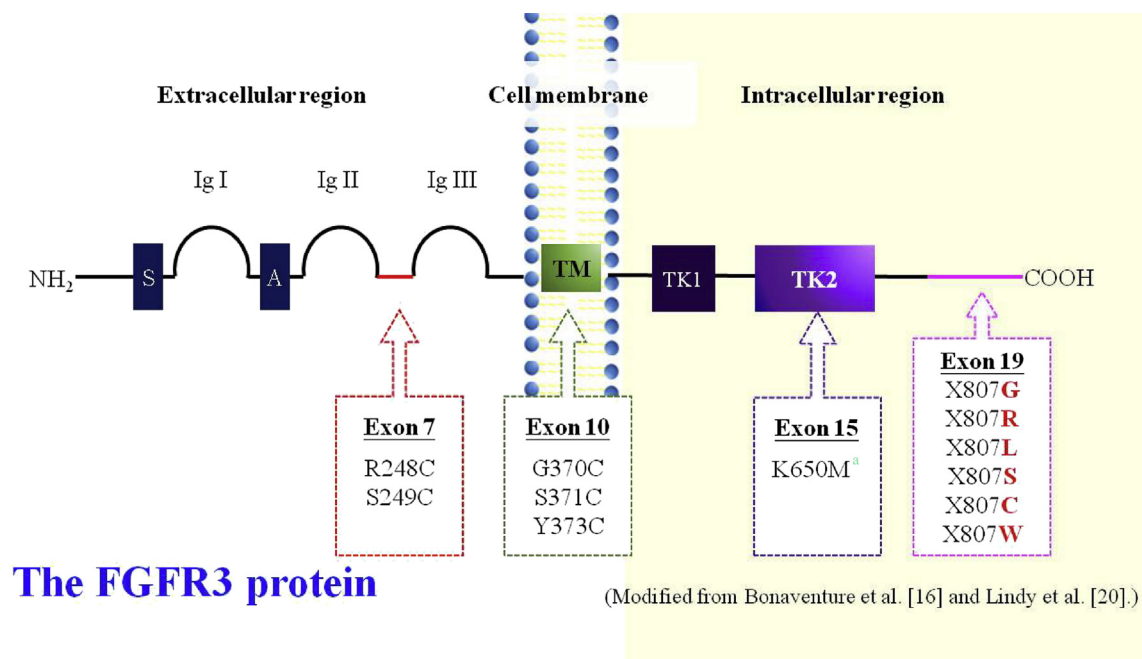
Thanatophoric dysplasia (TD) is a neonatal, lethal, short-limb dwarfism syndrome, with a prevalence rate of approximately 1:20,000–1:12,000 in prenatal cases [1,2] and 1:47,000–1:33,000 in live births [3].

According to the clinical features, TD is classified as TD type 1 (TD1) and TD type 2 (TD2). TD1 is characterized by short limbs (below the 5<sup>th</sup> centile at 20 weeks gestation) and curved femurs with or without cloverleaf skull, whereas TD2 is characterized by

short limbs with straight femurs and moderate-to-severe cloverleaf skull. The common features of TD1 and TD2 are short limbs, narrow thoracic cage, short ribs, macrocephaly, and brachydactyly [4–8].

TD is a sporadic, autosomal dominant skeletal dysplasia caused by mutations in the fibroblast growth factor receptor 3 gene (*FGFR3*). TD1 is caused by *FGFR3* missense or stop codon mutations [4,9–11], whereas TD2 is caused by only one *FGFR3* missense mutation of p.Lys650Glu (K650E) [12–14]. The *FGFR3* protein comprises three main parts: an extracellular region including three immunoglobulin (Ig) domains, a transmembrane segment, and an intracellular region comprising two tyrosine kinase (TK) domains (Figure 1) [15,16]. Here, we present perinatal imaging findings and molecular genetic analysis of TD1 in a fetus with a c.2419T>G (p.Ter807Gly) (X807G) mutation in *FGFR3*.

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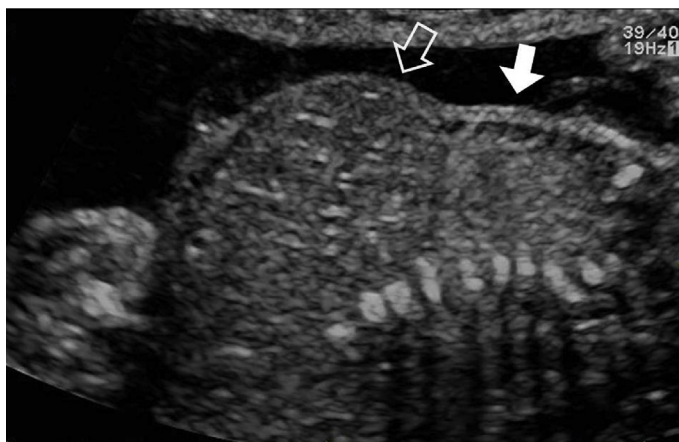
**Figure 1.** FGFR3 protein structure and reported locations of *FGFR3* gene mutations causing TD1. A = acid box; FGFR3 = fibroblast growth factor receptor 3; Ig, immunoglobulin-like domains (I, II, III); S = secretory peptide; TD1 = thanatophoric dysplasia type 1; TM = transmembrane domain; TK1 = first tyrosine kinase domain; TK2 = second tyrosine kinase domain. <sup>a</sup> Severe achondroplasia with developmental delay and acanthosis nigricans is caused by an amino acid change due to K650M in *FGFR3*.

## Case Report

A 28-year-old gravida 1, para 0 woman was referred for genetic counseling at 22 weeks gestation because of abnormal prenatal ultrasound findings. She and her 28-year-old husband were healthy, with no family history of skeletal anomalies. Level II ultrasound examination revealed a narrow chest, shortened and curved long limbs, protrusion of the abdomen, and macrocephaly with a biparietal diameter of 59.7 mm (24 weeks). The lengths of the long limbs were all below the fifth centile of normal biometry: right humerus length (HL) = 18.9 mm (15 weeks), left HL = 18.2 mm (15 weeks), right radius length (RL) = 15.4 mm (15 weeks), left RL = 12.6 mm (14 weeks), right ulna length (UL) = 18.2 mm (16 weeks), left UL = 14.2 mm (15 weeks), right femur length (FL) = 18.1 mm (15 weeks), left FL = 20.1 mm

(16 weeks), right tibia length (TL) = 14.7 mm (15 weeks), left TL = 14.0 mm (15 weeks), right fibula length = 14.0 mm (15 weeks), and left fibula length = 13.7 mm (15 weeks). The abdominal circumference (AC) was 175.5 mm (22 weeks) (Figures 2 and 3). The left- and right-side FL/AC ratios were 0.10 (18.1 mm/175.5 mm) and 0.11 (120.1 mm/175.5 mm), respectively. Both were < 0.16. Parilla et al [17] reported that an FL/AC ratio < 0.16 implies a specific diagnosis of TD. The amount of amniotic fluid was normal. A tentative diagnosis of TD1 was made.

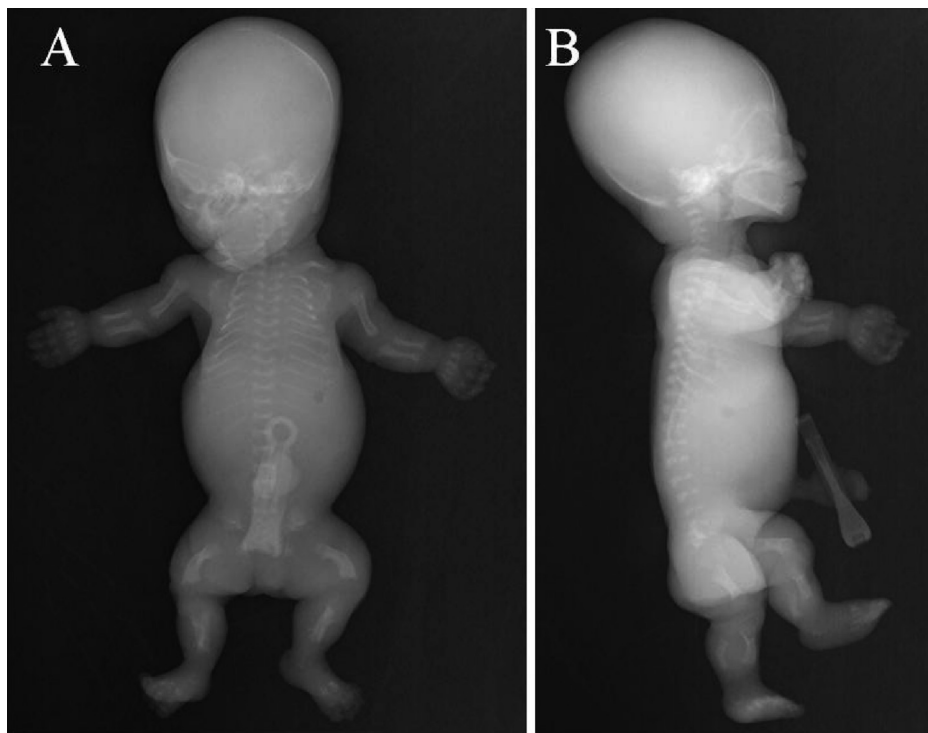
After genetic counseling, the pregnancy was subsequently terminated and a malformed fetus was delivered. Postnatal radiography findings were consistent with the diagnosis of TD1, with additional findings of short ribs, platyspondyly, and horizontal acetabular roofs (Figure 4). The fetal humerus and femur exhibited “telephone handle” bowing with metaphyseal flaring. Cytogenetic



**Figure 2.** Prenatal ultrasound of fetus at 22 weeks gestation in profile reveals a narrow chest (solid arrow) and protrusion of the abdomen (hollow arrow).



**Figure 3.** Prenatal ultrasound of fetus at 22 weeks gestation revealed short and curved limbs. (A) Right humerus with a length of 18.9 mm (15 weeks); (B) right femur with a length of 18.1 mm (15 weeks); (C) right tibia (solid arrow) with a length of 14.7 mm (15 weeks), and right fibula (hollow arrow) with a length of 14.0 mm (15 weeks).



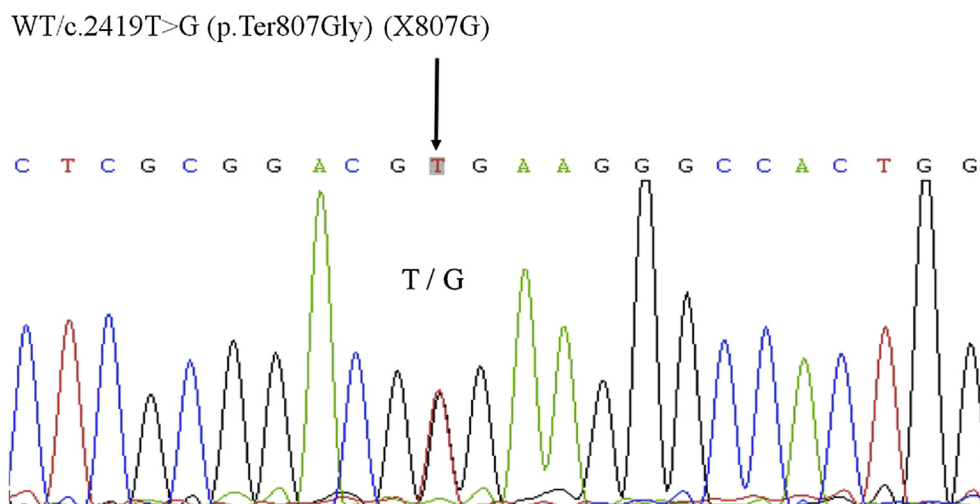
**Figure 4.** Postnatal radiography revealed a narrow chest, short limbs, short ribs, platyspondyly, horizontal acetabular roofs, and a large head. (A) Coronal view and (B) sagittal view.

analysis of the umbilical cord tissue revealed a karyotype of 46,XX. Molecular genetic analysis of the *FGFR3* gene using the genomic DNA sequence from the umbilical cord tissue revealed a heterozygous mutation of c.2419T>G (p.Ter807Gly) (X807G) (Figure 5).

## Discussion

We present a rare case of TD1 with a c.2419T>G (p.Ter807Gly) (X807G) mutation in *FGFR3*. To date, at least 14 different cDNA nucleotide changes in *FGFR3* have been reported, representing 12 different protein sequence changes associated with TD1 (Table 1 and Figure 1) [4,5,9,16,18–20]. The reported six missense mutations result in six different protein amino acid substitutions. The

mutations of c.742C>T (R248C) and c.746C>G (S249C) occur in Exon 7, which encodes the linker region between the Ig II and Ig III loops [16]. The mutations of c.1108G>T (G370C), c.1111A>T (S371C), and c.1118A>G (Y373C) occur in exon 10, which encodes the transmembrane domain [16]. The mutation of c.1949A>T (K650M) occurs in Exon 15, which encodes the TK2 domains [4,14,19]. Eight stop codon loss mutations in Exon 19, such as c.2419T>G (X807G), c.2419T>C (X807R), c.2419T>A (X807R), c.2420G>T (X807L), c.2420G>C (X807S), c.2421A>T (X807C), c.2421A>C (X807C), and c.2421A>G (X807W), result in six different protein sequence extensions, and an elongated coding frame caused by the mutations of chain termination stop codon [4,9,11,18,20].



**Figure 5.** Molecular genetic analysis of the *FGFR3* gene using the genomic DNA sequence from umbilical cord tissue reveals a heterozygous mutation of c.2419T>G (p.Ter807Gly) (X807G).



**Table 1**  
FGFR3 gene mutations in thanatophoric dysplasia type 1.

Mutation category	cDNA nucleotide change	Protein amino acid change	Exon
Missense mutations	c.742C>T	p.Arg248Cys	R248C
	c.746C>G	p.Ser249Cys	S249C
	c.1108G>T	p.Gly370Cys	G370C
	c.1111A>T	p.Ser371Cys	S371C
	c.1118A>G	p.Tyr373Cys	Y373C
Stop codon mutations	c.1949A>T <sup>a</sup>	p.Lys650Met	K650M
	c.2419T>G	p.Ter807Gly	X807G
	c.2419T>C	p.Ter807Arg	X807R
	c.2419T>A	p.Ter807Arg	X807R
	c.2420G>T	p.Ter807Leu	X807L
	c.2420G>C <sup>b</sup>	p.Ter807Ser	X807S
	c.2421A>T	p.Ter807Cys	X807C
	c.2421A>C	p.Ter807Cys	X807C
	c.2421A>G	p.Ter807Trp	X807W

Modified from Rousseau et al [9], Chen et al [5], Foldynova-Trantirkova et al [19], Xue et al [18], Karczeski et al [4], and Lindy et al [20].

<sup>a</sup> Severe achondroplasia with developmental delay and acanthosis nigricans is caused by an amino acid change due to K650M in *FGFR3*.

<sup>b</sup> The c.2420G>C mutation was reported by Xue et al [18] and Lindy et al [20].

In the cases of TD1, the c.742C>T (R248C) mutation has the highest frequency, followed by the c.1118A>G (Y373C) mutation, and stop codon lost mutations such as c.2419T>G (X807G), c.2419T>C (X807R), c.2419T>A (X807R), c.2420G>T (X807L), c.2420G>C (X807S), c.2421A>T (X807C), c.2421A>C (X807C), and c.2421A>G (X807W) [10,18]. The mutations of c.742C>T (R248C) and c.1118A>G (Y373C), account for 55.1–62.2% and 21.6–22.2% of TD1, respectively (Table 2) [10,18]. Passos-Bueno et al [10] reported that 11.9% (22 cases/185 cases) of TD1 were caused by stop codon mutations, and among the 22 cases with stop codon mutations, seven cases were caused by the c.2419T>G (p.Ter807Gly) (X807G) mutation. Xue et al [18] reported that 6.5% (12 cases/185 cases) of TD1 were caused by stop codon mutations, and among the 12 cases with stop codon mutations, three cases were caused by the c.2419T>G (p.Ter807Gly) (X807G) mutation.

Two-dimensional ultrasound imaging, with or without three-dimensional examination, is useful for prenatal diagnosis of TD [4,21]. If the prenatal sonographic imaging examination

**Table 2**  
Reported FGFR3 gene mutations in TD1.

Mutations	cDNA nucleotide change	Protein amino acid change	Passos-Bueno et al 1999		Xue et al 2014	
			No. of cases <sup>a</sup>	%	No. of cases <sup>b</sup>	%
Missense	c.742C>T	R248C	102	55.1%	115	62.2%
	c.746C>G	S249C	13	7.0%	11	5.9%
	c.1108G>T	G370C	2	1.1%	4	2.2%
	c.1111A>T	S371C	1	0.5%	— <sup>c</sup>	—
	c.1118A>G	Y373C	40	21.6%	41	22.2%
Stop codon	c.1949A>T	K650M	5	2.7%	2	1.1%
	c.2419T>G	X807G	7	3.8%	3	1.6%
	c.2419T>C	X807R	—	—	2	1.1%
	c.2419T>A	X807R	5	2.7%	2	1.1%
	c.2420G>T	X807L	2	1.1%	1	0.5%
	c.2420G>C	X807S	—	—	1	0.5%
	c.2421A>T	X807C	5	2.7%	—	—
	c.2421A>C	X807C	1	0.5%	—	—
	c.2421A>G	X807W	2	1.1%	3	1.6%
Total No.			185		185	

<sup>a</sup> Including reports by Rousseau et al [9,11], Tavormina et al [13,29,30], Bonaventure et al [16], Nerlich et al [31], Pokharel et al [32], Bellus et al [33], Camera et al [34], Wilcox et al [23], Kitoh et al [12], Brodie et al [35,36], and Wilcox and Kitoh [10].

<sup>b</sup> Including 93 cases of thanatophoric dysplasia type 1 and platyspondylic lethal skeletal dysplasia, San Diego type (PLSD-SD) reported by Tavormina et al [13], Kitoh et al [12], Wilcox et al [23] and Brodie et al [35,36].

<sup>c</sup> no information.

demonstrates short limbs, an FL/AC ratio < 0.16, a narrow chest, femoral telephone handle bowing especially after 20 weeks of gestation, and no cloverleaf head deformity, TD1 is likely a preliminary diagnosis [4,17,22]. However, even patients with the same *FGFR3* mutation may have phenotypic differences. The TD variants occasionally lack typical characteristics, such as facial deformation or different degrees of femur bowing [5]. Wilcox et al [23] and Castori et al [24] suggested that the phenotypic variability of TD may be due to nonallelic genetic variability, epigenetic/environmental, and stochastic factors. For example, severe achondroplasia with developmental delay and acanthosis nigricans (SADDAN), an allelic disease of TD1, is caused by an amino acid change due to c.1949A>T (K650M) in *FGFR3* [25–27]. The radiographic features and sonographic findings in SADDAN are similar to those in TD1, but the phenotypes are milder in SADDAN than in TD1 [14,28]. The most distinct difference between SADDAN and TD1 is longer-term survival, craniosynostosis, and acanthosis nigricans in patients with SADDAN [27,28].

Our case shows that a stop codon mutation of c.2419T>G (p.Ter807Gly) (X807G) can exhibit typical features of TD1. We suggest that prenatal diagnosis of TD1 by ultrasound should include a molecular genetic analysis of *FGFR3* to elucidate the molecular pathogenesis and the acquired information will provide useful information for genetic counseling.

## Conflict of interest

The authors have no conflicts of interest relevant to this article.

## Acknowledgments

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