



Prenatal diagnosis of severe glutaric acidemia type II due to a novel homozygous *ETFDH* frameshift variant: Case report and literature review

Yeni homozigot ETFDH çerçeve kayması varyantına bağlı şiddetli glutarik asidemi tip II'nin prenatal tanısı: Olgu sunumu ve literatür derlemesi

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Abstract

Glutaric acidemia type II (GA2) is a rare autosomal recessive fatty acid oxidation disorder that can present prenatally with bilateral hyperechoic cystic kidneys. We report a 23-year-old gravida 2 woman who was referred at 18+2 weeks for suspected fetal renal anomalies, with a history of consanguinity and a prior unexplained neonatal death. Quantitative fluorescent polymerase chain reaction and microarray were normal; whole-exome sequencing identified a novel homozygous *ETFDH* frameshift variant (c.1200_1203del; p.His401GlnfsTer3). The parents were heterozygous, and the variant was classified as likely pathogenic. The family terminated the pregnancy after counseling. This case highlights both GA2 in the differential diagnosis of fetal renal anomalies and the value of prenatal exome sequencing for diagnosis and counseling.

Keywords: Congenital abnormalities, *ETFDH* deficiency, glutaric acidemia type II, prenatal diagnosis, whole-exome sequencings

Öz

Glutarik asidemi tip II (GA2), prenatal dönemde bilateral hiperekojenik ve kistik böbreklerle prezente olabilen, nadir görülen otozomal resesif bir yağ asidi oksidasyon bozukluğudur. On sekiz hafta iki günlük gebelikte fetal renal anormali şüphesiyle yönlendirilen, akraba evliliği öyküsü ve açıklanamayan önceki neonatal kaybı bulunan 23 yaşındaki gravida 2 olgu sunulmuştur. Kantitatif fluoresan polimeraz zincir reaksiyonu ve kromozomal mikrodizin analizleri normal bulundu. Tüm ekzom dizilemesinde, her iki ebeveynde heterozigot olarak saptanan, yeni homozigot *ETFDH* çerçeve kayması varyantı (c.1200_1203del; p.His401GlnfsTer3) belirlenmiş ve muhtemel patojenik olarak sınıflandırılmıştır. Genetik danışmanlık sonrasında gebelik sonlandırılmıştır. Bu olgu, fetal renal anomalilerin ayırıcı tanısında GA2'nin dikkate alınması gerektiğini ve prenatal ekzom dizilemenin tanı ile genetik danışmanlıktaki değerini vurgulamaktadır.

Anahtar Kelimeler: Konjenital anomaliler, *ETFDH* eksikliği, glutarik asidemi tip II, prenatal tanı, tüm ekzom dizilemesi

Introduction

Glutaric acidemia type II (GA2), also referred to as multiple acyl-CoA dehydrogenase deficiency (MADD), is a rare autosomal recessive inborn error of metabolism characterized by impaired mitochondrial oxidation of fatty acids and certain amino acids. This disorder results from defects in the electron transfer flavoprotein (ETF) system, which plays a critical role in shuttling electrons from multiple flavoprotein dehydrogenases

to the mitochondrial respiratory chain. Pathogenic variants affecting this system disrupt cellular energy metabolism and lead to the accumulation of toxic metabolic intermediates, particularly during periods of increased metabolic demand, such as the perinatal and neonatal periods⁽¹⁾. The molecular basis of GA2 involves pathogenic variants in three genes encoding components of the ETF system: *ETFA* and *ETFB*, which encode the α and β subunits of ETF, and *ETFDH*, which encodes ETF-ubiquinone oxidoreductase (ETF-QO). Among these genetic

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causes, *ETFDH*s variants are the most frequently reported, particularly in severe early-onset forms of the disease. GA2 has a broad clinical spectrum and is traditionally classified into three phenotypic forms: a congenital-onset form associated with structural anomalies and neonatal lethality, a neonatal-onset form without congenital anomalies but with rapid metabolic decompensation, and a later-onset, often riboflavin-responsive form with a more favorable prognosis. The congenital and early neonatal forms are typically associated with severe metabolic acidosis, hypoglycemia, cardiomyopathy, hypotonia, and high mortality despite aggressive postnatal management⁽²⁾.

Although GA2 is recognized primarily as a postnatal metabolic disorder, accumulating evidence indicates that its most severe forms may manifest during fetal life. Prenatal involvement is increasingly reported, most commonly presenting with non-specific yet suggestive ultrasonographic findings. Among these, bilaterally enlarged, hyperechogenic, and cystic kidneys represent the most frequently described prenatal abnormalities, often accompanied by alterations in amniotic fluid volume and, in some cases, hepatomegaly or cardiomegaly. The pathophysiological mechanisms underlying fetal renal involvement in GA2 remain incompletely understood; however, it has been postulated that intrauterine accumulation of toxic metabolites may interfere with normal renal morphogenesis, leading to cystic or dysplastic changes⁽³⁾. Despite these observations, prenatal diagnosis of GA2 remains particularly challenging. The ultrasonographic features are not pathognomonic and overlap with a wide spectrum of fetal renal disorders, including autosomal recessive polycystic kidney disease (ARPKD), renal dysplasia, and other ciliopathies. Furthermore, conventional prenatal biochemical testing has limited sensitivity and specificity for fetal diagnosis, reducing its utility for definitive diagnosis. As a result, GA2 is frequently diagnosed only after birth, often following rapid neonatal deterioration or unexplained early neonatal death, and in many cases after missed opportunities for earlier recognition⁽⁴⁾.

Advances in prenatal genetic diagnostics, particularly the increasing availability of whole-exome sequencing (WES), have significantly improved the ability to identify rare monogenic disorders *in utero*. Prenatal WES has emerged as a powerful diagnostic tool for fetuses with structural anomalies who have normal conventional cytogenetic testing, enabling the detection of pathogenic variants in genes not routinely assessed by targeted panels. In the context of GA2, prenatal identification of biallelic pathogenic or likely pathogenic variants in *ETFA*, *ETFB*, or *ETFDH* can support a molecular diagnosis, inform counseling regarding the expected clinical course, and guide individualized pregnancy management. Moreover, establishing a molecular diagnosis during pregnancy has substantial implications for future reproductive planning, including targeted prenatal testing or preimplantation genetic testing (PGT-M) in subsequent pregnancies⁽⁵⁾. In this report, we describe the prenatal molecular diagnosis of GA2 in a fetus

presenting with bilateral hyperechogenic and cystic kidneys, in whom WES revealed a novel homozygous frameshift variant in *ETFDH*. This case expands the mutational spectrum associated with severe prenatal GA2 and underscores the importance of comprehensive prenatal genetic evaluation in fetuses with suggestive renal anomalies, particularly in the presence of consanguinity and a history of unexplained neonatal loss. To place this case in context, we searched PubMed/MEDLINE from inception through September 2026 using the terms “glutaric acidemia type II,” “glutaric aciduria type II,” “multiple acyl-CoA dehydrogenase deficiency,” “*ETFDH*,” “*ETFA*,” “*ETFB*,” “prenatal diagnosis,” and “fetal kidney,” and restricted the case-summary table to English-language reports with documented prenatal or perinatal presentation. The updated search identified a 2025 report providing functional evidence for *ETFDH* variants associated with fetal-onset MADD and polycystic kidneys and a 2026 series emphasizing combined biochemical and genetic assessment for early diagnosis and prenatal evaluation^(6,7).

Case Report

A 23-year-old gravida 2, para 1 woman was referred to our tertiary perinatology unit at 18+2 weeks' gestation because of suspected fetal renal anomalies detected during a routine second-trimester ultrasonographic examination at an external center. The pregnancy had been spontaneously conceived, and no first- or second-trimester aneuploidy screening tests had been performed. The patient and her partner were second cousins (second-cousin consanguinity); their fathers were first cousins. A detailed obstetric history revealed that the patient's first pregnancy resulted in a term delivery; however, the neonate died on postnatal day four due to unexplained clinical deterioration. No metabolic investigations, genetic testing, or postmortem examination had been performed at that time. According to the family's report, prenatal ultrasonography during the first pregnancy revealed fetal renal abnormalities, although no further diagnostic work-up was pursued.

Targeted fetal ultrasonography performed at our center demonstrated bilaterally enlarged kidneys with increased echogenicity and multiple cystic structures involving the renal parenchyma. The renal findings were symmetric and diffuse, with loss of normal corticomedullary differentiation (Figure 1). The fetal abdominal circumference was above the 99th percentile, attributable primarily to renal enlargement, whereas all other biometric parameters were within normal gestational-age-appropriate percentiles. No additional structural anomalies were identified in the central nervous system, cardiovascular system, gastrointestinal tract, or skeletal system. The volume of the amniotic fluid was within normal limits at the time of evaluation.

Given the combination of severe bilateral renal abnormalities, consanguinity, and a history of unexplained early neonatal death in a previous pregnancy, a genetic etiology was strongly suspected. The patient and her partner received comprehensive

genetic counseling, during which the differential diagnoses, invasive diagnostic options, outcomes, and prognostic implications were discussed in detail. Following counseling, the couple opted for invasive prenatal testing.

Diagnostic Assessment, Therapeutic Intervention, Follow-up, and Outcomes

Amniocentesis was performed under continuous ultrasound guidance without complications at 18+3 weeks' gestation. The obtained amniotic fluid sample was subjected to stepwise genetic evaluation. Quantitative fluorescent polymerase chain reaction analysis excluded common aneuploidies, including trisomies 13, 18, and 21, and sex chromosome abnormalities. Conventional karyotyping and chromosomal microarray analysis revealed no pathogenic copy number variations or chromosomal abnormalities.

Given the strong suspicion of a monogenic disorder, trio-based WES was subsequently performed on fetal DNA, with parallel analysis of parental samples. WES identified a homozygous frameshift variant in the *ETFDH* gene in the fetus, designated c.1200_1203del (*p.His401GlnfsTer3*). Parental testing confirmed that both the mother and father were heterozygous carriers of the same variant (Figure 2). This deletion results in a frameshift and a premature termination codon, and is predicted to cause loss of normal protein function, an established disease mechanism for *ETFDH*-related MADD. According to the American College of Medical Genetics and Genomics/Association for Molecular Pathology criteria, the variant was classified as likely pathogenic based on PVS1 and PM2_supporting. PVS1 was applied because

the frameshift variant was predicted to result in loss of function, whereas PM2_supporting was applied because the variant was absent from major population databases. This specific variant had not previously been reported in dbSNP, ClinVar, gnomAD, or the published literature at the time of analysis.

On the basis of the biallelic *ETFDH* finding, parental segregation, and concordant fetal phenotype, the molecular diagnosis was considered consistent with severe early-onset GA2. The couple was counseled that congenital-onset MADD with structural anomalies is frequently associated with rapid neonatal metabolic decompensation and high mortality, but it was emphasized that the precise postnatal course cannot be predicted with certainty from a single novel variant. After thorough discussion of the expected clinical course and available management options, the family elected to proceed with termination of the pregnancy.

Termination was performed at 23+4 weeks of gestation in accordance with local regulations and institutional protocols. The family declined fetal autopsy, so postmortem pathological examination could not be performed. Following the procedure, additional genetic counseling was provided. Given the confirmed autosomal recessive inheritance and identification of a likely pathogenic *ETFDH* variant, the couple was informed of a 25% risk of recurrence in future pregnancies and counseled regarding available reproductive options, including targeted prenatal diagnosis (amniocentesis/chorionic villus sampling) and PGT-M. A chronological summary of the diagnostic investigations, genetic analyses, and subsequent management decisions during the course of this pregnancy is provided in Table 1.

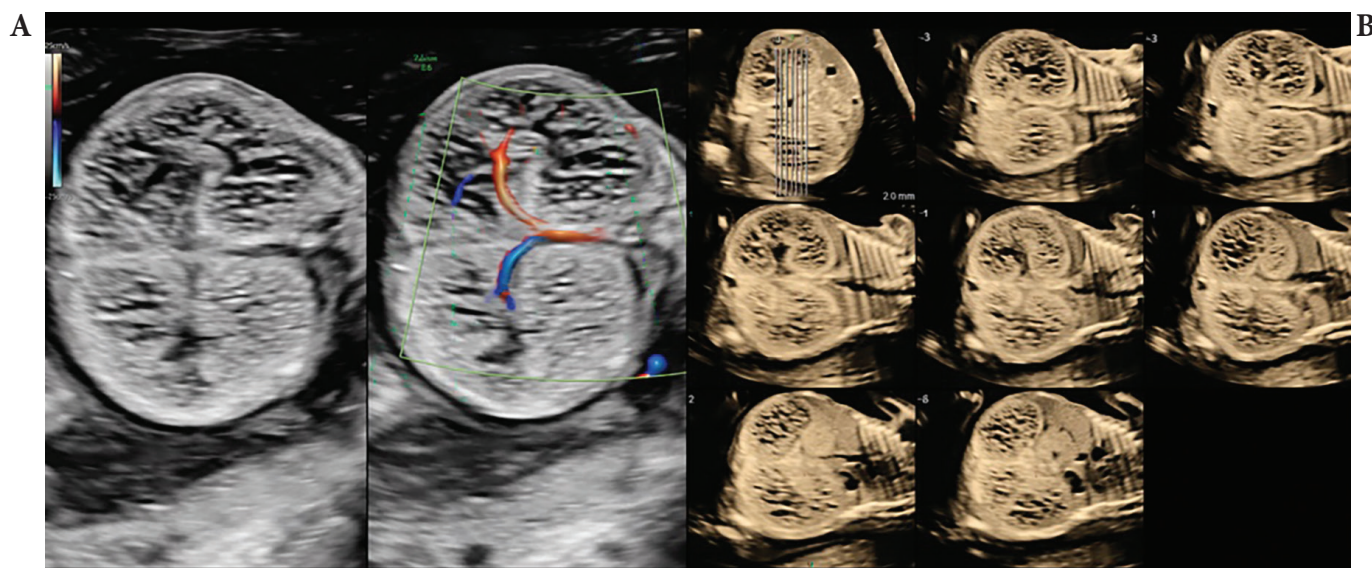


Figure 1. Prenatal ultrasonographic findings of fetal kidneys at 18+2 weeks of gestation

(A) Two-dimensional grayscale ultrasound with color Doppler demonstrates bilaterally enlarged, markedly hyperechogenic kidneys with loss of normal corticomedullary differentiation and multiple cortical microcysts

(B) Multislice three-dimensional ultrasonographic reconstruction illustrating diffuse bilateral renal involvement, symmetrical parenchymal enlargement, and internal cystic architecture

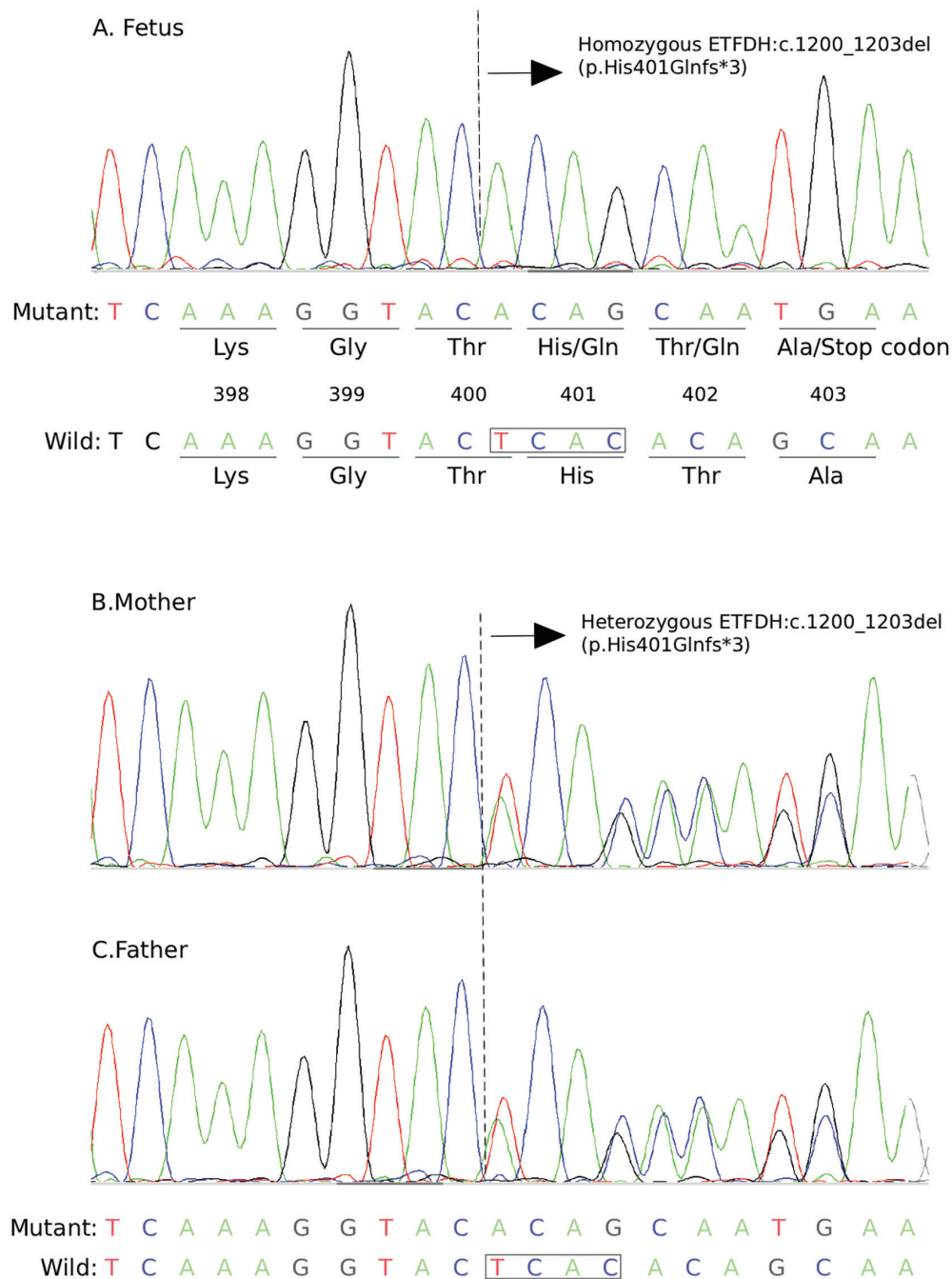


Figure 2. Sanger sequencing analysis of the ETFDH c.1200_1203del (p.His401GlnfsTer3) variant in the fetus and parents

(A) **Fetus:** Sanger sequencing chromatogram showing the homozygous 4-bp deletion (TCAC) in exon 10 of *ETFDH*, characterized by clean, single-sequence peaks downstream of the deletion site. The aligned wild-type (WT) and mutant sequences illustrate the deleted nucleotides (boxed) and the resulting frameshift, with altered amino acid residues and premature termination at codon 403

(B) **Mother:** Sanger sequencing chromatogram demonstrating heterozygous carrier status, with overlapping nucleotide peaks beginning at the deletion breakpoint due to the superimposition of wild-type and mutant alleles

(C) **Father:** Sanger sequencing chromatogram confirming heterozygous carrier status, with overlapping peaks downstream of the deletion breakpoint, consistent with the maternal findings. The aligned WT and mutant sequences shown below the chromatogram illustrate the 4-bp deletion

The vertical dashed lines and black arrows indicate the deletion breakpoint. Nucleotide and amino acid annotations illustrate the sequence alteration and its predicted protein-level consequence

Table 1. Timeline of clinical events and diagnostic pathway

Gestational age/time point	Clinical event
Previous pregnancy (term)	Prenatal renal anomalies reported; neonate died on postnatal day 4 due to unexplained clinical deterioration.
Early first trimester (current pregnancy)	Spontaneous conception; no first-trimester aneuploidy screening performed.
18+0 weeks	Routine second-trimester ultrasound at external center revealed suspected fetal renal abnormalities.
18+2 weeks	Referral to tertiary perinatology unit; detailed fetal ultrasonography demonstrated bilaterally enlarged, markedly hyperechogenic kidneys with multiple cystic changes and loss of corticomedullary differentiation.
18+3 weeks	Comprehensive genetic counseling provided; ultrasound-guided amniocentesis performed without complications.
19+1 weeks	QF-PCR analysis excluded common aneuploidies (13, 18, 21, and sex chromosomes).
20+0 weeks	Chromosomal microarray analysis showed no pathogenic copy number variants. Trio-based WES initiated.
22+4 weeks	Homozygous <i>ETFDH</i> frameshift variant (c.1200_1203del; p.His401GlnfsTer3) identified in the fetus; parents confirmed as heterozygous carriers.
23+0 weeks	Multidisciplinary counseling regarding the molecular findings, the high-risk of severe neonatal disease and mortality, prognostic uncertainty, and management options.
23+4 weeks	Pregnancy terminated in accordance with local regulations and institutional protocols.
Post-termination	Post-test genetic counseling provided regarding 25% recurrence risk and future reproductive options (PGT-M/targeted PND).
<i>ETFDH</i> : Electron transfer flavoprotein dehydrogenase, PGT-M: Preimplantation genetic testing for monogenic disorders, PND: Prenatal diagnosis, QF-PCR: Quantitative fluorescent polymerase chain reaction, WES: Whole-exome sequencing	

Discussion

GA2, also known as MADD, represents a heterogeneous group of mitochondrial fatty acid oxidation disorders with a broad phenotypic spectrum, ranging from late-onset, treatable forms to devastating congenital and early-neonatal presentations. The most severe forms, typically associated with congenital anomalies and early neonatal lethality, remain diagnostically challenging in the prenatal period owing to their rarity, phenotypic variability, and the non-specific nature of fetal imaging findings. The present case illustrates several clinically important aspects of severe prenatal GA2, including its sonographic presentation, molecular basis, diagnostic pathway, and implications for pregnancy management and future reproductive counseling. Early reports highlighted potential deleterious intrauterine effects and demonstrated the feasibility of prenatal diagnosis via biochemical investigations^(8,9).

One of the most striking features of severe prenatal GA2 is the frequent involvement of the fetal kidney. In our patient, bilaterally enlarged, hyperechogenic kidneys with multiple cystic changes were detected during the second trimester, representing the primary abnormal findings that prompted further evaluation. Similar renal phenotypes have been repeatedly described in prenatally diagnosed GA2 cases and appear to be a recurring hallmark of the congenital-onset form⁽¹⁰⁾. Although the exact mechanism underlying renal cyst formation in GA2 remains unclear, intrauterine accumulation of toxic metabolic intermediates is hypothesized to interfere

with normal nephrogenesis, leading to dysplastic or cystic renal changes. This hypothesis is supported by pathological findings in previously reported cases demonstrating abnormal renal architecture and evidence of metabolic injury^(10,11).

Despite their frequency, renal abnormalities in GA2 patients are not pathognomonic and overlap considerably with other fetal renal disorders, most notably ARPKD, renal dysplasia, and ciliopathies. This overlap poses a significant diagnostic challenge in prenatal practice. In the absence of additional anomalies or a known family history, GA2 may not be immediately considered in the differential diagnosis of cystic or hyperechogenic fetal kidneys. In our case, however, the presence of consanguinity and a previous unexplained early neonatal death substantially increased the index of suspicion for an inherited metabolic disorder, underscoring the importance of a detailed obstetric and family history in guiding prenatal diagnostic strategies.

Pathogenic variants in *ETFDH* are an established cause of MADD and have been reported in both severe neonatal and later-onset phenotypes; pathogenic variants in *ETFA* and *ETFB* can also cause severe perinatal disease. Across published prenatal and perinatal reports, renal abnormalities such as bilateral enlargement, increased echogenicity, and cystic or dysplastic changes recur in affected fetuses and neonates. Loss-of-function variants, including non-sense, frameshift, and canonical splice-site variants, have been reported in several congenital-onset cases, but the limited number of prenatally characterized patients and marked allelic heterogeneity preclude

a deterministic genotype-phenotype correlation. Accordingly, fetal renal anomalies should be regarded as an important phenotypic clue to MADD rather than as a gene-specific or prognostically definitive finding⁽¹²⁾.

The identification of the novel homozygous *ETFDH* frameshift variant c.1200_1203del (*p.His401GlnfsTer3*) represents a key contribution of this report. The variant is predicted to introduce a premature termination codon and to cause loss of normal ETF-QO function. Loss-of-function is an established mechanism in *ETFDH*-related MADD, and biallelic truncating or splice-disrupting variants have been described in congenital-onset cases with severe renal and metabolic manifestations. Nevertheless, functional studies were not performed for the

present variant, and outcome prediction based solely on variant type remains uncertain. The concordant renal phenotype, autosomal-recessive segregation, and previous neonatal history support its clinical relevance without establishing that every fetus carrying this genotype would follow an identical course⁽⁶⁻¹¹⁾.

Selected individually verifiable prenatal and perinatal reports of GA2 are summarized in Table 2. The review confirms that bilateral renal enlargement, increased echogenicity, and cystic or dysplastic changes are recurrent antenatal findings, sometimes accompanied by oligohydramnios or hepatomegaly. Molecularly characterized reports include disease-associated variants in *ETFDH* and *ETFA*, underscoring genetic heterogeneity.

Table 2. Selected, verified prenatal and perinatal reports of glutaric acidemia type II

Author (year)	Gene/variant	Prenatal/perinatal findings	Diagnostic approach	Outcome	Consanguinity
Goodman et al. ⁽⁸⁾ (1983)	Gene not available (premolecular era)	Congenital anomalies with deleterious intrauterine effects; renal cystic changes described	Clinical, biochemical, and pathological evaluation	Severe congenital/neonatal disease	NR
Bennett et al. ⁽⁹⁾ (1984)	Gene not available (premolecular era)	At-risk pregnancy; no gene-level testing available	Reduced palmitate oxidation in cultured amniotic cells; postnatal biochemical confirmation	Live birth; treated; died at 4 months from cardiac failure	NR
Whitfield et al. ⁽⁵⁾ (1996)	Gene/variant NR	Fetal polycystic kidneys and oligohydramnios	Prenatal US; postmortem biochemical/pathological investigation	Perinatal death	NR
Chisholm et al. ⁽¹⁴⁾ (2001)	Gene/variant NR	Growth restriction, cystic renal disease, oligohydramnios; two consecutive affected pregnancies	Prenatal US; elevated maternal/amniotic AFP; amniotic-fluid acylcarnitines	Pregnancy termination in the reported affected fetus	No
Hackl et al. ⁽¹⁰⁾ (2017)	<i>ETFDH</i> , homozygous c.1117-2A>G	Prenatal ARPKD-like enlarged hyperechogenic/cystic kidneys	Prenatal US; postnatal biochemical and molecular testing	Early neonatal death	NR
Martinez-Aracil et al. ⁽¹²⁾ (2020)	<i>ETFDH</i> , homozygous c.706dupG (<i>p.Glu236GlyfsTer5</i>)	Hyperechogenic enlarged kidneys with cystic changes; recurrent affected pregnancies	Prenatal US; molecular testing; fetal autopsy	Severe perinatal disease/neonatal death in the family	Yes
Kucinska-Chahwan et al. ⁽¹¹⁾ (2021)	<i>ETFDH</i> , compound heterozygous novel variants	Bilateral enlarged, hyperechogenic and cystic kidneys	Prenatal US and exome sequencing	Pregnancy termination after prenatal diagnosis	NR
Carmant et al. ⁽¹³⁾ (2021)	<i>ETFA</i> , homozygous c.3G>A (<i>p.Met1?</i>)	Large hyperechoic microcystic kidneys and hepatomegaly; later oligohydramnios	Prenatal US; postnatal biochemical, molecular, and pathological evaluation	Live birth at 36 weeks; neonatal death on day 3	Yes
Zhai et al. ⁽¹⁵⁾ (2023)	<i>ETFDH</i> , c.1285+1G>A and c.343_344delTC	Bilateral enlarged hyperechogenic kidneys with oligohydramnios	Prenatal US and fetal WES	NR in English abstract	NR
Zhang et al. ⁽⁶⁾ (2025)	<i>ETFDH</i> , c.487+2T>A with c.1395T>G (<i>p.Tyr465Ter</i>) and c.1773_1774delAT in cis	Polycystic renal malformation detected at 23 weeks	Prenatal US; trio-WES; testing of fetal tissue; functional splice studies	Pregnancy termination	NR

AFP: Alpha-fetoprotein, ARPKD: Autosomal recessive polycystic kidney disease, *ETFDH*: Electron transfer flavoprotein dehydrogenase, GA2: Glutaric acidemia type II, NR: Not reported, US: Ultrasonography, WES: Whole-exome sequencing

Outcomes in reported congenital-onset cases were often poor, but survival has also been described; therefore, the published evidence supports cautious, case-specific counseling rather than categorical prediction of lethality⁽⁵⁻¹⁵⁾.

The identification of a novel homozygous frameshift variant in *ETFDH* in this fetus expands the mutational spectrum associated with prenatal GA2. Confirmation that both parents were heterozygous carriers supports autosomal-recessive segregation and enables targeted testing in future pregnancies. The recurrence of a similar renal phenotype and neonatal death in the previous pregnancy is clinically suggestive, although that neonate was not genetically or biochemically tested and cannot be considered molecularly confirmed. This case also underscores the growing importance of WES in prenatal diagnostics. Conventional karyotyping and chromosomal microarray cannot detect most single-gene causes of fetal renal disease, whereas prenatal WES can identify relevant coding variants when cytogenetic testing is non-diagnostic. In the present case, WES, followed by parental segregation analysis, supported a molecular diagnosis that directly informed counseling and reproductive planning⁽¹¹⁾.

From a clinical perspective, prenatal molecular diagnosis of GA2 can substantially inform decision-making.

Congenital-onset MADD with structural anomalies is frequently associated with rapid neonatal metabolic decompensation and high mortality despite intensive care, although individual prognosis remains variable and cannot be inferred with certainty from a novel genotype alone. Postnatal dietary modification, avoidance of catabolism, and supplementation with riboflavin and other cofactors may benefit selected patients, particularly in milder disease or in riboflavin-responsive cases, while responses in severe neonatal presentations tend to be limited and inconsistent. Prenatal recognition, therefore, permits balanced counseling about uncertainty, anticipated neonatal needs, and pregnancy options. Identification of the familial variant also enables targeted prenatal testing and PGT-M in future pregnancies⁽⁵⁻¹⁵⁾.

Study Limitations

The strengths of this report include detailed prenatal phenotyping, a clearly documented diagnostic pathway, and trio-based genetic analysis with parental segregation. The fetus carried a homozygous, likely pathogenic, *ETFDH* variant concordant with the renal phenotype and the family history, thereby providing a molecular diagnosis of *ETFDH*-related MADD. The absence of a postmortem examination precluded pathological confirmation of the renal abnormalities and assessment of additional microscopic or systemic manifestations; however, an autopsy is not required to establish the molecular diagnosis. Additional limitations include the absence of fetal biochemical or functional assays, and the uncertainty inherent in predicting the clinical course of a novel variant.

Conclusion

This case highlights the need to include GA2 in the differential diagnosis of fetuses presenting with bilaterally hyperechogenic, cystic kidneys, particularly in the context of consanguinity and an adverse obstetric history. Prenatal WES with segregation analysis can support a molecular diagnosis, facilitate balanced counseling, and enable targeted reproductive planning; however, the prognosis should be communicated cautiously when the identified variant is novel.

Ethics

Informed Consent: Written informed consent was obtained from the patient for the publication of this case report and any accompanying images.

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Footnotes

Authorship Contributions

Concept: S.K., R.M., Design: B.B.P., Data Collection or Processing: S.K., Analysis or Interpretation: R.M., Literature Search: S.K., B.B.P., Writing: S.K., B.B.P., R.M.

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