

CHARGE syndrome associated with *de novo* (I1460Rfs*15) frameshift mutation of CHD7 gene in a patient with arteria lusoria and horseshoe kidney

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Abstract. CHARGE syndrome is an autosomal dominant condition caused by mutations in the chromodomain helicase DNA binding protein 7 (CHD7) gene. The present study reported on the case of a 16-month-old female with plurimalformative syndrome, whose etiology was identified by clinical whole-exome sequencing (WES) analysis. Clinical and follow-up assessments identified multiple craniofacial dysmorphisms, congenital defects and functional symptoms, including dysphagia and Marcus Gunn jaw winking synkinesis. Trio-WES analysis was performed for the patient and their parents and the presence of CHARGE syndrome was further indicated using single-molecule real-time sequencing. A *de novo* pathogenic variant, c.4379_4380del (p. Ile1460Argfs*15), was identified in exon 19 of the CHD7 gene, which resulted in a premature translational stop signal. Trio-WES analysis was used for further investigation, indicating that neither of the patient's parents had the mutation and confirming its *de novo* nature. To the best of our knowledge, the case of the present study was the first reported case of CHARGE syndrome in Romania with congenital

defects including an aberrant right subclavian artery and a horseshoe kidney. CHARGE syndrome was diagnosed in the patient based on the pathogenic mutation in the CHD7 gene. To the best of our knowledge, the present case report is the first to suggest that the CHD7 gene variant is associated with CHARGE syndrome.

Introduction

CHARGE syndrome is a rare, autosomal dominant disorder characterized by multiple congenital anomalies. According to Orphanet, CHARGE syndrome Online Mendelian Inheritance of Man entry no. 214800; <https://www.orpha.net/consor/cgi-bin/>) has a prevalence of 1-9/100,000. CHARGE is an acronym for the most common symptoms observed in patients with the condition: Coloboma, heart defects, atresia of the choanae, retarded growth and/or development, genital hypoplasia and ear abnormalities (1). However, other clinical manifestations have also been identified in diagnosed cases. Patients with CHARGE syndrome exhibit complex symptoms that differ from one case to another, indicating the variable clinical expression of the disorder. Cranial nerve (CN) dysfunction, external ear anomalies, semicircular canal anomalies, coloboma, choanal atresia, genital hypoplasia, congenital cardiovascular defects, cleft lip and/or palate and anosmia are identified in >50% of patients. Motor retardation, swallowing and severe feeding problems, and intellectual disability are also frequent among patients with CHARGE syndrome (2).

The identification of clinical features is important for the diagnosis of patients with suspected CHARGE syndrome (3). Sanlaville and Verloes (4) divided the clinical aspects of CHARGE syndrome into major and minor criteria, but the highly variable clinical expression and the lack of obligatory elements have continued to pose major diagnostic problems. Major and minor clinical criteria have been refined and updated (4,5), and a new checklist organized by body system and age has been developed to aid the diagnosis of CHARGE syndrome (6). Recently, a novel genetic approach has changed

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the importance of clinical criteria for the diagnosis of the disorder. Hale *et al* (7) suggested that difficulties regarding the clinical diagnosis of CHARGE syndrome may be overcome by including the pathogenic chromodomain helicase DNA binding protein 7 (CHD7) variant as a major diagnostic criterion. Accordingly, a pathogenic CHD7 variant status plus one major feature would be sufficient for the diagnosis of the disorder (7,8). It is important for each novel mutation that extends the spectrum of pathogenic mutations in the CHD7 gene to be included in the databases, to facilitate the diagnosis and estimate the prevalence of the disorder (3). Since the publication of the new criteria in 2016, only a few case reports discussing patients with CHARGE syndrome with a pathogenic mutation in the CHD7 gene, previously considered as atypical CHARGE, have been published (9,10). By understanding the different genotypes of CHARGE syndrome, it was possible to make clear genotype-phenotype associations for all CHD7 variants.

In the present study, a case with a pluriformative syndrome, whose etiology was identified by clinical whole-exome-sequencing (WES) analysis, was described. According to the criteria of Hale *et al* (7), the patient was diagnosed with CHARGE syndrome due to the presence of the pathogenic CHD7 variant. By reporting a novel case of CHARGE syndrome, the present study emphasizes the importance of the new criteria, which may encourage clinicians to perform extensive genetic testing, e.g., WES, for an accurate diagnosis of the disorder.

Materials and methods

Clinical and paraclinical evaluation. Physical examination of the patient was followed by: Ear, nose and throat assessment, audiogram, thoracic computed tomography (CT) and abdominal and heart Doppler ultrasonography.

Genetic analysis. Genomic DNA was extracted from peripheral venous blood, as previously described by Miller *et al* (11). Clinical WES was used to detect an exonic pathogenic variant that may explain the phenotype of the patient. Gene sequencing was performed by the Invitae Laboratory. Genomic DNA was enriched for targeted regions using a hybridization-based protocol and sequenced using Illumina technology (Illumina, Inc.). The average coverage depth of the WES of all targeted regions was $\geq 50\times$. Reads were aligned to a reference sequence Genome Reference Consortium human build 37 (GRCh37) (12) and sequence changes were identified and interpreted in the context of a single clinically relevant transcript. Exonic deletions and duplications were identified using an algorithm that determined the copy number at each target. Subsequently, the biological and clinical implications of each variant were identified. All reported pathogenic or likely pathogenic variants that had potential medical implications for the patient were verified by orthogonal technologies. Single molecule real-time (SMRT) sequencing technology (Pacific Biosciences, Inc.) was used to further verify the results of the WES analysis. Using a combination of public tools and databases, a comprehensive search of phenotype-genotype associations was performed. Disruptive variants, including

variants that caused premature truncation events, interfered with canonical splice sites or resulted in initiator, frameshift or multi-exon deletions that were detected in genes associated with Mendelian conditions that corresponded to the patient's presentation, were reported.

Subsequently, trio-WES analysis was performed on samples obtained from the parents of the patient, which identified the mutation as a *de novo* variant that was only present in the patient.

The variants that were identified as potentially explaining the clinical features of the patient were reported according to the guidelines established by the American College of Genetics and Genomics (13). Sequence variants with a minor allele frequency of >0.05 in the Human Genetic Variation Database (<http://www.genome.med.kyoto-u.ac.jp/SnpDB/>) and the NHLBI Grand Opportunity Exome Sequencing Project (<http://evs.gs.washington.edu/EVS/>) were excluded.

Results

Case presentation. The present study described the case of a 16-month-old female who was evaluated in the Louis Turcanu Emergency Hospital for Children and in the Pediatric Cardiology Department of Pius Brînzeu Emergency County Clinical Hospital, Timisoara, Romania, in February 2019, for dysmorphic features and multiple congenital defects in order to establish a diagnosis and to aid in the management of a future pregnancy. The patient was born post-term via normal spontaneous delivery. The parents (mother, 33 years; father, 34 years) were non-consanguineous and appeared healthy. The patient had no siblings. Ultrasonography performed during the pregnancy did not detect any pathological changes in the patient. Anthropometric measurements at birth were within the normal ranges: Body weight, 3,630 g; body height, 52 cm; and cranial perimeter, 35 cm. The Apgar scores of the patient were 5/6/10 and the family history of the patient was unremarkable.

Medical history. The patient displayed facial dysmorphism from birth, which is the reason for further investigation performed by the neonatology and pediatric services. At birth, severe dysphagia was reported; therefore, enteral nutrition was the recommended feeding route. The cause of dysphagia was investigated and neuromuscular dysphagia, tumors and hemangioma were excluded as causes of the condition. In time, the patient's condition improved and at 3 months of age, the patient was fed orally. Thoracic and abdominal CT scans were performed, revealing an aberrant right subclavian artery (arteria lusoria) and a horseshoe kidney. The patient was not receiving any medication at the time of presentation.

Clinical evaluation. At 16 months of age, the anthropometric measurements of the patient upon first physical examination in the Genetics Department were as follows: Body height, 75 cm; body weight, 8,730 g; and cranial perimeter, 45.5 cm (in the normal range) (14). Upon physical examination at 21 months of age, the following anthropometric measurements were recorded: Body height, 78 cm; body weight, 10 kg (in the normal range); and cranial perimeter, 46.6 cm (in the normal range) (14). At 16 and 21 months of age, the patient was fed only with liquids and semisolids.

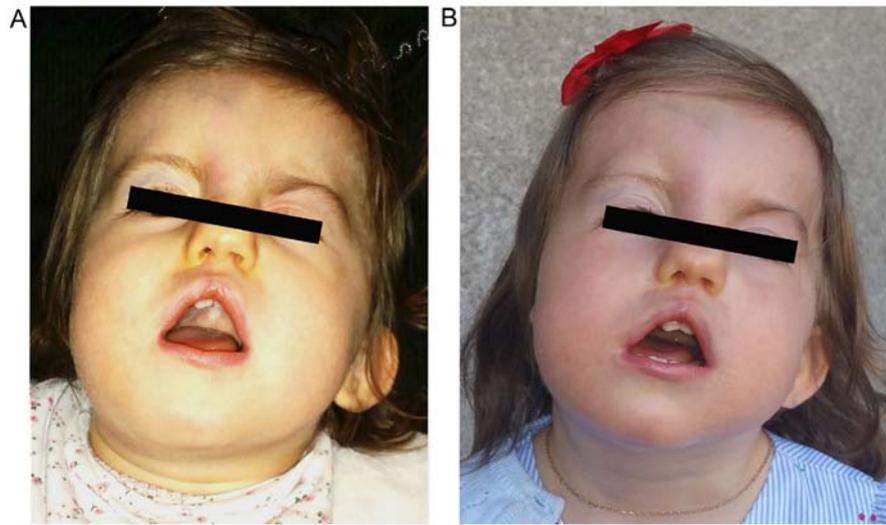


Figure 1. Facial dysmorphism of the patient included craniofacial asymmetry, square face, prominent forehead, high palate, triangular-shaped open mouth, asymmetric and low-set left ear, left palpebral ptosis, left facial palsy and head retroflexion. Facial images at (A) 16 months and (B) 21 months of age.

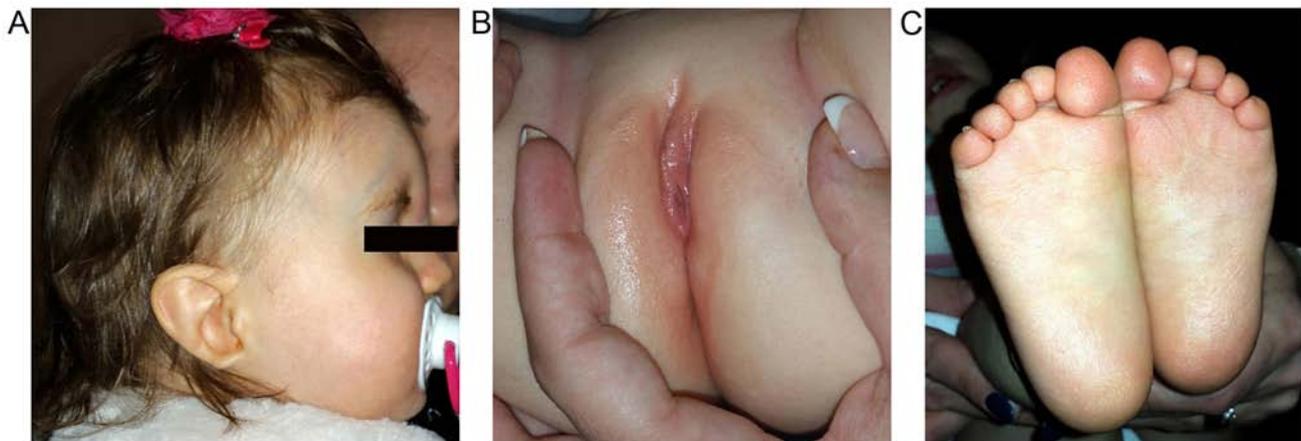


Figure 2. (A) Patient's profile: Low-set left ear, ear lobe agenesia on the right side, (B) labia minora hypoplasia, (C) soles without furrows, but with fine sole dermatoglyphics.

The patient displayed dysmorphic facial features, which included square face, craniofacial asymmetry, prominent forehead, wide nasal ridge, high palate, triangular-shaped open mouth, low-set left ear, asymmetry of the shape and size of the ears, abnormality of the pinna cartilage of the outer ear, ear lobe agenesia on the right side and unilateral left blepharoptosis with associated upper eyelid contraction (Figs. 1 and 2). Ophthalmic examination revealed choroidal coloboma.

The patient also presented with fixed head retroflexion, congenital craniofacial dysostosis, facial palsy (left hemi-face), general facial hypotonia, facial grimacing, abnormal conjugate eye movement and Marcus Gunn jaw winking synkinesis. The aforementioned symptoms, together with the left blepharoptosis, conferred a peculiar facial expression. Cranial nerves (CN) VII, VIII, IX and X were affected. The patient suffered from profound deafness.

Further anomalies that were identified by systemic examination included labia minora hypoplasia, abnormality of the plantar skin and abnormal plantar dermatoglyphics (Fig. 2). In addition, the patient was only able to walk with support.

Nasal endoscopic exam revealed that the patient did not have choanal atresia, while audiogram revealed severe bilateral hearing impairment. The patient did not speak, but she smiled and was able to cooperate. The left auditory nerve was not visualized on cranial CT.

Thoracic CT identified an aberrant origin of the right subclavian artery (arteria lusoria) without obstructive manifestations of the esophagus or trachea (Fig. 3).

Heart ultrasonography revealed that the patient did not display any intracardiac structural abnormalities; therefore, the only cardiac defect identified that was associated with CHARGE syndrome was the aberrant origin of the right subclavian artery (Fig. 4).

The patient did not receive any medication. After receiving kinesiotherapy for 2 h daily, the patient was able to maintain equilibrium on the feet and walk short distances without support and retroflexion of the head and left palpebral ptosis were reduced. Cardiology follow-up for evaluation of the cardiac status was recommended. A cochlear implant was scheduled.

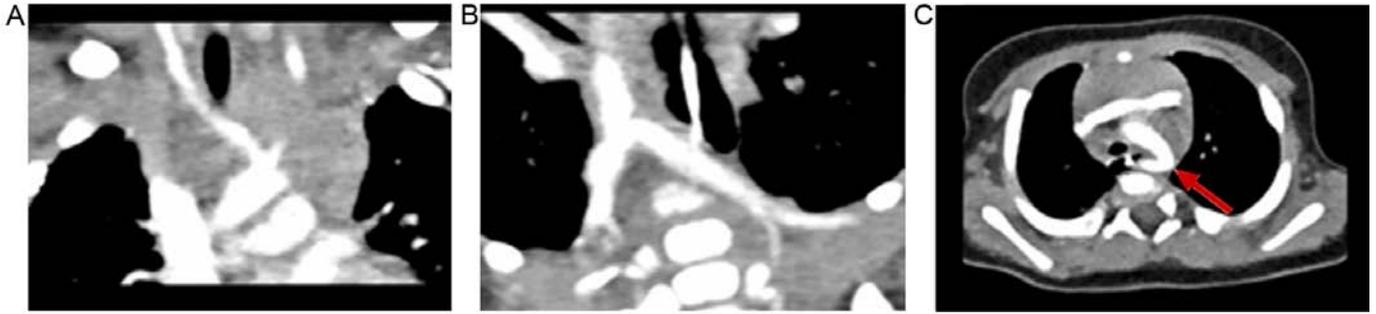


Figure 3. Computed tomograms displaying (A) the right common carotid artery and left common carotid artery, both arising from the aortic arch; (B) the left subclavian artery and right subclavian artery with aberrant origin and diverticulum of Kommerell (the distal remnant of the right aortic arch), and (C) the left-sided aortic arch with an aberrant right subclavian artery arising from the proximal part of the descending aorta, with retrotracheal and retro-oesophageal course, but without obstruction. The arrow indicates the right subclavian artery emerging from proximal descending aorta.

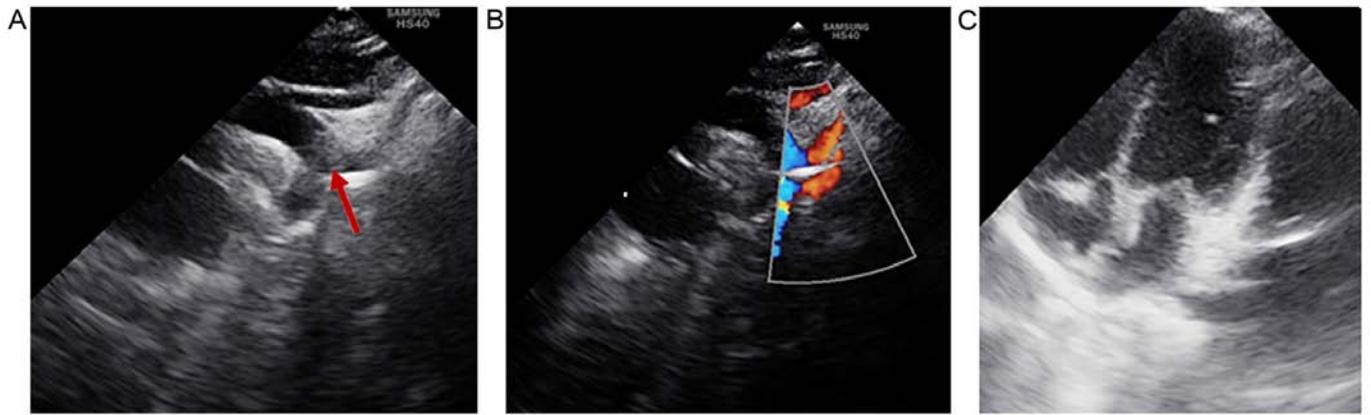


Figure 4. Heart ultrasonography. (A) The suprasternal window displays the left-sided aortic arch with the aberrant origin of the right subclavian artery (arrow), which arises from the proximal part of the descending aorta. (B) The suprasternal window with color Doppler flow displays the left-sided aortic arch with flow across the aberrant right subclavian artery (arrow), right common carotid artery and left subclavian artery. (C) Apical four-chamber window displaying normal cardiac structures.

Mutation. A *de novo* pathogenic variant, c.4379_4380del (p.Ile1460Argfs*15), was identified in exon 19 of the CHD7 gene. The variant consisted of one thymine deletion from position 4,379 and one adenine deletion from position 4,380 (rs398124319). The mutation led to a reading frameshift starting from isoleucine at codon 1,460, which resulted in a premature translational stop signal (p.Ile1460Argfs*15) and was hypothesized to result in an absent or disrupted protein product. The analysis identified a monoallelic deletion in the CHD7 gene, NM_017780.3 (CHD7, c.4379_4380del), which was also identified by SMRT sequencing (Fig. 5).

The mutation was present in the Human Gene Mutation Database (<http://www.hgmd.org>) and the Clinical Variance database (<http://www.ncbi.nlm.nih.gov/clinvar>). The heterozygous frameshift mutation was not detected in the parents of the patient, suggesting that it was a *de novo* mutation.

Discussion

CHARGE syndrome is a variable disorder that affects a number of different parts of the body and is characterized by a non-random cluster of congenital anomalies and dysmorphisms, with significant variation between patients (15). The diagnosis relies on a set of major and minor clinical

criteria (4,5). According to the criteria of Sanlaville and Verloes (4), a patient must display the following: Three major criteria, or two major and two minor criteria for diagnosis with the typical form; two major and one minor criterion for diagnosis with the partial form; two major but no minor criterion, or one major and two minor criteria for diagnosis with the atypical form (4). Hale *et al* (7), proposed an update to the clinical diagnostic criteria, suggesting that a pathogenic CHD7 variant status should be considered as a major diagnostic criterion, which, when present together with one other major criterion, is sufficient for the diagnosis of typical CHARGE syndrome.

The majority of patients with CHARGE syndrome display distinctive facial features, including a square-shaped face and facial asymmetry, which were also observed in the case described in the present study (3). Patients with CHARGE syndrome also display ear abnormalities, which may contribute to hearing problems. The case reported in the present study displayed abnormalities of the shape and position of the bilateral ears, as well as ear lobe agenesis on the right side.

The central nervous system is also frequently affected in patients with CHARGE syndrome, with CN dysfunction reported in >90% of cases. Different clinical manifestations occur when >1 CN is dysfunctional. In the case reported in the

phenotype and a pathogenic variant (c.4379_4380del) was identified. The mutation resulted in a premature translational stop signal (p.Ile1460Argfs*15) in exon 19 of the CHD7 gene. Several studies have reported that frameshift mutations are the most common type of mutation in patients with CHARGE syndrome, with a frequency of 34-73% (8,27,28). Clinical WES analysis takes into account information regarding the target genes associated with the major symptoms, as well as the verification of the genes indicated by the American College of Medical Genetics (13,29,30). Compared to classical sequencing, WES analysis has a shorter analysis time, lower costs and offers a more precise diagnosis. In the present study, Trio-WES analysis was performed, which allowed the *de novo* mutation to be identified, as neither of the patient's parents displayed the mutation in the CHD7 gene. In a large study, parental DNA profiles were assessed and all pathogenic variants were identified as *de novo* mutations, except for one case (8). An intragenic deletion was identified in two brothers, but was not identified in the blood samples of the parents. It was hypothesized that one parent had germinal mosaicism (8). Considering this possibility, prenatal diagnosis should be recommended for each future pregnancy (31,32). *De novo* mutations are more frequent than inherited mutations and the majority are frameshift mutations (33-35). Although rare, pathogenic variants may be inherited from a mildly affected parent; therefore, parents should be carefully examined (3,4). An analysis of a French cohort suggested that 66.38% of patients with CHARGE syndrome had different pathogenic variants and 90% of these variants were novel (8). It is estimated that 74% of patients with CHARGE syndrome have congenital heart defects due to a CHD7 mutation (25). Congenital heart defects are more frequent in patients with truncating variants of the gene (80%) compared with patients with missense or splice-site variants (58%) (25). Aortic arch anomalies, frequently including an aberrant subclavian artery or right aortic arch, were reported in 14% of cases in a previous study (18). In the present study, the patient was the first case of reported CHARGE syndrome in Romania presenting with a truncating CHD7 mutation and an aberrant subclavian right artery. Another case with an unspecified mutation in the CHD7 gene has also been reported in Romania (36).

The variant identified in the present study, c.4379_4380del in the CHD7 gene, was not present in population databases (Exome Aggregation Consortium: No frequency) and appeared to have not been reported in the literature. ClinVar contains an entry for this variant (variation ID: 95789) that is considered to be a pathogenic and germinal mutation. Over 500 mutations in the CHD7 gene have been reported (28), but only one case had the mutation (<https://www.ncbi.nlm.nih.gov/clinvar/variation/95789/>) that was identified in the present study and it has not been reported in a published scientific journal associated with CHARGE syndrome. The rare variant c.4379_4380del in the CHD7 gene is consistent with a loss-of-function variant, which is known to be pathogenic (37), and haploinsufficiency is the most likely pathogenic mechanism (38).

CHD7 mutations cause inactivation of remodeling activity of varying degrees. Remodeling of nucleosomes is a key function of CHD7 during developmental processes, which may

explain why CHD7 mutations cause developmental defects but do not prevent the development of pregnancy (39-42).

To the best of our knowledge, the present study reported the first case of CHARGE syndrome in Romania that displayed an aberrant right subclavian artery and a horseshoe kidney, and was clearly diagnosed on the basis of the pathogenic mutation in the CHD7 gene. The frameshift mutation resulted in the formation of a premature stop codon leading to the inactivation of the CHD7 protein. CHARGE syndrome is a rare disease; therefore, every newly reported case improves the understanding of the spectrum of mutations in the CHD7 gene and extends the knowledge of genotype-phenotype correlations.

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Availability of data and materials

The datasets used and/or analyzed during the present study are available from the corresponding author on reasonable request.

Authors' contributions

CG and DS contributed to the conceptualization of the study, literature search as well as writing, editing and critically reviewing the manuscript; CG, AL and FB performed data analysis; EVG and MAV performed data analysis, critical review and supervision. MP treated the patient in the clinic throughout the admission and provided patient data. All authors have read and approved the final manuscript for publication.

Ethics approval and consent to participate

The study described in this article was carried out in accordance with the Code of Ethics of the World Medical Association (Declaration of Helsinki) for experiments involving humans and Uniform Requirements for manuscripts submitted to biomedical journals. The study was approved by the Local Ethics Commission for Scientific Research of Pius Brînzeu Emergency County Clinical Hospital Timisoara, Romania; (approval no. 172/05.08.2019). The parents of the patient provided written informed consent regarding genetic testing and participation in the study.

Patient consent for publication

The parents of the patient provided written informed consent regarding the publication of the medical data and images of the case.

Competing interests

The authors declare that they have no competing interests.

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