

# World Journal of *Clinical Cases*

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Editorial Board Member of *World Journal of Clinical Cases*, Rajesh Kumar Rajnish, MBBS, MS, Assistant Professor, Department of Orthopaedics, All India Institute of Medical Sciences, Bilaspur, Bilaspur 174001, Himachal Pradesh, India. [duktiraj@gmail.com](mailto:duktiraj@gmail.com)

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## Novel frameshift mutation in the *AHDC1* gene in a Chinese global developmental delay patient: A case report

Shuang-Zhu Lin, Hong-Yan Xie, Yan-Lai Qu, Wen Gao, Wan-Qi Wang, Jia-Yi Li, Xiao-Chun Feng, Chun-Quan Jin

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**Shuang-Zhu Lin, Hong-Yan Xie, Yan-Lai Qu, Xiao-Chun Feng, Chun-Quan Jin,** Diagnosis and Treatment Center for Children, The First Affiliated Hospital to Changchun University of Chinese Medicine, Changchun 130021, Jilin Province, China

**Wen Gao, Wan-Qi Wang, Jia-Yi Li,** Changchun University of Chinese Medicine, Changchun 130000, Jilin Province, China

**Corresponding author:** Chun-Quan Jin, MD, Professor, Diagnosis and Treatment Center for Children, The First Affiliated Hospital to Changchun University of Chinese Medicine, No. 1478 Gongnong Road, Chaoyang District, Changchun 130021, Jilin Province, China. [jinchunquan@126.com](mailto:jinchunquan@126.com)

### Abstract

#### BACKGROUND

Xia-Gibbs syndrome (XGS, OMIM: 615829), caused by mutations within the AT-Hook DNA-binding motif-containing protein 1 (*AHDC1*) gene (OMIM: 615790), located on the short arm of chromosome 1 within the cytogenetic band 1p36.11, contains five noncoding 5 exons, a single 4.9-kb coding exon, and a noncoding 3 exon.

#### CASE SUMMARY

In this case report, we diagnosed and treated a 6-mo-old girl with XGS. The primary clinical symptoms included global developmental delay, hypotonia, and mild dysmorphic features. Using high-throughput whole-exome sequencing to sequence the patient and her parents, and the results showed a novel frameshift mutation of c.1155dupG (p.Arg386Alafs\*3) in the *AHDC1* gene. The paternal gene was wild type.

#### CONCLUSION

This report extends the mutation spectrum of the *AHDC1* gene to provide the diagnostic basis for genetic counseling in families with XGS.

**Key Words:** Xia-Gibbs syndrome; AT-Hook DNA-binding motif-containing protein 1; Children; Global developmental delay; Case report

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**Core Tip:** We report a 6-mo-old girl with Xia–Gibbs syndrome (XGS). The main clinical manifestations were global developmental delay, hypotonia, and other mild dysmorphic features. DNA sequencing showed that there was a novel frameshift mutation of c.1155dupG (p.Arg386Alafs\*3) in the AT-Hook DNA-binding motif-containing protein 1 (*AHDC1*) gene. This study extends the mutation spectrum of the *AHDC1* gene, and provides a molecular basis for the etiological diagnosis of XGS and genetic consultation for the family.

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## INTRODUCTION

Xia–Gibbs syndrome (XGS) is an autosomal dominant genetic disease caused by mutation of the AT-Hook DNA-binding motif-containing protein 1 (*AHDC1*) gene. Typical features include global developmental delay, hypotonia, obstructive sleep apnea, seizures, delayed myelination, micrognathia, and other mild dysmorphic features[1,2]. The *AHDC1* gene is located on the short arm of chromosome 1 within the cytogenetic band 1p36.11, and consists of seven exons with only one coding exon (exon 6), five noncoding 5 exons, and a noncoding 3 exon[3].

In this case, a novel frameshift mutation of c.1155dupG (p.Arg386Alafs\*3) in the *AHDC1* gene was found by high-throughput whole-exome sequencing (WES) in a patient with global developmental delay, hypotonia, micrognathia, and other mild dysmorphic features.

## CASE PRESENTATION

### Chief complaints

A 6-mo-old female patient presented to our hospital due to global developmental delay.

### History of present illness

In June 2021, the patient presented with a 6-mo history of global developmental delay. Since birth, the child had lagged behind in developmental milestones. She could not raise her head until she was age 4 mo, and she still shook her head sometimes. She could not sit alone without the help of others, and turning over was not flexible. She could not crawl, and the stability of her lower limbs was too poor to support her weight. She had no difficulty in pronunciation.

### History of past illness

The patient weighed 3.7 kg and was 52 cm long after full-term normal delivery without a history of asphyxiation and resuscitation. The patient did not have a history of feeding difficulties. There was no history of encephalitis and brain trauma since disease onset.

### Personal and family history

Her parents were clinically normal. Genetic history or family history of infectious diseases were denied.

### Physical examination

At her visit at 6 mo of age, we performed a physical examination. Her weight was 9.0 kg and length 70.0 cm. Mild dysmorphic features were observed, such as micrognathia. Grasping reflex was present, and limb muscle tension showed hypotonia. Ankle clonus was positive. Muscle strength was level 4. Physiological reflexes were present.

### Laboratory examinations

We performed a series of examinations of the patient, including liver function, kidney function, electrolytes, and organic acids in blood and urine, which showed no abnormalities.

### Imaging examinations

In June 2021, brain magnetic resonance imaging showed bilateral frontal subdural effusion, hydrocephalus, and hydrops in the mastoid area. Electroencephalography (EEG) was abnormal,

showing sharp waves and spike waves in the Rolandic area or right forehead region.

#### **Further diagnostic work-up**

The patient underwent a Peabody Developmental Motor Scales (PDMS-2) test on May 14, 2021[4]. The Fine Motor Quotient (FMQ) was 9 points, with a motor quotient of 67, and the Gross Motor Quotient (GMQ) was 21 points with a motor quotient of 81; both measures were worse than those of her peers. Griffiths Mental Development Scales (GMDS) showed that motor ability was equivalent to that of a 3-mo-old child, with a development quotient (DQ) of 46 points; human-social ability was equivalent to that of a 4-mo-old child, with a DQ of 62 points; hearing and language ability was equivalent to that of a 4.5-mo-old child with a DQ of 69 points, and hand and eye coordination was equivalent to that of a 3.5-mo-old child, with a DQ of 54 points. The patients' overall performance was equivalent to that of a 3.5-mo-old child, with a DQ of 54 points.

#### **High throughput WES and mitochondrial sequencing**

Informed parental consent was obtained for WES, mitochondrial sequencing, and publication of photographs on behalf of the proband. DNA samples were extracted from the peripheral blood of the child and her parents to detect whole-exome sequences and whole-genome copy number variants. The results revealed a novel frameshift mutation of c.1155dupG (p.Arg386Alafs\*3) in the *AHDC1* gene. Polymorphic sites were detected in each sample data using GATK software and statistical analysis was performed on 1000 human genomes and ExAC databases. The reported pathogenic locus has been confirmed using the Human Gene Mutation Database (HGMD) and the Human Online Mendelian Genetic Database (OMIM). The pathogenicity of the mutation locus was comprehensively assessed using the American College of Medical Genetics and Genomics (ACMG) standards and guidelines for the interpretation of sequence variation.

#### **Gene detection and pathogenicity analysis**

The WES results showed the presence of a novel frameshift variant in the *AHDC1* gene, which was an unreported frameshift mutation, c.1155dupG (p.Arg386Alafs\*3), and may result in altered gene function. The frequency at which variation occurs in the normal population database is unknown, and is a low-frequency variation. The results of protein function prediction are unknown, and are not reported in the HGMD database.

According to Sanger sequencing, the variation occurred in the child, while the parental genes were wild type (Figures 1-3). The mutation was suspected to be a pathogenic according to the ACMG guidelines[5].

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## **FINAL DIAGNOSIS**

Sanger sequencing showed that there was a novel frameshift variation of c.1155dupG (p.Arg386Alafs\*3) in the *AHDC1* gene. Based on clinical presentation, laboratory tests and gene sequencing results, the clinical diagnosis was XGS.

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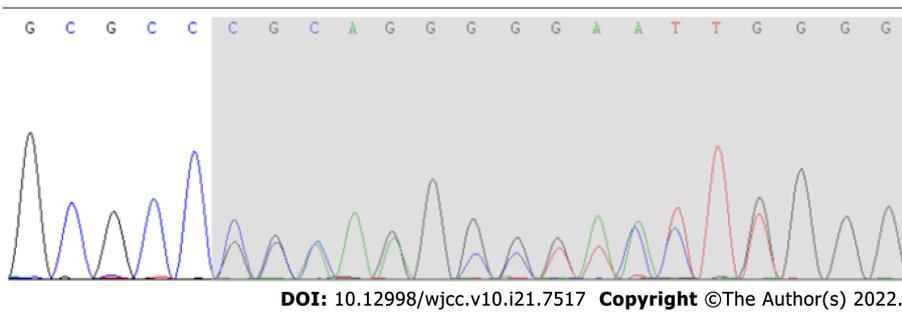
## **TREATMENT**

To improve quality of life of the patient, she has been provided with rehabilitation training and behavioral guidance therapy since June 2021.

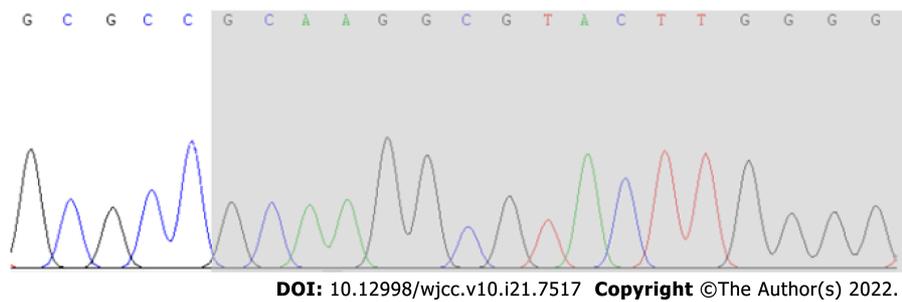
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## **OUTCOME AND FOLLOW-UP**

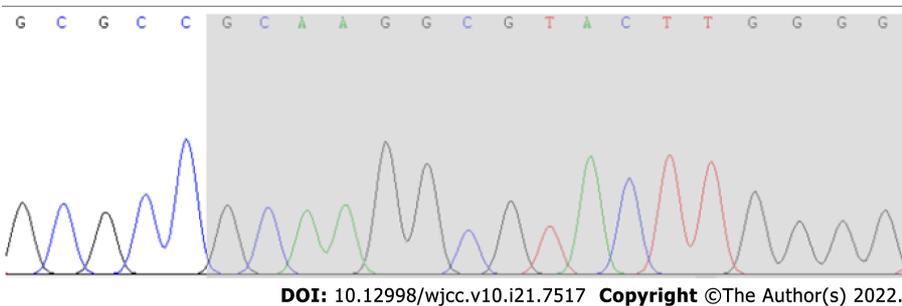
The patient had been receiving rehabilitation treatment for nearly 6 mo. The patient is now age 11 mo, her weight is 11.0 kg and length is 74.0 cm. She can sit alone, and her hands can engage in more elaborate movements, and have increased responses to external stimuli, and she is able to speak some simple vowels. The patient underwent the PDMS-2 test in November 2021. The FMQ was 13 points with a motor quotient of 79, and GMQ was 17 points with a motor quotient of 72. GMDS showed that motor ability was equivalent to that of a 5.3-mo-old child, with a DQ of 46 points. Performance was equivalent to that of a 6.5-mo-old child, with a DQ of 56 points.



**Figure 1** A novel frameshift variation in c.1155dupG (p.Arg386Alafs\*3) of the AT-Hook DNA-binding motif-containing protein 1 gene was revealed by Sanger sequencing.



**Figure 2** No anomalies were found in the AT-Hook DNA-binding motif-containing protein 1 gene in the child's father as revealed by Sanger sequencing.



**Figure 3** No anomalies were found in the AT-Hook DNA-binding motif-containing protein 1 gene in the child's mother as revealed by Sanger sequencing.

## DISCUSSION

The *AHDC1* gene is located on chromosome 1p36.11, and likely functions in DNA binding. The *AHDC1* gene is part of the CBX family of proteins associated with human chromodomain-containing Polycomb proteins. It encodes a protein of 1603 amino acids, consisting of five noncoding 5 exons, a noncoding 3 exon and a single 4.9-kb coding exon (exon 6) containing 2 AT hooks[1,3]. Previous studies have shown that *AHDC1* interacts with nuclear proteins involved in epigenetic regulation during development, mainly at neural loci and neuronal protein transport. Mutation of the *AHDC1* gene can lead to XGS.

XGS (OMIM: 615829) is an autosomal dominant genetic disease caused by mutation of the *AHDC1* gene. Typical features include global developmental delay, intellectual disability, structural abnormalities of the brain, global hypotonia, feeding problems, sleep difficulties, apnea, and short stature[6]. In addition to neurological seizures, delayed myelination, micrognathia, and other mild dysmorphic manifestations[7], XGS patients may also have a broad clinical range and multisystem involvement[8,9]. Not all XGS patients show a typical phenotype, and there are differences in the disease manifestations [10,11].

The present patient first attended hospital due to delayed motor milestones over 2 mo when she was age 6 mo. In order to clarify the cause of the disease, we used high-throughput WES and identified an unreported mutation of the *AHDC1* gene.

According to previous studies, more than 90% of patients had motor and speech delay, hypotonia occurred in approximately 85% of patients, and less than 40% of patients had short stature. About 30% of patients had symptoms of autism. Some patients showed sleep apnea (34.33%), laryngomalacia (14.93%), and other manifestations. Approximately 35% of patients developed epileptic seizures[8,12,13].

In this case report, the child conformed to the typical clinical manifestations of XGS. The child developed significant motor delay and hypotonia, but speech ability was not delayed. She was able to respond positively to external stimuli. There was no sufficient evidence of sleep apnea and laryngomalacia. Although the child's EEG showed the distribution of spike waves and sharp waves, she did not appear to have the related actions, and she did not have other related manifestations of epilepsy [14,15].

Our patient has not yet developed growth hormone deficiency or short stature. Height and weight were within the mean range of normal, in contrast to two previously reported Chinese children who exhibited partial growth hormone deficiency and attended hospital due to short stature[16].

In this report, we describe a Chinese patient with XGS, with a new mutation c.1155dupG (p.Arg386Alafs\*3) in the *AHDC1* gene identified by WES, and compared the results with those from two Chinese cases reported in the literature, to better understand the clinical phenotype and the association with the *AHDC1* gene.

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## CONCLUSION

Previous studies have shown that global developmental delay occurs in the *AHDC1*-related phenotype of XGS. Our patient was found to have a novel frameshift variation of c.1155dupG (p.Arg386Alafs\*3) in the *AHDC1* gene, which was an unreported frameshift mutation. Typical features of XGS include global developmental delay, hypotonia, obstructive sleep apnea, seizures, delayed myelination, micrognathia, and other mild dysmorphic features. This report result showed clinicians could consider XGS in patients with similar clinical characteristics. Genetic testing can help physicians confirm the diagnosis and help with further genetic counseling.

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## FOOTNOTES

**Author contributions:** Lin SZ and Xie HY collected and analyzed all clinical data and wrote the manuscript; Qu YL and Gao W participated in the collation of the literature and the chart research; Jin CQ was involved in the genetic diagnosis and treatment of the patients; Lin SZ, Wang WQ, Li JY and Feng XC substantially participated in drafting and revising the important intellectual content of the manuscript; All authors involved have read and approved the final manuscript.

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**Country/Territory of origin:** China

**ORCID number:** Shuang-Zhu Lin 0000-0001-5333-2138; Hong-Yan Xie 0000-0002-4116-5173; Yan-Lai Qu 0000-0001-8039-5345; Wen Gao 0000-0001-9230-368X; Wan-Qi Wang 0000-0002-8247-7616; Jia-Yi Li 0000-0002-7729-4479; Xiao-Chun Feng 0000-0001-5780-2811; Chun-Quan Jin 0000-0002-6082-6467.

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