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ABOUT COVER

Editorial board member of World Journal of Clinical Cases, Dr. Elia de Maria is Adjunct Professor of Arrhythmology Lab in the Cardiology Unit, Ramazzini Hospital in Carpi, Italy. He graduated in Medicine and Surgery from the University of Napoli in 1999, continuing on to obtain specialization in Cardiology in 2003. He also holds the distinction of High Degree Master in Electrophysiology and Cardiac Stimulation. Since 2005, he has practiced as a Permanent Consultant Cardiologist in the Italian Public Hospitals, and since 2015 as an External Contract Professor in the Faculty of Medicine and Surgery of University of Verona. His clinical and research interests encompass pharmacological therapy in acute and chronic cardiac conditions, temporary and definitive pacing, thoracentesis and pericardiocentesis, and hemodynamic monitoring. (L-Editor: Filipodia)

AIMS AND SCOPE

The primary aim of World Journal of Clinical Cases (WJCC, World J Clin Cases) is to provide scholars and readers from various fields of clinical medicine with a platform to publish high-quality clinical research articles and communicate their research findings online.

WJCC mainly publishes articles reporting research results and findings obtained in the field of clinical medicine and covering a wide range of topics, including case control studies, retrospective cohort studies, retrospective studies, clinical trials studies, observational studies, prospective studies, randomized controlled trials, randomized clinical trials, systematic reviews, meta-analysis, and case reports.

INDEXING/ABSTRACTING

The WJCC is now indexed in Science Citation Index Expanded (also known as SciSearch®), Journal Citation Reports/Science Edition, PubMed, and PubMed Central. The 2020 Edition of Journal Citation Reports® cites the 2019 impact factor (IF) for WJCC as 1.013; IF without journal self cites: 0.991; Ranking: 120 among 165 journals in medicine, general and internal; and Quartile category: Q3.

RESPONSIBLE EDITORS FOR THIS ISSUE

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Novel deletion mutation in Bruton’s tyrosine kinase results in X-linked agammaglobulinemia: A case report

Xiao-Mei Hu, Ke Yuan, Hong Chen, Chun Chen, Yan-Lan Fang, Jian-Fang Zhu, Li Liang, Chun-Lin Wang

Authorization: Hu XM and Wang CL conceived and designed the study; Yuan K, Hu XM, Chen H, and Fang YL performed the experiments; Chen C and Zhu JF provided clinical research; Hu XM wrote the paper; Hu XM, Yuan K, Liang L and Wang CL reviewed and edited the manuscript; all authors read and approved the manuscript.

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Abstract

BACKGROUND
X-linked agammaglobulinemia is a primary immunodeficiency disease caused by gene mutations of Bruton’s tyrosine kinase (BTK). We found a new mutation point and summarized the correlation analysis and performed a literature review.

CASE SUMMARY
The proband was a 5-year-old boy. He was admitted to our hospital due to a recurrent cough and a fever that had persisted for a month. He had a history of multiple respiratory infections and sinusitis. There was no immunodeficiency or recurrent infection history among his family members. Agammaglobulinemia was characterized as follows: Immunoglobulin (Ig) A, 90.0 mg/dL (90-450 mg/dL); IgG, 20.0 mg/dL (800-1800 mg/dL); and IgM, 18.0 mg/dL (60-280 mg/dL). Notably, the assessment of IgG subtypes revealed the following very low levels: Subtype 1, 0.26 g/L (3.62-12.28 g/L); subtype 2, 0.10 g/L (0.57-2.9 g/L); subtype 3, 0.009 g/L (0.129-0.789 g/L); and subtype 4, 0.003 g/L (0.013-1.446 g/L). Cellular immunological test results were as follows: CD3, 74.6% (50%-84.0%); CD4, 47.3% (27.0%-51.0%); and CD8, 24.9% (15.0%-44.0%). A de novo hemizygous deletion in BTK was detected: c.902_c.904delAAG/p.E301del. Transcript levels of the mutant BTK were similar to those of the wild-type gene, though overexpression resulted in markedly reduced levels of mutant BTK (9.49% ± 1.58%), relative to the wild-type BTK (75.8% ± 2.98%, P < 0.01).

CONCLUSION
This case of X-linked agammaglobulinemia was attributed to a de novo hemizygous deletion mutation in BTK (c.902_c.904delAAG/p.E301del). The mutation resulted in markedly reduced BTK protein stability in vitro.

Key words: Agammaglobulinemia; Bruton’s tyrosine kinase; Mutation; Immunodeficiency; Case report
INTRODUCTION

X-linked agammaglobulinemia (XLA, OMIM 300755; also known as Bruton’s disease) is a primary immunodeficiency disease caused by mutations of the Bruton’s tyrosine kinase (BTK) gene. The BTK protein, discovered in 1993, is named after Ogden Bruton, who first described XLA in 1952. XLA is a developmental disorder characterized by severely reduced mature peripheral B lymphocyte counts and serum immunoglobulin (Ig) levels[1]. Typically, patients with XLA suffer from various bacterial infections caused by many extracellular bacteria. They are also vulnerable to viruses and parasites. The presentation and severity of XLA differ among patients, with some BTK mutations being associated with severe and complex disease processes[2-4]. However, the relationship between in vitro findings and clinical phenotypes of BTK mutations remains poorly understood.

In the present study, we report the case of a Chinese boy with a typical clinical XLA phenotype carrying a de novo hemizygous deletion in BTK. We identified the mutation (c.902_c.904delAAG/p. E301del) and conducted a predictive analysis of its effect on the tertiary structure of BTK. The present study was approved by the Ethics Committee of The First Affiliated Hospital, College of Medicine, Zhejiang University, and conducted in accordance with the Declaration of Helsinki Principles. Furthermore, written informed consents were obtained from the patient’s parents.

CASE PRESENTATION

Chief complaints

A 5-year-old boy was admitted to our hospital due to recurrent cough and fever that had persisted for more than a month.

History of present illness

The patient’s symptoms started over a month ago with recurrent cough and fever, which had worsened over the previous week.

History of past illness

The patient had a history of multiple respiratory infections and sinusitis episodes since the age of 1 year, but no peripheral lymphadenopathy, tonsil enlargement, or hepatosplenomegaly were observed.

History of past illness

The boy was the first child of Han Chinese nonconsanguineous parents. He was born full term with a birth weight of 4000 g and a length of 50 cm. There was no family history of immunodeficiency or recurrent infections.

Physical examination

The patient’s temperature was 36.6°C, heart rate was 90 bpm, respiratory rate was 25 breaths per minute, blood pressure was 121/60 mmHg and oxygen saturation in room
air was 97%. His mind was clear, he had shortness of breath, middle trachea, hyperemia of the pharynx, no obvious enlargement of the tonsils, thick breath sounds in both lungs, obvious moist rale, homogeneous rhythm, no obvious pathological Mur, soft abdomen, normal bowel sound, no obvious abnormalities during nervous system examination.

**Laboratory examinations**
The patient’s routine blood results were as follows: White blood cell count, \(21.5 \times 10^9/L\) (4.0-12.0 \(\times 10^9/L\)); neutrophils, 67.9% (50%-70%); lymphocytes, 18.1% (20%-40%); hemoglobin, 131 g/L (120-140 g/L); platelet count, 401 \(\times 10^9/L\) (100-300 \(\times 10^9/L\)); and high-sensitivity C-reactive protein, 112.7 mg/dL (0–8 mg/dL). Agammaglobulinemia was characterized as follows: IgG, 20.0 mg/dL (800-1800 mg/dL); IgG subtype 1, 0.26 g/L (3.62-12.28 g/L); IgG subtype 2, 0.10 g/L (0.57-2.9 g/L); IgG subtype 3, 0.009 g/L (0.129-0.789 g/L); IgG subtype 4, 0.003 g/L (0.013-1.446 g/L); IgA, 90.0 mg/dL (90-450 mg/dL); and IgM, 18.0 mg/dL (60-280 mg/dL) (determined by enzyme-linked immunosorbent assay kits from Shanghai Langton Biotechnology Co., Ltd.). Complement C4 and C3 levels were found to be 18.0 mg/dL (7-149 mg/dL) and 106.0 mg/dL (58-160 mg/dL), respectively.

**CD3\(^+\), CD4\(^+\), and CD8\(^+\) T lymphocytes** were 74.6% (50%-84.0%), 47.3% (27.0%-51.0%), and 24.9% (15.0%-44.0%), respectively.

**Imaging examinations**
A chest spiral computed tomography scan revealed a bilateral lung infection.

**Further diagnostic work-up**
Due to the patient’s history of repeated respiratory tract infections, his very low serum IgG levels (< 2.5 g/L), and general agammaglobulinemia, he was treated with Ig infusions every four weeks. This treatment markedly reduced the patient’s respiratory infection incidence.

**Genetic analysis:** Genomic deoxyribonucleic acid (DNA) was extracted from peripheral blood samples obtained from the proband and his parents. Sequence variants detected in \(BTK\) were described according to the National Center of Biotechnology Information entry NM_000061.2. An analysis of pathogenicity and mutation conservation was performed with the bioinformatics Mutation Taster (http://www.mutationtaster.org) and University of California Santa Cruz Genome Browser (http://genome.UCSC.edu) programs.

**Molecular modeling:** The three-dimensional structure of the mutation was generated in the Swiss-Model program (https://swissmodel.expasy.org/interactive).

**BTK expression:** The wild-type (WT) full-length human \(BTK\) messenger ribonucleic acid (mRNA) (NM_000061.2), which includes NheI and BamH1 restriction enzyme sites, was synthesized (Tsingke, China), and cloned into the plasmid vector pEGFP-N1. The mutation 902-904delAAG was introduced into the \(BTK\) sequence via two polymerase chain reaction (PCR) rounds with mutagenic primers. The two PCR products were connected by homologous recombination with a TreliC\(^\text{TM}\) SoSoo cloning kit (Tsingke, China). The connection product was transformed into \(Escherichia\ coli\) DH5\(^\alpha\). Positive clones were selected, and the full-length mutant cDNA was sequenced to confirm the site-directed mutation.

For transient transfection, HEK-293T cells were cultured in 24-well plates to 70%-80% confluence and transfected with 500 ng of pEGFP-N1 containing no insert, pEGFP-N1-WT-\(BTK\) (WT), or pEGFP-N1-Mutation-\(BTK\) (Mut) with Lipofectamine\(^\text{TM}\) 3000 transfection reagent (Thermo Fisher Scientific). Cells were collected 24 h later.

**Quantitative real-time PCR:** Cells were collected from 24-well plates and total RNA preparations were obtained with a MiniBEST Universal RNA Extraction Kit (Takara). cDNA was produced with a Primescript RT reagent kit with gDNA Eraser, applied prior to reverse transcription to remove genomic DNA (Takara, AK3920). Glyceraldehyde 3-phosphate dehydrogenase gene fragment was used as an internal reference, and quantitative PCR was performed with a real-time fluorescence quantitative PCR instrument (BIO-RAD CFX Connect). The forward and reverse primers used for the PCR amplification were 5’ GAA AGG TTC CCT TAT CCC TTC C 3’ and 5’ GAA TCC ACC GCT TCC TTA GTT 3’, respectively.

**Western blotting:** Cell protein was extracted with a whole cell extraction kit (Abcam), and 10-μg protein aliquots were subjected to 12% sodium dodecyl sulfate polyacrylamide gel electrophoresis. Protein bands were electro transferred onto a
polyvinylidene difluoride membrane and detected with monoclonal anti-BTK antibody (Abcam) and horseradish peroxidase-conjugated goat anti-rabbit secondary antibody. Immunoreactive bands were visualized with enhanced chemiluminescence reagent (Super Signal, Pierce) and observed with a gel imaging system.

Genetic diagnosis and protein structure modeling: Genetic analysis revealed that the proband had a de novo hemizygous deletion in BTK: c.902_c.904delAAG/p.E301del. No BTK variants were detected in the proband’s parents’ genomes (Figure 1). Bioinformatics analysis in Mutation Taster indicated that BTK c.902_c.904delAAG/p.E301del would be highly pathogenic. Furthermore, sequence alignment revealed that the E301 residue lost in this deletion is conserved across diverse vertebrates (e.g. Homo sapiens, Pan troglodytes, Macaca mulatta, Felis catus, Mus musculus, Gallus gallus, and Xenopus tropicalis), a finding consistent with it being functionally important (Figure 2). The deletion did not produce a frameshift. However, three-dimensional structural modeling indicated that the deletion altered the Src homology (SH) 2 domain of the mutant BTK protein relative to WT BTK (Figure 3).

Reduction in steady-state levels of BTK: Quantitative PCR results revealed similar BTK mRNA levels between WT and mutant cDNAs, indicating that the mutation was not disruptive to transcription (Figure 4). Western blotting revealed plentiful overexpression of WT BTK (75.8% ± 2.98%) and markedly reduced overexpression of the BTK c.902_c.904delAAG/p.E301del deletion mutant (9.49% ± 1.58%, P < 0.01) (Figure 5). Hence, mutant BTK protein levels were depressed despite the deletion mutation not being disruptive to transcription, providing evidence of a posttranslational loss.

FINAL DIAGNOSIS

X-linked agammaglobulinemia.

TREATMENT

Regular injections of intravenous immunoglobulin.

OUTCOME AND FOLLOW-UP

The child’s immune function was basically normal, and there were no obvious abnormalities during long-term follow-up.

DISCUSSION

The history of repeated infections and reduced serum Ig levels in the proband in the present case led to a clear diagnosis of Ig deficiency. This phenotype together with the identified BTK mutation led to the final diagnosis of XLA. As BTK-mediated signaling plays an important role in the differentiation, development, proliferation, and apoptosis of B lymphocytes, mutations in BTK that disrupt BTK function result in the severe Ig deficiency characteristic of XLA[1,3]. Affected patients exhibit typical development in infancy while they are protected by maternal IgGs, after which patients become susceptible to repeated bacterial infections. The disrupted B-cell development in bone marrow in patients with XLA leads to severe insufficiencies of B cells and antibodies in the circulation.

Human BTK is located on the X chromosome at q21.33-22 (total length, 37.5 kb) and expressed in all hematopoietic cells. It contains 21 exons.

Approximately 900 different BTK mutations have been identified in patients with XLA, most of which are missense mutations, followed by nonsense, deletion, insertion, and splice mutations. Some two-thirds of patients with XLA have a family history of XLA, with the remainder having a de novo mutation.

The BTK protein consists of five functional domains: A pleckstrin-homology domain [amino acids (aa) 1-138], a Tec homology domain (aa 139-215), an SH3 domain (aa 216-
Figure 1  No Bruton’s tyrosine kinase variants were detected in the proband’s parents’ genomes. Polymerase chain reaction direct sequencing revealed a compound heterozygous Bruton’s tyrosine kinase sequence variant (c.902_c.904delAAG/p.E301del) in the proband. The parents of the proband both had normal Bruton’s tyrosine kinase genes.

Figure 2  Bruton’s tyrosine kinase sequence conservation analysis. Amino acid E301 (arrow) was found to be conserved across diverse vertebrates.

280), an SH2 domain (aa 281-377), and the tyrosine kinase-SH1 domain (aa 375-659)\textsuperscript{14}. BTK mutations, such as L295P, G302E, G302R and G302del, have been reported to severely disrupt protein activity, leading to XLA\textsuperscript{6-8}. Although the deletion mutation in our patient (c.902_c.904delAAG/p.E301del) did not result in a frameshift and did not alter the structure of the whole protein (Figure 3), it is located in the important functional SH2 domain. The evolutionary conservation of the residue lost in our patient’s mutant BTK (E301) across diverse vertebrates suggests that it is functionally critical.

BTK genotypes have been related, to some extent, with disease phenotypes\textsuperscript{9,10}. Patients with some mild missense mutations causing just a single change have
relatively intact Ig levels and mild clinical manifestations. However, patients with more severe mutations, including frameshift and nonsense mutations, may exhibit a wide range of severe phenotypes. Notwithstanding, the same mutation may result in different clinical manifestations in different individuals\[^{11-14}\]. In the present case, we found that BTK mutation was associated with a clinically typical presentation of XLA. The pathogenesis appears to be attributable to a loss of stability of the mutant protein, whose stability level upon overexpression \textit{in vitro} was only about that of the WT protein.

**CONCLUSION**

In summary, a \textit{de novo} hemizygous deletion mutation in BTK was identified as the cause of XLA in the present case. The mutation was shown to cause a significant reduction in protein stability \textit{in vitro}.
Figure 5  Western blot and relative translation analysis of E301 deletion mutant Bruton’s tyrosine kinase relative to wild-type Bruton’s tyrosine kinase. Markedly reduced protein band (A) and relative translation (B) were observed with the E301 deletion mutant relative to the wild-type gene. PEGFP-1 is the empty vector control group. Reduced glyceraldehyde-phosphate dehydrogenase was the loading control. Mean ± standard deviation levels are shown; *P < 0.001. BTK: Bruton’s tyrosine kinase; WT: Wild-type.

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