

CASE REPORT

Open Access



Unilateral buphthalmos, corneal staphyloma and corneal fistula caused by pathogenic variant in the PITX3 gene: a case report

Lin Zhou¹, Zhike Xu², Qianying Wu¹ and Xin Wei^{1*}

Abstract

Introduction: *PITX3* has been reported to be associated with congenital cataracts, anterior segment mesenchymal dysgenesis, Peters' anomaly, and microphthalmia. In this case, an infant with unilateral buphthalmos, corneal staphyloma and corneal fistula carrying a variant in *PITX3* was reported.

Case description: We describe a 4-month-old female infant who was referred to our Eye Clinic because of gradual enlargement of the eyeball in the right eye and whitish opacity in both eyes. Buphthalmos with long axial length (22.04 mm), macrocornea with diffuse corneal oedema and opacity (14.50 mm*14.50 mm) and high intraocular pressure (23.78 mmHg) were detected in the right eye. Microphthalmia with short axial length (16.23 mm), microcornea with diffuse corneal oedema and opacity (7.50 mm*6.50 mm) were detected in the left eye. A 360° trabeculotomy was performed for the right eye. However, corneal staphyloma and corneal fistula in the right eye were detected 6 months after the surgery. A variant in exon 4 of *PITX3* (c.640_656dup (p. Gly220Profs*95)) was identified in the proband but was not detected in her healthy parents.

Conclusion: A novel phenotype characterized by unilateral buphthalmos, corneal staphyloma and corneal fistula in an infant were reported to be associated with *PITX3* in our study. Our study expands the scope of the clinical heterogeneity of *PITX3* variants. It also improves our understanding and increases the attention given to patients with *PITX3* variants.

Keywords: *PITX3*, Variant, Unilateral buphthalmos, Corneal staphyloma, Corneal fistula

Introduction

Buphthalmos is derived from “ox-eyed” in Greek. It describes the visible enlargement of the eyeball at birth or soon after due to increased intraocular pressure (IOP) [1]. Primary congenital glaucoma (onset at birth) and primary infantile glaucoma (onset after birth to 3 years) are the most frequent causes of buphthalmos [2, 3]. Corneal oedema, increased corneal diameter, and optic disc cupping are the classical manifestations

in patients with buphthalmos [4]. *PITX3* is the third *PITX* gene in the *PITX/RIEG* homeobox family and plays a critical role in normal lens development during vertebrate eye formation [5, 6]. *PITX3* is responsible for various ocular defects, including congenital cataract, anterior segment dysgenesis (ASD), Peters' anomaly, and microphthalmia [7, 8]. In this case, our aim is to report novel phenotype (unilateral buphthalmos and corneal opacity) of a 4-month-old female infant with variants in *PITX3*.

*Correspondence: mseng1121@126.com

¹ Department of ophthalmology, West China Hospital, Sichuan University, Address 37, Guo Xue Lane, Chengdu 610041, Sichuan, China
Full list of author information is available at the end of the article



© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

Case description

The proband in this study is a 4-month-old female infant. She was born after a full-term uneventful pregnancy and did not suffer a significant perinatal history. Physical examination after birth revealed a birth weight of 3015 g, a head circumference of 34 cm, and a body length of 47 cm. She had no systemic anomalies and no remarkable family history.

She was referred to our Eye Clinic because of an enlarged and cloudy right eye. Ophthalmologic examination (including B-scan and slit lamp examination) showed the following manifestations before surgery: right eye buphthalmos with long axial length (22.04 mm), macrocornea with diffuse corneal oedema and opacity (14.50 mm*14.50 mm), left eye microphthalmia (short axial length: 16.23 mm) and microcornea with diffuse corneal oedema and opacity (7.50 mm*6.50 mm) (Fig. 1). The IOP was 23.78 mmHg and 17.30 mmHg in the right and left eyes, respectively. Additionally, an inferiorly decentred excavation within the superficial optic disc tissue was revealed by the B-scan in the right eye (Fig. 1). A 360° trabeculotomy was immediately performed on the right eye. She did not return for routine follow-up. Six months after the trabeculotomy, corneal staphyloma and corneal fistula with iris plugging of the perforated ulcer

were detected according to the telephone follow-up. Oophthalmectomy was performed for the right eye at the local hospital.

Informed consent was obtained from the parents of the proband according to the protocol approved by West China Hospital Sichuan University. Whole exome sequencing has been performed on the proband's genomic DNA sample. S220 Focused-ultrasonicator (Covaris, Massachusetts, USA) was used to shear Genomic DNA (1–3 µg) into an average size of 150-bp. The preparation of standard Illumina libraries was conducted by DNA Sample Prep Reagent Set (MyGenostics, Beijing, China).

To acquire the DNA library, genomic DNA (1–3 µg) and the probes were mixed and then PCR amplification was performed. A DNBSEQ-T7RS sequencer for paired reads of 150 bp (average sequencing depth: 1485.68; target area coverage: 10X: 99.93 20X: 99.87) was used for next-generation sequencing. Variants in genes responsible for glaucoma, microphthalmia and macrophtalmia (Table S1) were selected and analysed through multiple bioinformatic analytic steps. Variants with a minor allele frequency (MAF) smaller than 0.01 (based on the 1000 genome, ESP6500, dbSNP, EXAC) and sequencing quality with a coverage of more than 5 were included. Additionally,

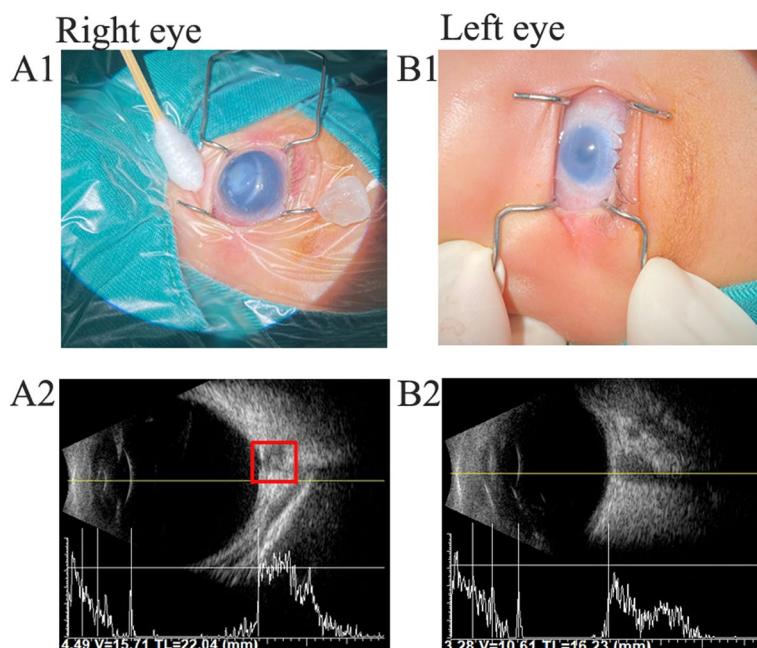


Fig. 1 The phenotype of the proband with variant in *PITX3*. Fig. **A1** The photography of the right eye. Buphthalmos with macrocornea (14.50 mm*14.50 mm), corneal opacity and edema were detected. Fig. **A2** B-scan of the right eye. Buphthalmos with axial length of 22.04 mm was present and an inferiorly decentred excavation within the superficial optic disc tissue revealed in the red box. Fig. **B1** The photography of the left eye. Microcornea (7.50 mm*6.50 mm) and corneal opacity were detected. Fig. **B2** Microphthalmia with axial length of 16.23 mm was detected

synonymous variants without a splice site change and benign variants predicted by online tools (SIFT, PolyPhen-2, MutationTaster, GERP++ and REVEL) were excluded.

Only one truncation in exon 4 (c.640_656dup (p.Gly220Profs*95)) of *PITX3* was identified (Fig. 2). No pathogenic variants were identified in other genes. Sanger sequencing validation, including amplification, sequencing, and target sequence analysis, was performed following a previously described method [9]. Additionally, segregation analysis was conducted, and her healthy parents did not carry the same variant.

Conclusions

PITX3 has been reported to be mapped close to aphakia on mouse chromosome 19. The lens develops normally in mice with *Pitx3* knockdown until an arrest occurs around embryonic Days 10.5–11. This timing corresponds to the moment of initial expression of *Pitx3* in the lens [10]. Microphthalmos or aphakia could be detected in mice with knockdown of *Pitx3* [11]. Mutations of this gene have been reported to be associated with congenital cataract, anterior segment dysgenesis (ASD), Peters' anomaly, and microphthalmia (Table 1 and Fig. 3).

Presently, twelve variants have been reported in 32 families. These variants include two missense variants in two families and ten truncations in 32 families [6–8, 12–24]. Four homozygote individuals with

more severe phenotypic abnormalities were reported because of consanguineous marriage in three families (Table 1). Six Asian families and 26 Caucasian families have been reported to have these variants in previous studies. Congenital cataracts without other abnormalities were more common in Asians than Caucasians with variants in *PITX3*. The c.640_656dup (p.Gly220Profs*95) mutation hot spot was detected in 18 families. For these affected individuals with heterozygous variants, cataracts were the most common manifestations and were detected in 92.74% of patients with *PITX3* variants. Anterior segment dysgenesis and corneal opacity could be found in 14.53 and 2.13% of patients harbouring *PITX3* variants, respectively. Microphthalmia (0.43%), microcornea (1.28%), nystagmus (0.85%), iridocorneal adhesions (0.85%), and glaucoma (0.43%) could also be detected (Table 1 and Fig. 3). However, no studies have reported corneal staphyloma and corneal fistula in patients with *PITX3* variants. Here, we report a 4-month-old female infant carrying a variant in *PITX3*. Unilateral buphthalmos, corneal staphyloma and corneal fistula were detected, and 360° trabeculectomy was conducted on the right eye. However, ophthalmeectomy was performed for the right eye at the local hospital because of the protruding opaque cornea and corneal fistula that presented 6 months after the 360° trabeculectomy.

In summary, we report a novel phenotype characterized by unilateral buphthalmos, corneal staphyloma

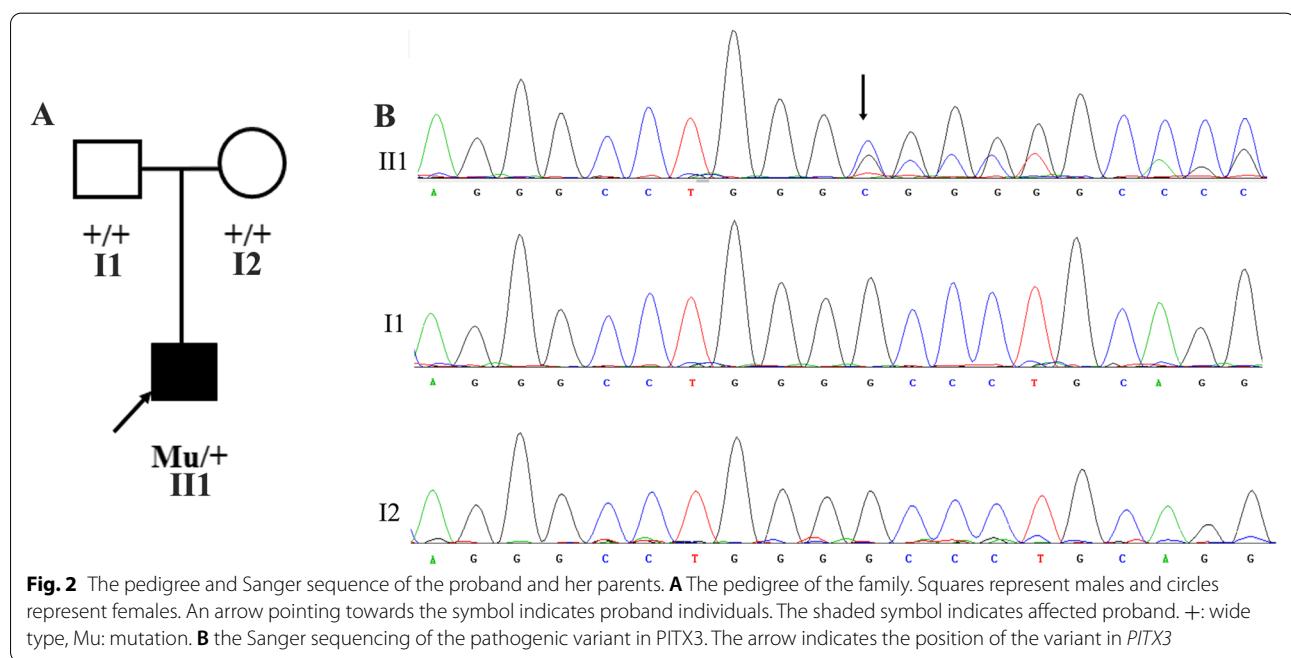


Fig. 2 The pedigree and Sanger sequence of the proband and her parents. **A** The pedigree of the family. Squares represent males and circles represent females. An arrow pointing towards the symbol indicates proband individuals. The shaded symbol indicates affected proband. +: wild type, Mu: mutation. **B** the Sanger sequencing of the pathogenic variant in *PITX3*. The arrow indicates the position of the variant in *PITX3*

Table 1 Summary of the reported variants in *PTX3*

PMID	Variant	Family	Numbers	Phenotype						
				Family Members	Cataract	Anterior segment dysgenesis	Peters anomaly	Corneal opacity	Microcornea	Microphthalmia
Homozygous										
21836522	c.640_656del (p.Ala214Argfs*42)	Family 1	1	1	-	-	-	-	-	Y
16563358	c.650del (p.Gly217Alafs*92)	Family 1	1	1	Y	-	-	Y	-	Y
16563358	c.650del (p.Gly217Alafs*92)	Family 1	1	1	Y	-	-	Y	-	Y
29405783	c.669del (p.Leu225Trpfs*84)	Family 2	1	2	-	Y	-	-	-	-
Heterozygous										
29405783	c.38G>A (p.Ser13Asn)	Family 5	1	1	-	-	-	Y	-	-
29405783	c.38G>A (p.Ser13Asn)	Family 5	1	1	-	-	-	Y	-	-
29405783	c.38G>A (p.Ser 3Asn)	Family 5	1	1	Y	-	-	-	-	-
9620774	c.94G>A (p.Gly32Ser)	Family 2	1	2	Y	-	-	-	-	-
216333712	c.542del (p.Pro181Leufs*128)	Family 1	1	8	Y	-	-	-	-	-
26885225	c.573del (p.Leu182Trpfs*127)	Family 1	1	8	Y	-	-	-	-	-
24555714	c.573del (p.Ser192Alafs*117)	Family 5	1	1	Y	-	-	Y	Y	-
24555714	c.573del (p.Ser192Alafs*117)	Family 5	1	1	Y	-	-	Y	Y	-
24555714	c.573del (p.Ser192Alafs*117)	Family 5	1	1	Y	-	-	Y	Y	-
29405783	c.582del (p.Ile 94Metfs*115)	Family 4	1	1	Y	-	-	Y	-	-
28249924	c.608del (p.Ala203Glyfs*106)	Family 1	1	1	Y	-	-	-	-	-
28249924	c.608del (p.Ala203Glyfs*106)	Family 1	1	1	Y	-	-	-	-	-
28249924	c.608del (p.Ala203Glyfs*106)	Family 1	1	1	Y	-	-	-	-	-
28249924	c.608del (p.Ala203Glyfs*106)	Family 1	1	1	Y	-	-	-	-	-
28249924	c.608del (p.Ala203Glyfs*106)	Family 1	1	1	Y	-	-	-	-	-
28249924	c.608del (p.Ala203Glyfs*106)	Family 1	1	1	Y	-	-	-	-	-
30816539	c.608del (p.Ala203Glyfs*106)	Family 10003	1	5	Y	-	Y	-	-	-
9620774	c.640_656dup (p.Gly220Profs*95)	Family 1	1	6	-	-	-	-	-	-
15286169	c.640_656dup (p.Gly220Profs*95)	Family 1	1	6	Y	-	-	-	-	-
15286169	c.640_656dup (p.Gly220Profs*95)	Family 1	1	1	Y	-	-	Y	Y	-
15286169	c.640_656dup (p.Gly220Profs*95)	Family 2	1	7	-	-	-	Y	Y	-
15286169	c.640_656dup (p.Gly220Profs*95)	Family 2	1	4	Y	-	-	-	-	-
15286169	c.640_656dup (p.Gly220Profs*95)	Family 3	1	14	Y	-	-	-	-	-
15286169	c.640_656dup (p.Gly220Profs*95)	Family 4	1	12	Y	-	-	-	-	-
15286169	c.640_656dup (p.Gly220Profs*95)	Family 5	1	5	Y	-	-	-	-	-

Table 1 (continued)

PMID	Variant	Family	Phenotype				Nystagmus
			Family Members	Family	Cataract	Peters anomaly	
15665340	c.640_656dup (p.Gly220Profs*95)	Family 1	1	7	Y	-	-
15665340	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
15665340	c.640_656dup (p.Gly220Profs*95)	Family 2	1	6	Y	-	-
15665340	c.640_656dup (p.Gly220Profs*95)	Family 2	4	Y	Y	-	-
15665340	c.640_656dup (p.Gly220Profs*95)	Family 3	1	14	Y	-	-
16272057	c.640_656dup (p.Gly220Profs*95)	Family 1	1	20	Y	-	-
16636655	c.640_656dup (p.Gly220Profs*95)	Family 1	1	29	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	-	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
18989383	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-	-
24555714	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	Y	-
24555714	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	Y	-
24555714	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	Y	-
24555714	c.640_656dup (p.Gly220Profs*95)	Family 2	1	1	Y	-	-
24555714	c.640_656dup (p.Gly220Profs*95)	Family 3	1	1	Y	-	-
24555714	c.640_656dup (p.Gly220Profs*95)	Family 3	1	1	Y	Y	-
24555714	c.640_656dup (p.Gly220Profs*95)	Family 4	1	1	Y	-	-
24555714	c.640_656dup (p.Gly220Profs*95)	Family 4	1	1	Y	Y	-

Table 1 (continued)

PMID	Variant	Family	Phenotype			
			Family Members	Cataract	Peters anomaly	Microcornea
		Numbers				Nystagmus
29405783	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	Y	-
29405783	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	-	-
29405783	c.640_656dup (p.Gly220Profs*95)	Family 1	1	Y	-	-
29405783	c.640_656dup (p.Gly220Profs*95)	Family 3	1	-	-	-
29405783	c.640_656dup (p.Gly220Profs*95)	Family 3	1	Y	-	-
30816539	c.640_656del (p.Ala214Argfs*42)	Family 10094	1	Y	-	-
30816539	c.640_656del (p.Ala214Argfs*42)	Family 10178	1	Y	-	-
16565358	c.650del (p.Gly217Alafs*92)	Family 1	1	26	Y	-
29405783	c.669del (p.Leu225Trpfs*84)	Family 2	1	Y	-	-
30894134	c.797_814del (p.Ser266_Ala271del)	Family 1	1	Y	-	-
30894134	c.797_814del (p.Ser266_Ala271del)	Family 1	1	Y	-	-

Table 1 (continued)

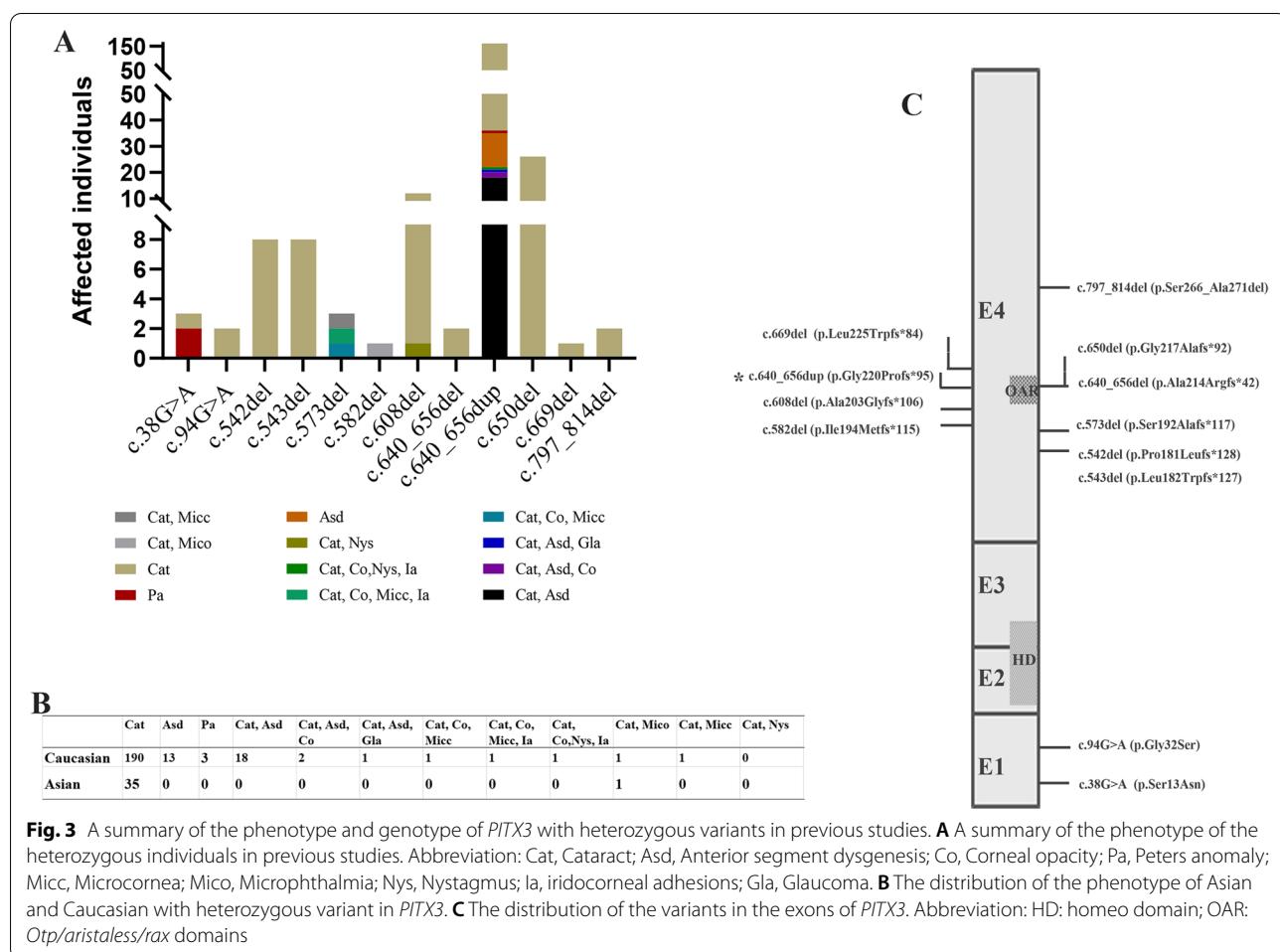
PMID	Variant		Family	Phenotype			Country	Ethnicity	Years	Ref.
				Sclerocornea	iridocorneal adhesions	buphthalmos				
Homozygous										
21836522	c.640_656del (p.Ala214Argfs*42)		Family 1	Y	-	-	Saudi Arabia	Caucasian	2011	Aldahmesh et al., 2011 [12]
16565358	c.650del (p.Gly217Alafs*92)		Family 1	-	-	-	Lebanese	Caucasian	2006	Bidinost et al 2006 [13]
16565358	c.650del (p.Gly217Alafs*92)		Family 1	-	-	-	Lebanese	Caucasian	2006	Bidinost et al 2006 [13]
29405783	c.669del (p.Leu225Trpfs*84)		Family 2	Y	-	-	Iraq	Caucasian	2018	Celia et al., 2018
Heterozygous										
29405783	c.38G>A (p.Ser13Asn)		Family 5	-	-	-	French	Caucasian	2018	Celia et al., 2018
29405783	c.38G>A (p.Ser13Asn)		Family 5	-	-	-	French	Caucasian	2018	Celia et al., 2018
29405783	c.38G>A (p.Ser13Asn)		Family 5	-	-	-	USA	Caucasian	1998	Semina et al., 1998 [14]
9620774	c.94G>A (p.Gly32Ser)		Family 2	-	-	-	UK	Caucasian	2011	Berry et al., 2011 [15]
21633712	c.542del (p.Pro181Leufs*128)		Family 1	-	-	-	Chinese	Asian	2015	Xiangyu Ye et al., 2015
26885225	c.543del (p.Leu182Trpfs*127)		Family 1	-	-	-	Belgo-Romanian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.573del (p.Ser192Alafs*117)		Family 5	Y	-	-	Belgo-Romanian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.573del (p.Ser192Alafs*117)		Family 5	-	-	-	Belgo-Romanian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.573del (p.Ser192Alafs*117)		Family 5	-	-	-	North Ireland	Caucasian	2018	Celia et al., 2018
29405783	c.582del (p.Ile194Metfs*115)		Family 4	-	-	-	Chinese	Asian	2017	Liu et al., 2017 [16]
28249924	c.608del (p.Ala203Glyfs*106)		Family 1	-	-	-	Chinese	Asian	2017	Liu et al., 2017 [16]
28249924	c.608del (p.Ala203Glyfs*106)		Family 1	-	-	-	Chinese	Asian	2017	Liu et al., 2017 [16]
28249924	c.608del (p.Ala203Glyfs*106)		Family 1	-	-	-	Chinese	Asian	2017	Liu et al., 2017 [16]
28249924	c.608del (p.Ala203Glyfs*106)		Family 1	-	-	-	Chinese	Asian	2017	Liu et al., 2017 [16]
28249924	c.608del (p.Ala203Glyfs*106)		Family 1	-	-	-	Chinese	Asian	2017	Liu et al., 2017 [16]
28249924	c.608del (p.Ala203Glyfs*106)		Family 1	-	-	-	Chinese	Asian	2017	Liu et al., 2017 [16]
28249924	c.608del (p.Ala203Glyfs*106)		Family 1	-	-	-	Chinese	Asian	2017	Liu et al., 2017 [16]
28249924	c.608del (p.Ala203Glyfs*106)		Family 1	-	-	-	Chinese	Asian	2017	Liu et al., 2017 [16]
30816539	c.608del (p.Ala203Glyfs*106)		Family 10003	-	-	-	Chinese	Asian	2019	Zehua Wu et al., 2019
9620774	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	USA	Caucasian	1998	Semina et al., 1998 [14]
15286169	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	UK	Caucasian	2004	Berry et al., 2004 [15]
15286169	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	UK	Caucasian	2004	Berry et al., 2004 [15]

Table 1 (continued)

Table 1 (continued)

PMD	Variant		Family	Phenotype	Sclerocornea	Iridocorneal adhesions	buphthalmos	Glaucoma	Country	Ethnicity	Years	Ref.
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
18989383	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Australian	Caucasian	2008	Summers et al., 2008 [20]
24555714	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Belgian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Belgian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	Belgian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.640_656dup (p.Gly220Profs*95)		Family 2	-	-	-	-	-	Belgian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.640_656dup (p.Gly220Profs*95)		Family 3	-	-	-	-	-	Belgian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.640_656dup (p.Gly220Profs*95)		Family 3	-	-	-	-	-	Belgian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.640_656dup (p.Gly220Profs*95)		Family 4	-	-	-	-	-	Belgian	Caucasian	2014	Verdin et al., 2014 [6]
24555714	c.640_656dup (p.Gly220Profs*95)		Family 4	Y	-	-	-	-	Belgian	Caucasian	2014	Verdin et al., 2014 [6]
29405783	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	French	Caucasian	2018	Celia et al., 2018
29405783	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	French	Caucasian	2018	Celia et al., 2018
29405783	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	French	Caucasian	2018	Celia et al., 2018
29405783	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	French	Caucasian	2018	Celia et al., 2018
29405783	c.640_656dup (p.Gly220Profs*95)		Family 1	-	-	-	-	-	French	Caucasian	2018	Celia et al., 2018
30816539	c.640_656del (p.Ala214Argfs*42)		Family 10094	-	-	-	-	-	Chinese	Asian	2019	Zehua Wu et al., 2019
30816539	c.640_656del (p.Ala214Argfs*42)		Family 10178	-	-	-	-	-	Chinese	Asian	2019	Zehua Wu et al., 2019
16565358	c.650del (p.Gly217Alafs*92)		Family 1	-	-	-	-	-	Lebanese	Caucasian	2006	Bidinost et al., 2006 [13]
29405783	c.669del (p.Leu225Trpfs*84)		Family 2	-	-	-	-	-	Iraq	Caucasian	2018	Celia et al., 2018
30894134	c.797_814del (p.Ser266_Ala271del)		Family 1	-	-	-	-	-	Chinese	Asian	2019	Fan, Q et al., 2019 [21]
30894134	c.797_814del (p.Ser266_Ala271del)		Family 1	-	-	-	-	-	Chinese	Asian	2019	Fan, Q et al., 2019 [21]

Notes: NA not reported in original article; F family member; M family member; /het heterozygous; /Hom homozygous; Y carry the relevant phenotype; —, normal



and corneal fistula this is associated with a *PITX3* variant. Our study expands the scope of the clinical heterogeneity of *PITX3* variants. It also improves our understanding and increases the attention given to patients with *PITX3* variants.

Abbreviations

IOP: Increased intraocular pressure; ASD: Anterior segment dysgenesis; ESP: Exome Sequencing Project v. 6500; ExAC: Exome Aggregation Consortium; MAF: Minor allele frequency; dbSNP: The Single Nucleotide Polymorphism database.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12886-022-02573-x>.

Additional file 1.

Acknowledgements

Not applicable.

Authors' contributions

Conception and design: LZ and XW; Data collection: LZ, ZX, QW, XW; Analysis and interpretation: LZ, ZX, QW, XW; Writing the article: LZ and XW. All authors have read and approved the manuscript.

Funding

Supported by grants from the National Science Foundation of China (No.82070954); The Applied Basic Research Programs of Science and Technology Commission Foundation of Sichuan Province (No.19YYJC0790); The Innovative Spark Grant of Sichuan University (No.2018SCUH0062). The funding bodies played no role in the design of the study and collection, analysis, and interpretation of data and in writing the manuscript.

Availability of data and materials

The sequence data were deposited in NCBI Gene bank and can be retrieved using GenBank accession number: BankIt2572599 seq ON236641. Other data and supplementary information are included in this published article.

Declarations

Ethics approval and consent to participate

The case report was adhered to the tenets of the Declaration of Helsinki and approved by the ethics committee of West China Hospital, Sichuan University. Written informed consent was obtained from the parents of the proband.

Consent for publication

Written informed consent for publication of identifying images or other personal or clinical details was obtained from all of the individuals and the parents of proband.

Competing interests

The authors report no conflicts of interest in this work.

Author details

¹Department of ophthalmology, West China Hospital, Sichuan University, Address 37, Guo Xue Lane, Chengdu 610041, Sichuan, China. ²Department of ophthalmology, The people's hospital of Leshan, Leshan 614700, China.

Received: 3 September 2021 Accepted: 15 August 2022

Published online: 24 September 2022

References

- Feroze KB, Patel BC. Buphthalmos. Treasure Island (FL): StatPearls; 2021.
- Mark HH. Buphthalmos: early glaucoma history. Acta Ophthalmol. 2011;89:591–4. <https://doi.org/10.1111/j.1755-3768.2009.01783.x>.
- Bouhenni RA, Ricker I, Hertle RW. Prevalence and clinical characteristics of childhood Glaucoma at a tertiary care Children's hospital. J Glaucoma. 2019;28:655–9. <https://doi.org/10.1097/JG.00000000000001259>.
- Vasileiadis GT, Frangoulis O. Unilateral congenital buphthalmos. BMJ Case Rep. 2015;2015. <https://doi.org/10.1136/bcr-2015-210979>.
- Shi X, Bosenko DV, Zinkevich NS, et al. Zebrafish pitx3 is necessary for normal lens and retinal development. Mech Dev. 2005;122:513–27. <https://doi.org/10.1016/j.mod.2004.11.012>.
- Verdin H, Sorokina EA, Meire F, et al. Novel and recurrent PITX3 mutations in Belgian families with autosomal dominant congenital cataract and anterior segment dysgenesis have similar phenotypic and functional characteristics. Orphanet J Rare Dis. 2014;9:26. <https://doi.org/10.1186/1750-1172-9-26>.
- Anand D, Agrawal SA, Slavotinek A, Lachke SA. Mutation update of transcription factor genes FOXE3, HSF4, MAF, and PITX3 causing cataracts and other developmental ocular defects. Hum Mutat. 2018;39:471–94. <https://doi.org/10.1002/humu.23395>.
- Wu Z, Meng D, Fang C, et al. PITX3 mutations associated with autosomal dominant congenital cataract in the Chinese population. Mol Med Rep. 2019;19:3123–31. <https://doi.org/10.3892/mmr.2019.9989>.
- Chen Y, Zhang Q, Shen T, et al. Comprehensive mutation analysis by whole-exome sequencing in 41 Chinese families with Leber congenital amaurosis. Invest Ophthalmol Vis Sci. 2013;54:4351–7. <https://doi.org/10.1167/iovs.13-11606>.
- Semina EV, Reiter RS, Murray JC. Isolation of a new homeobox gene belonging to the Pitx/Rieg family: expression during lens development and mapping to the aphakia region on mouse chromosome 19. Hum Mol Genet. 1997;6:2109–16. <https://doi.org/10.1093/hmg/6.12.2109>.
- Wada K, Matsushima Y, Tada T, et al. Expression of truncated PITX3 in the developing lens leads to microphthalmia and aphakia in mice. PLoS One. 2014;9:e111432. <https://doi.org/10.1371/journal.pone.0111432>.
- Aldahmesh MA, Khan AO, Mohamed J, Alkuraya FS. Novel recessive BFSP2 and PITX3 mutations: insights into mutational mechanisms from consanguineous populations. Genet Med. 2011;13:978–81. <https://doi.org/10.1097/GIM.0b013e31822623d5>.
- Bidinost C, Matsumoto M, Chung D, et al. Heterozygous and homozygous mutations in PITX3 in a large Lebanese family with posterior polar cataracts and neurodevelopmental abnormalities. Invest Ophthalmol Vis Sci. 2006;47:1274–80. <https://doi.org/10.1167/iovs.05-1095>.
- Semina EV, Ferrell RE, Mintz-Hittner HA, et al. A novel homeobox gene PITX3 is mutated in families with autosomal-dominant cataracts and ASMD. Nat Genet. 1998;19:167–70. <https://doi.org/10.1038/527>.
- Berry V, Yang Z, Addison PK, et al. Recurrent 17 bp duplication in PITX3 is primarily associated with posterior polar cataract (CPP4). J Med Genet. 2004;41:e109. <https://doi.org/10.1136/jmg.2004.020289>.
- Liu H, Liu H, Tang J, et al. Whole exome sequencing identifies a novel mutation in the PITX3 gene, causing autosomal dominant congenital cataracts in a Chinese family. Ann Clin Lab Sci. 2017;47:92–5.
- Addison PK, Berry V, Ionides AC, et al. Posterior polar cataract is the predominant consequence of a recurrent mutation in the PITX3 gene. Br J Ophthalmol. 2005;89:138–41. <https://doi.org/10.1136/bjo.2004.053413>.
- Finzi S, Li Y, Mitchell TN, et al. Posterior polar cataract: genetic analysis of a large family. Ophthalmic Genet. 2005;26:125–30. <https://doi.org/10.1080/13816810500229124>.
- Burdon KP, McKay JD, Wirth MG, et al. The PITX3 gene in posterior polar congenital cataract in Australia. Mol Vis. 2006;12:367–71.
- Summers KM, Withers SJ, Gole GA, Piras S, Taylor PJ. Anterior segment mesenchymal dysgenesis in a large Australian family is associated with the recurrent 17 bp duplication in PITX3. Mol Vis. 2008;14:2010–5.
- Fan Q, Li D, Cai L, et al. A novel mutation in the OAR domain of PITX3 associated with congenital posterior subcapsular cataract. BMC Med Genet. 2019;20:42. <https://doi.org/10.1186/s12881-019-0782-2>.
- Zazo Seco C, Plaisancie J, Lupasco T, et al. Identification of PITX3 mutations in individuals with various ocular developmental defects. Ophthalmic Genet. 2018;39:314–20. <https://doi.org/10.1080/13816810.2018.1430243>.
- Berry V, Francis PJ, Prescott Q, et al. A novel 1-bp deletion in PITX3 causing congenital posterior polar cataract. Mol Vis. 2011;17:1249–53.
- Ye X, Zhang G, Dong N, Meng Y. Human pituitary homeobox-3 gene in congenital cataract in a Chinese family. Int J Clin Exp Med. 2015;8:22435–9.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations. **Notes:** NA not reported in original article; F family; M family member; Het heterozygous; Hom homozygous; Y carry the relevant phenotype; —, normal

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

