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A novel missense mutation of *GJA8* causes congenital cataract in a large Mauritanian family

Mouna Hadrami[1] • Crystel Bonnet[2,3,4]• Fatimetou Veten1 • Christina Zeitz[5]• Christel Condroyer[5]•, Panfeng Wang7 • Sidi cheikh[6] • MohamedBiya[1] • Med AhmedSidiAhmed[6,12] • Qingjiong Zhang[7] • Isabelle Audo[5,8,9] • Christine Petit[2,3,4 10,11]• Ahmed Houmeida[1]

1 Unité de Recherche sur les Biomarqueurs dans la Population Mauritanienne, Université´ des Sciences de Technologies et de médecine (USTM), Nouakchott, Mauritanie.

2 Syndrome de Usher et Autres Atteintes Rétino-Cochléaires, Institut de la Vision, Paris, France.

3 UMRS 1120, Institut National de la Santé et de la Recherche Médicale, Paris, France.

4 Sorbonne Universités, UPMC Université Paris 06, Complexité du Vivant, Paris, France.

5 Sorbonne Universités, UPMC Univ Paris 06, INSERM, CNRS, Paris, France.

6 Service Ophtalmologie,Centre Hospitalier National,Nouakchott, Mauritanie.

7 Zhongshan Ophthalmic Center, Sun Yat-sen University, China

8 Centre Hospitalier National d'Ophtalmologie des Quinze-Vingts, DHU Sight Restore, INSERM-DHOS CIC 1423, Paris, France.

9 Institute of Ophthalmology, University College of London, London, UK.

10Unité de Génétique et Physiologie de l'Audition, Institut Pasteur, Paris, France.

11Collège de France, Paris, France.

12 Programme national de lutte contre cécités; Nouakchott ; Mauritanie

Corresponding author: Ahmed Houmeida :houmeida@hotmail.com

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Abstract

Background: Congenital cataract is the most frequent cause of childhood blindness. To date, more than 40 loci associated with cataract have been identified, including at least 26 genes on different chromosomes associated with inherited cataract. Here, we describe nine generations of a Mauritanian consanguineous family affected with congenital cataract. This study aimed to identify the genetic mutation in this Mauritanian family.

Methods: A detailed nine-generation autosomal dominant Mauritanian cataract family history and clinical data of the family members were recorded. A total of 14 family members, including 10 affected and 4 unaffected individuals were recruited. Targeted next-generation sequencing was performed to determine the disease-causing mutation. Sanger sequencing was used to confirm the results.

Results: A novel heterozygous missense mutation, c.166A>C (p.Thr56Pro), in *GJA8* was identified. This mutation co-segregated with all affected individuals and was not observed in the unaffected family members. The prediction of secondary structure from the protein sequence showed that the structure of the mutant protein was different with that wild-type GJA8.

Conclusions: We describe for the first time a missense mutation, c.166A>C in *GJA8*, which is associated with autosomal dominant congenital cataract in a Mauritanian family.

Introduction:

Cataract is commonly considered as an age related condition. This pathology may also be secondary to various after birth events or inborn[1-2]. Blindness from congenital cataract is indeed estimated to affect about 1-15 per 10,000 children in the developing world as the disease goes often undetected in early childhood resulting in most cases in permanent visual loss[3-4]. Hereditary congenital cataracts account for at least a third of all congenital cataract forms with the autosomal dominant being the most common familial form. They can also be transmitted as autosomal recessive or X-linked[4].

Of the thirty fourgenetic loci to which congenial cataracts, isolated or primary, have been mapped, a quarter of the known mutant genes are gap junction channel protein (connexins) encoding genes. Two of these genescodefor α-connexinsCx46 (GJA3) and Cx50 (GJA8) which are the most abundant proteins in lens fiber cells and essential, respectively,in the lens transparency and development [5].

Although about 50% of blindness in African populations is resulting from cataract, studies on the etiologies of this often avoidable disorder are very limited. Besides, there is no data, to our knowledge, on the genes implicated in hereditary cataract in these populations.

Here, we described the segregation profile of a congenital nuclear cataract in a nine generation Mauritanian family living in an isolated village located in the south of Mauritania. Using next-generation sequencing of whole exome, we also investigated the underlying genetic defect and analyzed the potential structural organization of the mutant region.

Materials and methods

This Mauritanian family living in the village of Dali Gumba, in the Hodh region of southern Mauritania has been affected, over nine generations, by a blindness which develops in early years following a congenital cataract. A team of eye specialists from the CNH (Centre National Hospitalier) and biologists from the University of Sciences technologies and medicine has clinically examined and interviewed the members of the living family members. A pedigree and family medical history were recorded.Opthtalomological assessment including slit lamp was carried out for all family members. Fourteen individuals (10 patients and 4unaffected subjects)were recruited for molecular investigation (figure 1a).

Targeted next-generation sequencing

DNA extraction, from peripheral blood collected in EDTA tubes, was carried out using QIAampDNA Blood Midi Kit (Qiagen, Hilden, Germany). Next-generation sequencing (NGS)was selectively conducted on the index case (figure 1a), using a custom-designed in-solution capture array targeting a panel of 116 cataract underlying genes. Details of the relevant genes are provided in **Appendix1**.Library preparation, qualification and NGS on the HiSeq2000 platform (Illumina, Inc., San Diego, CA) were performed as described previously [6]. The patient DNA, along other DNA samples, was multiplexed then randomly fragmented, ligated and amplified via ligation-mediated polymerase chain reaction (LM-PCR) [7]. After purification and hybridization, a quantitative PCR was then performed on LM-PCR products to assess the level of enrichment.

Bioinformatic analyses

Sequence reads alignment to the reference human genome 19 (hg19) with UCSC and nucleotide variation annotations were performedusing single nucleotide polymorphism (SNP) databases, includingHapMap project(http://hapmap.ncbi.nlm.nih.gov/), 1000 Genome Project(http://www.1000genomes.org/), Exome Variant Server (EVS, http://evs.gs.washington.edu/EVS/), and Exome Aggregation Consortium (EXAC, http://exac.broadinstitute.org/). In the Pathogenicity evaluation, amino acid change was considered as potentially disease causing if predicted by at least one of the programs (PolyPhen2, http://genetics.bwh.harvard.edu/pph2/), Sorting Intolerant From Tolerant (SIFT, http://sift.jcvi.org/) andMutation Taster (http://www.mutationtaster.org/).(**Appendix2**) Amino acid conservation across species was studied with UCSC Genome Browser (https://genome.ucsc.edu/). (figure2). The conformational change induced by the DNA variation on the mutant protein was analyzed and compared to wild-type protein structure using CFSSP server (http://www.biogem.org/tool/chou-fasman/).

Sanger sequencing

The protein variant identification, following NGS, was confirmed in the index proband and thirteen other affected family members by Sanger sequencing (ref) using (human GJA8 reference sequence NM_005267.4, Forward: 5’- GCTCTTGCCTTCTCCCTCAT -3’ and

Reverse: 5'- TGGCTTTCTGGATGGAGGAG-3').The primers were designed using Primer3 (http://bioinfo.ut.ee/primer3-0.4.0/).

Approval to this study was given by the ethics committee of the University of Sciences, Technologies and Medicine, Nouakchott, Mauritania. The purpose of the study was explained to the participants and their informed and signed consent was obtained. For children, the parents approval was obtained.

Results

Clinical exploration

Inborn cloudiness of the eye natural lens was reported in all the interviewed patients. Following clinical examination, nuclear congenital bilateral cataract was confirmed in all suspected cases from both genders. Initials signs of interference with the vision werereported to be in the first two years of life. The disease progression varied slightly among patients. Preliminary examination did not reveal association with any common ocular anomalies or systemic condition.Cataract was observed in each generation and all affected individuals had at least one parent who carries the disease. These characteristics were consistent with an autosomal dominant inheritance.

Genetic screening

Next generation sequencing performed on the proband's DNA (Fig 1.a, *) and selectively targeting the coding exons of 116 congenital cataract associated genes showed, after filtration and validation, a pathogenic DNA missense variation, A>C at position 166 (c.166 A>C) in the Cx50 α-connexin gene (*GJA8*).(**Appendix1**).

This mutation, not reported before,resulted in the substitution of an evolutionarily highly conserved threonine at position 56by a proline(p. T56P) (figure 1.c). This change was not observed in any of DNA samples from15individuals affected by other ocular pathologies and sequenced along the proband's DNA using the same NGS approach.

Sanger sequencing of the exon 2of *GJA8* in the fourteen affected family members, including the proband, showed the same A>C mutation, at position 166 from the translation start site (figure 1.b). This co-segregation with the disease was found only in the cataract patients as none of the unaffected family members or the healthy controls showed this mutation.

Bioinformatics analysis

Using the wild type Cx-50 protein as template, the predicted three-dimensional structure impacted by the amino acid point mutation p.T56P showed a localized alteration, with a score of 1.00 using CFSSP , in the first extra membrane loop which consisted of the disruption of the wild-type sheet and its replacement, in the mutant protein, by a turn then coil(figure2). This conformational change was assessed functionally as probablydamagingwith a score of 1.0 by SIFT and PolyPhen-2, respectively.

Discussion

Although blindness resulting from cataract is a primary health issue, data on the etiologies of this disease remained very limited in devolving countries. In this study, we reported a bilateral nuclear cataract present at birth in a nine generation family living in a remote village of Southern Mauritania. The age of onset varied but in most patients, the vision impairment was noticedwithin the two first years with a progressive evolution. Surgery did not confer a visual benefitmore likely due to the relatively advanced age, mostly above 6 years, of the patientsat presentation.The timing of extraction in congenital cataract is indeed critical in ensuring visual rehabilitation as the ideal recommended age of itsremoval isabout ten weeks to one year at the latest if the lens opacification is bilateral (8). These poor outcomes have greatlyaffected the trust of thefamily rulers in the medical benefit of the operation which resulted in that nearly all cataractsaffected children became blind or greatly visually impaired.

Although the age at onset does not necessary indicate the etiology, the presence of this cataract at birth and in several family members was evocative of an inherited cause. Besides, physical examination and personal medical history of patients did not reveal any underlying defined metabolic or infectious disorder. As in most inherited cataracts, the medical pedigree of the cataract phenotype in this family was consistent with an autosomal dominant pattern (9).

About 10 to 25 % of all cataracts are inherited and most of the genetically categorized congenital forms of this disorder were associated with known candidate genes (10-11). However, as no data were available on the specific implication of these cataract related genes in any African or Arab population, we opted foracomprehensive NGSscreening approach

using a large panel of 116 cataract underlying genes (6-12). This sequencing, confirmed by direct Sanger sequencing, showed a new missense variationat position 166 (c.166 A>C) in*GJA8*gene, on chromosome 1, whichresulted, at protein level, in a p.T56P substitutionin Cx50 α-connexin, awell known gap junction channel forming protein (13). This change was not observed in non affected family members or the healthy controls which supported the potential disease contributing effect of this mutation. This likelyeffect was also consistent withtheposition-specific independent count (PSIC) score of 1.000, as "probably damaging", produced by PolyPhen-2,a well approved pathogenity predicting software (**Appendix2**). The effect of the substitution on the protein function was also signified using the CFSSP server(figure2).

Different functional studies on expressed *GJA3* and *GJA8* mutant proteins have shown abnormalities likely to affect intercellular commutation through channel alteration or cellular trafficking impairment resulting in the reduction of the number of efficient gap junction channels within the plasma membrane.Thus, in mouse lines, targeted deletions of Cx50 protein have been linked to inheritance of cataractthrough their effect on lenssize and onset ofdisease phenotype (14). Data from transgenic mice also showed that alteration of the level of Cx50 production could result in lens opacification (15). Expressed human connexin mutants associated with congenital cataract have too showed biochemical and cellular aberration ranging from substantial reduction in gap junction plaques, generation of non-functional intercellular channels and formation of hemichannels with altered gating or charge selectivity properties (16-17).

In human families, more than forty missense Cx50 mutations, all transmitted in autosomaldominant mode, have so far been linked to congenital cataract on the basis of their disease segregation patternand clinical appearance (table 1). The protein tertiary structure of Connexin 50, like otherconnexin family members, showed, besides the four highly ordered transmembrane segments TM1-TM4, the C and N cytoplasmic termini,three loops (two extra-cellular: EL1 - EL2 and one cytoplasmic: CL) (18). Nearly 50 % of all cataract related mutations have been mapped to E1 and E2 loops which, by several analysis, were found to be structurally fundamental for gap junction generation (19). Although we did not performa protein stability or cell localization testingonthe mutant proteinfound in this family, the positions ofour mutation with respect to the membrane topology of the wild type C50 connexin showed that the replacement (p. T56P) concerned a highlyconservedaminoacid. This mutation, in loop E1, is also positioned in a site where numerous other congenital cataract

linked mutations have been identified (Table1). For instance, Cx50-S50P mutation (figure 1.c), close to our mutation T56P and also involving the introduction of a proline amino acid has been shown to affect lens physiopathology (21). The site of p.T56P substitution may therefore be determinant in the physiological contribution of connexin Cx50 and its integrity could affectthelens normal survival.In that respect, the conformational disruption predicted here i.e. the replacement of a β sheet in the wild type Cx50 connexin by the turn then coilin the mutant protein, is reasonable giving the known distinctive rigidity of the proline's side chain. Proline is indeed the only proteiogenic amino acid with a constrainedφ angle (approximatively at −65°) due the covalent locking of the nitrogen atom in the side chain five-membered ring. As a result of this angular restriction, interference of proline amino acid with the regular protein neighboring secondary structure (α helix or β sheet) is well documented (22).

As highlighted above, cataract phenotypes have been linked to severalcandidate genes.Although the mutations were largely in the same gene (*GJA8*), their respective occurrence appearedto reflect a population related distribution as most of these variants were reported in population of different origin (table1). A similar population allocation pattern has been reported for another heterogeneous monogenic disease i.e. beta thalassemia. This inherited blood disorder is indeed often caused, in a defined group, by a very limited number of β-gene mutations. For instance, in North African populations, nonsense mutation such as codon 39 (A >T) and splice junction IVSI-1were the most common cause of β thal cases (23). In sub-Saharan African populations, Substitution (A >G) at position -29 in the Tata box and IVS2-849 have been reported respectively in β^+ and β^0 U.S. black African patients (24). Giving the absence of any dataon inherited cataract in African populations, we could not relate our mutation to an existing cataract variant in these populations.However, the affected family belongs to the Moors (Maures) which is the predominant ethnic group of the Mauritanian population. This group of berber-arab origin ethnically self-identifies with the neighboring North Africa populations (25). Although no cataract associated mutation has so far been reported in this region and the specific ethnic occurrence of 166 (c.166 A>C) remains to be ascertained, this finding may be relevant in the population distribution analysis of future cataract related gene mutations in these populations.

Looking at the broader contribution of variantc.166 A>C, this newmutationexpands the spectrum of cataract associated DNA variants (table1). Besides, it was found in a remotely located family. Characterization of biomarkers in ethnically or geographically restricted

groups has indeed been reported to be more pertinent, than in general population studies, in understanding the heritability of population common genetic traits and diseases associated variants.This mutation, giving its protein location and specific ethnic occurrence may therefore contribute in assessingthe physiopathology of inherited cataract.

Conclusion

In this study, we identified a family new mutation (c.166 A>C) in GJA8 segregating with a nuclear congenital cataract. Giving that no other associated mutation was found in the proband'DNA using the powerful screening technique of NGS and its segregation with the phenotype, this mutation might be useful as a predicting marker of the diseaseonset before the clinical manifestation of the lens opacification.

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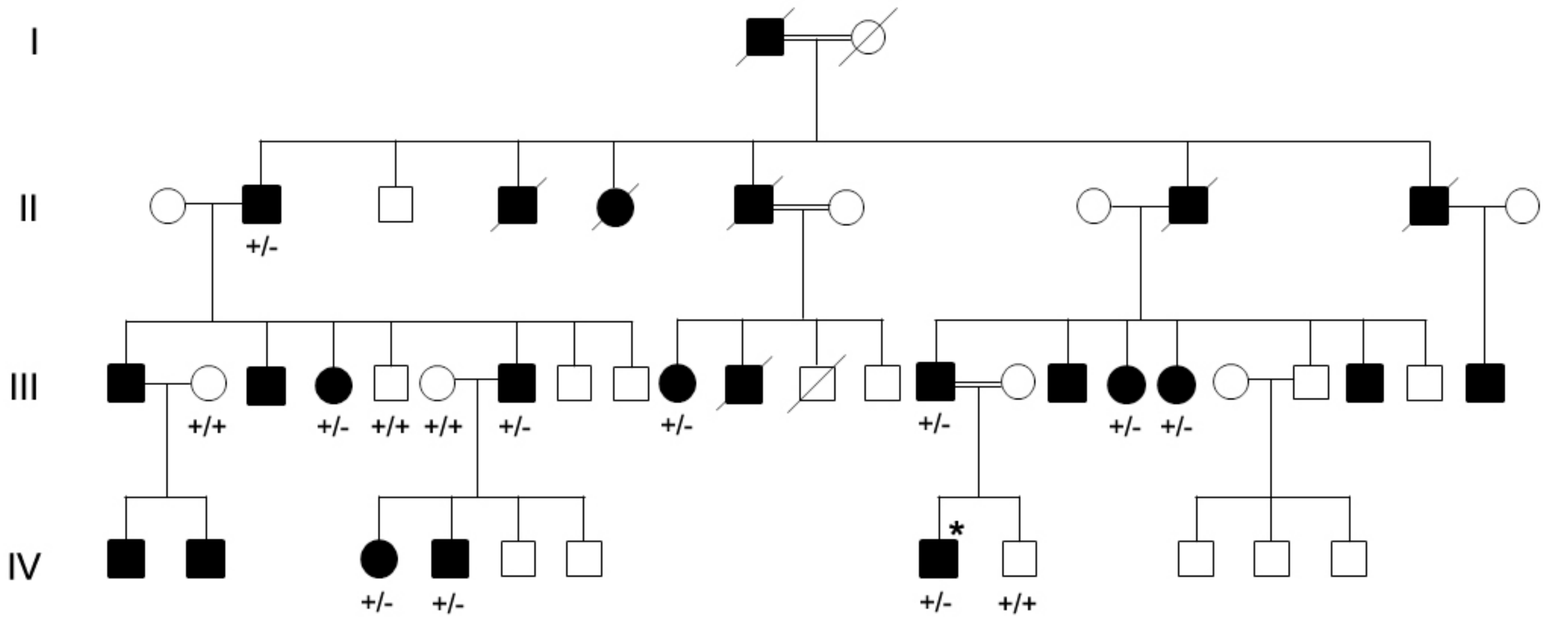
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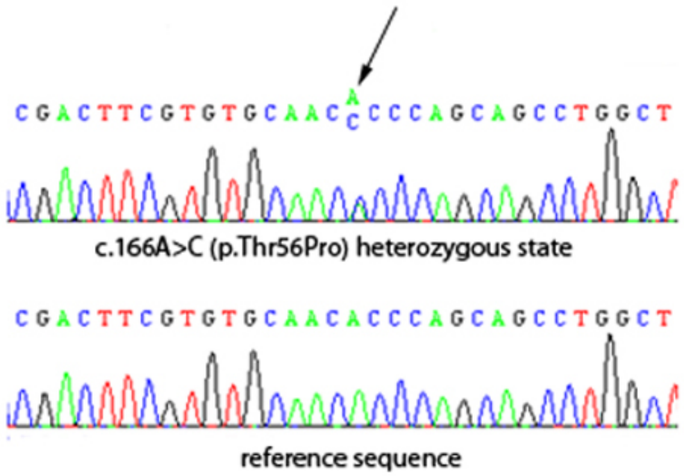
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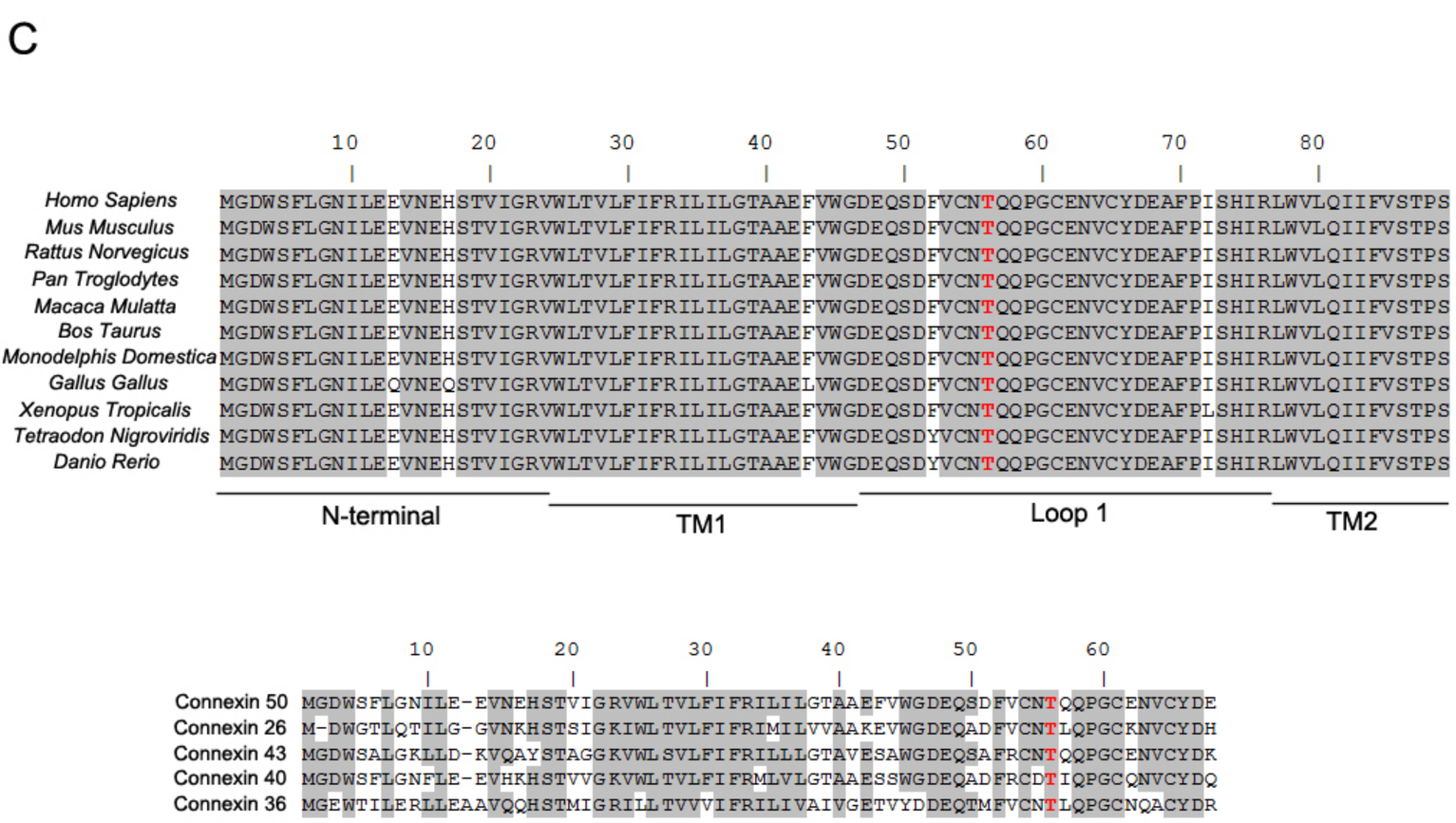
A


I
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B

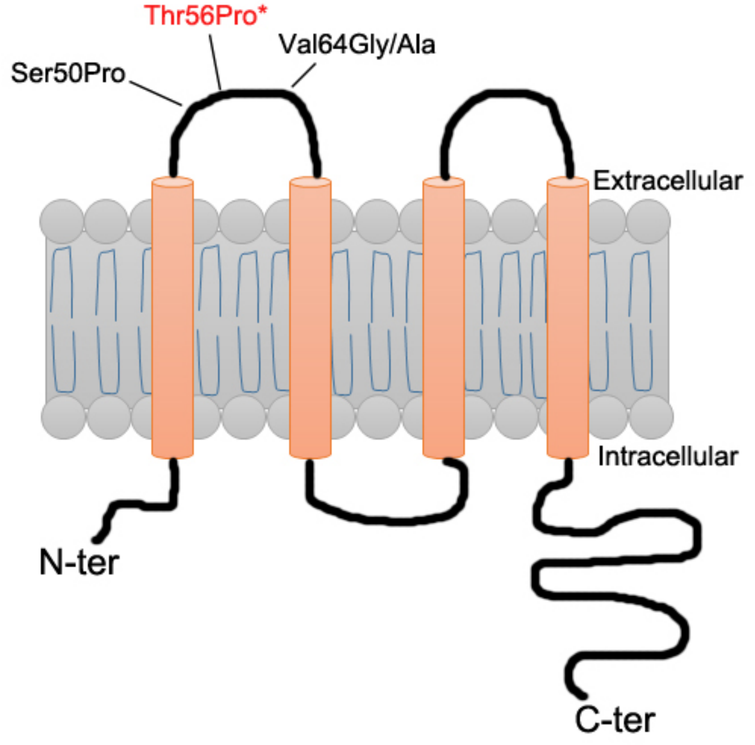

CGACTTCGTGTGCAACACCCAGCAGCCTGGCT
c.166A>C (p.Thr56Pro) heterozygous state
CGACTTCGTGTGCAACACCCAGCAGCCTGGCT
reference sequence

C

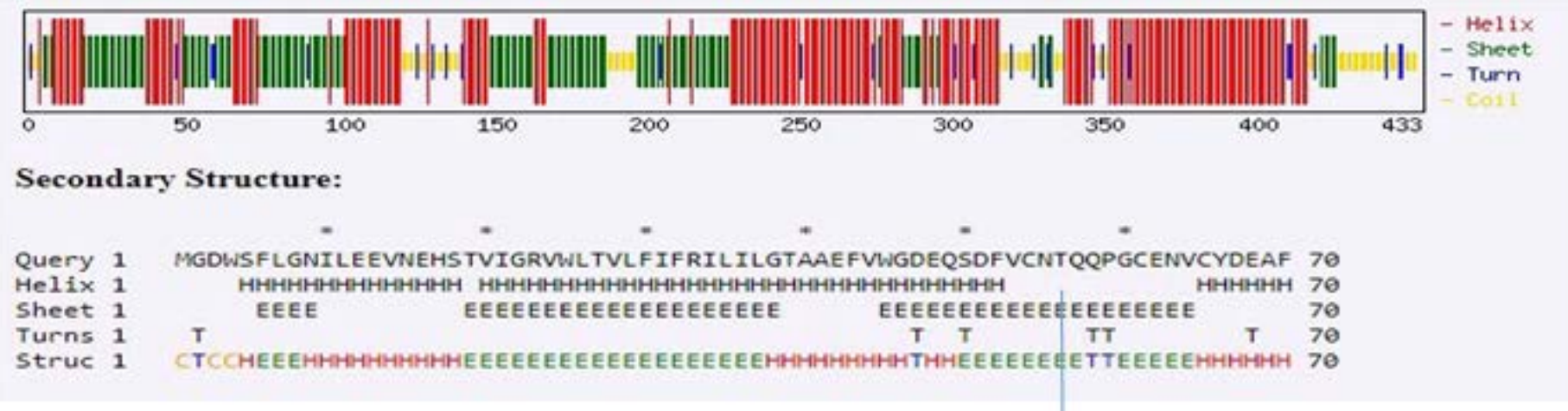

10 20 30 40 50 60 70 80
Homo Sapiens MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
Mus Musculus MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
Rattus Norvegicus MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
Pan Troglodytes MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
Macaca Mulatta MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
Bos Taurus MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
Monodelphis Domestica MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
Gallus Gallus MGDWSFLGNILEQVNEQSTVIGRVWLTVLFIFRILILGTAAELVWGDEQSDFVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
Xenopus Tropicalis MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFVCNTQQPGCENVCYDEAFPLSHIRLWVLQIIFVSTPS
Tetraodon Nigroviridis MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDYVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
Danio Rerio MGDWSFLGNILEEVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDYVCNTQQPGCENVCYDEAFPISHIRLWVLQIIFVSTPS
N-terminal
TM1
Loop 1
TM2

10 20 30 40 50 60
Connexin 50 MGDWSFLGNILE-EVNEHSTVIGRVWLTVLFIFRILILGTAAEFVWGDEQSDFVCNTQQPGCENVCYDE
Connexin 26 M-DWGTLQTILG-GVNKHSTSIGKIWLTVLFIFRIMILVVAAKEVWGDEQADFVCNTLQPGCKNVCYDH
Connexin 43 MGDWSALGKLLD-KVQAYSTAGGKVWLSVLFIFRILLLGTAVESAWGDEQSAFRCNTQQPGCENVCYDK
Connexin 40 MGDWSFLGNFLE-EVHKHSTVVGKVWLTVLFIFRMLVLGTAAESSWGDEQADFRCDTIQPGCQNVCYDQ
Connexin 36 MGEWTILERLLEAAVQQHSTMIGRILLTVVVIFRILIVAIVGETVYDDEQTMFVCNTLQPGCNQACYDR

D


Thr56Pro*
Ser50Pro
Val64Gly/Ala
Extracellular
Intracellular
N-ter
C-ter

Wildtype



Mutant

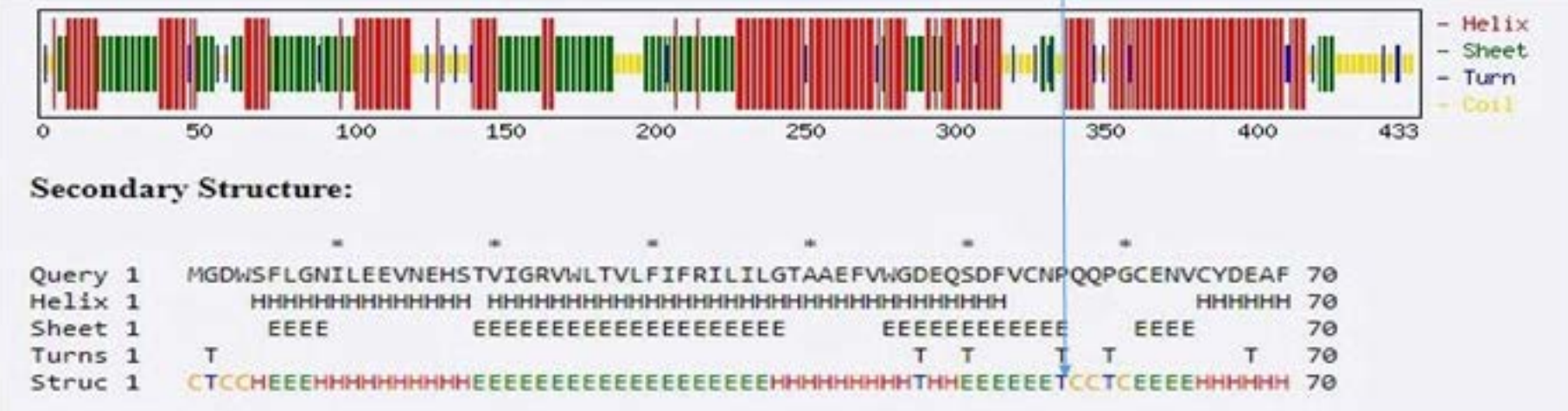


Figure 2

Table 1: List of novel and reported *GJA8* mutations associated with congenital cataract

Mutation	Amino acid change	Location	Cataract types	Inheritary	Family origin	Reference
c.20T>C	p.L7P	NT	Nuclear	AD	Caucasian	[8]
c.68G>C	p.R23T	NT	Nuclear	AD	Iranian	[9]
c.89dupT	p.fs	NT	Nuclear	AD	Caucasian	[10]
c.92T>C	p.I31T	M1	Nuclear	AD	Chinese	[11]
c.116C>G	p.T39R	M1	and microcoma and iris hypoplasia	AD	Chinese	[12]
c.119C>T	p.Ala40Val	M1	Cataract, microphthalmia, and sclerocornea	AD	Caucasian	[10]
c.130G>A	p.V44M		Nuclear	AD	Iranian	[26]
c.131T>A	p.V44E	M1	Cataract and microcoma	AD	Indian	[27]
c.131T>C	p.V44A	M1	Suture-sparing nuclear	AD	Chinese	[28]
c.134G>C	p.W45S	M1	Jellyfish-like bilateral and microcornea	AD	Indian	[29]
c.134G>T	p.W45L	M1	cataract	AD	Iranian	[13]
c.136G>A	p.G46R	M1	Complete and microcornea	AD	Chinese	[12]
c.137G>T	p.G46V	M1	Total cataract	AD	Pakistani	[30]
c.139G>A	p.D47N	E1	Nuclear pulverulent	AD	British	[31]
c.139G>T	p.D47Y	E1	Nuclear	AD	Chinese	[32]
c.139G>C	p.D47H	E1	Nuclear	AD	Chinese	[33]
c.142G>A	p.E48K	E1	Zonular nuclear pulverulent	AD	Pakistani	[34]
c.151G>A	p.Asp51Asn	M1	Cataract, microphthalmia, and sclerocornea	AD	Caucasian	[10]
c.166A>C	**p.T56P**	**E1**	**Nuclear**	**AD**	**Mauritania**	**This study**
c.175C > G	p.P59A	E1	Nuclear	AD	Chinese	[35]
c.191T>G	p.V64G	E1	Nuclear	AD	Chinese	[36]
c.218C>T	p.S73F	E1	Various locations in the nucleus or the poles	AD	Danish	[37]
c.227G > A	p.R76 C	M2	Zonular pulverulent	AD	Chinese	[38]
c.227G > A	p.R76 H	M2	Zonular pulverulent	AD	Chinese	[35]
c.235G>C	p.V79L	M2	" Full moon " Y-sutural opacity	AD	Indian	[39]
c.262C>T	p.P88S	M2	Zonular pulverulent	AD	British	[40]
c.262C>A	p.P88Q	M2	Lamellar pulverulent	AD	British	[41]
c.264C>T	p.P88T	M2	Total cataract	AD	Chinese	[42]
c.293A>G	p.H98R	E2	Cataract	AD	UK	[43]
c.293A>C	p.H98P	E2	Cataract	AD	American	[8]
c.301G>T	p.R101L	E2	posterior polar cataract	AD	Iranian	[13]
c.367G>A	p.G123S	E2	Nuclear	AD	Chinese	[44]
c.460C>G	p.H154D	E2	Cataract	AD		[45]

c.565C>T	p.P189S	E2	Cataract and microcornea	AD	Brasil	[46]
c.566C>T	p.P189L	E2	Cataract and microcornea	AD	Danish	[37]
c.569A>G	p.N190S	E2	Cataract and microcornea	AD	Chinese	[47]
c.586G>A	p.V196M	E2	Cataract	AD	Indian	[48]
c.93G>A	p.R198Q	E2	Cataract and microcornea	AD	Indian	[27]
c.592C>T	p.R198W	E2	Cataract and microcornea	AD	Chinese	[49]
c.595C>T	p.P199S	E2	Cataract	AD	Indian	[50]
c.601G>A	p.E201K	E2	Perinuclear cataracts	AD	Chinese	[51]
c.607insA	p.203fs	E2	Cataract	AR	Indian	[48]
c.741T>G	p.I247M	CT	zonular pulverulent	AD	Russian	[52]
c.773C>T	p.S258F	CT	Nuclear	AD	Chinese	[53]
c.776insG	p.fs	CT	Triangular	AD	Germany	[54]
c.836C>A	p.S259Y	CT	Nuclear pulverulent	AD	Danish	[37]
c.823G>A	p.V275I		Cataract		Chinese	[55]
c.827C>T	p.S276F	CT	Nuclear pulverulent	AD	Chinese	[56]
c.829C>T	p.H277Y	CT	Nuclear pulverulent	AD	Chinese	[57]
c.905T>C	p.L278C	CT	Lamellar zonular	AD	Indian	[58]
c.842T>C	p.L281S	CT	Cataract, congenital		Indian	[58]
c.1273C>T	p.R425*	CT	Nuclear	AD	UK	[43]

Annotation variation

ID	concentration	ID-ZOC	possible dia	I260	I280	260/280
D24	50,6ng/ul	QT2137	Cataracte	1,011	0,553	1,83

NGS informations

Sequencing depth	150 folders
Supporting Reads	%≥30%
Total Reads	≥10
dbSNP Allele Frequency	≤0.01

gene	Chromosor	position	variants	consequen	Zygosity	EXAC	HGMD	SIFT_pred (
GJA8	chr1	147380248	c.166A>C	p.(Thr56Pr	hetero	no record	novel	Damaging

Polyphen2_	Polyphen2_	LRT_pred (	MutationTaster_pred
Possibly_da	Possibly_da	Deleterious	Disease_causing

congenital cataract gene	GJA8	CRYGC	CRYBB2
gene that mutation caused phenotype accompany cataract	ABHD12	ABHD5	ACTA2

Appendix1. Genes associated with congenital cataract

CRYGD	HSF4	EPHA2	CRYAA	CRYBA1	PITX3	BFSP2	GCNT2	GJA3
ADAMTS10	ADAMTS17	ADAMTSL4	AGK	ALDH18A1	ALDH1A3	APOA1	ASPH	B3GALTL

MIP	CRYAB	CRYBB1	FYCO1	LIM2	CRYGS	MAF	CRYBB3	CRYBA4
BCOR	BFSP1	BFSP2	BMP4	BUB1B	CHMP4B	CHRDL1	CNBP	COL11A1

VIM	CHMP4B	BFSP1	TDRD7	AGK	CRYGB	NHS	WFS1	CRYBA2
COL11A2	COL18A1	COL2A1	COX14	COX7B	CRYAA	CRYAB	CRYBA1	CRYBA2

UNC45B	LSS							
CRYBA4	CRYBB1	CRYBB2	CRYBB3	CRYGB	CRYGC	CRYGD	CTDP1	CYP27A1

DPAGT1	EBP	ELP4	EPG5	EPHA2	ERCC5	ERCC6	ESCO2	EYA1

FAM111A	FAM126A	FBN1	FKRP	FLNB	FOXE3	FREM1	FTL	FYCO1

GALK1	GALT	GCNT2	GDF3	GFER	GJA3	GJA8	HCCS	HDAC6

HMGB3	HSF4	ISPD	JAM3	LIM2	LOXL1	MAF	MIP	NAA10

NHS	P3H2	PDE6D	PEX16	PEX7	PITX3	PTCH1	PTH	RARB

RDH11	RECQL4	SDHB	SDHD	SEC23A	SIL1	SIX3	SIX5	SLC16A12

SLC33A1	SLC4A4	SMOC1	SORD	SOX2	SRD5A3	TBC1D20	TBC1D32	TDRD7

TENM3	TMEM114	TMEM127	TMEM5	TMEM98	TMX3	UNC45B	VAX1	VIM

VLDLR	VSX2	WNT3	WRN	WT1