

CRISPR Base Editing as a Potential Therapeutic Approach for Kir7.1 Channelopathy

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BACKGROUND

- Leber Congenital Amaurosis 16 (LCA16) is a severe form of inherited ocular channelopathy caused by point mutations in *KCNJ13*, which affect the retinal pigment epithelial (RPE).
- AAV-gene therapy related immune responses, CRISPR/Cas9 gene editing associated off-targets, and un-intended indels pose some challenges in clinical use of such treatments.

Kir7.1 protein depicting the disease causing mutations



 We used Adenosine and Cytosine CRISPR base editors (ABE and CBE) for proof-of-concept correction of W53X (c.158G>A) and L144P (c.431T> C) in KCNJ13 using electroporation or silica nanoparticle-mediated delivery to induced pluripotent stem cell derived RPE (iPSC-RPE).

METHODS

- Base editing was carried out using either ABE or CBE mRNA with a guide RNAs specific to the W53X or L144P mutant allele.
- A HEK293-FRT stable cells (Kir7.1-L144P and Kir7.1- W53X) were base edited via electroporation.
- LCA16-W53X patient-specific fibroblasts and iPS-RPE cells were targeted with ABE mRNA delivered using nanoparticles.
- efficiency (by deep sequencing), protein Base editing expression and localization (Immunocytochemistry), and channel function (electrophysiology) were assessed in edited cells and were compared with non-edited mutant and WT cells. Potential off-targets were screened to evaluate the accuracy and efficacy of CRISPR BEs.





ABE for W53X correction in fibroblasts and hiPS-RPE



ABEmax mRNA; Indel frequency <2%

GGGGAATCCTAATGGACATGCGCTAGCGTTGGATGATGTTGGTCTTTT--- Wⁱ TAATGGACATGCGCTGGCGTTGGATGATGTTGGTC TAATGGACATGCGCTAGCGTTGG<mark>G</mark>TGATGTTGGTCTTT---0.2 GGGAAACCTAATGGACATGCGCTAGCGTTGGATGATGTTGGTCTTTT--0.15 GAGAATCCTAATGGACATGCGCTAGCGTTGGATGATGTTGGTCTTTT---0.15%

A8NG mRNA; Indel frequency <3%

GGGGAATCCTAATGGACATGCGCTAGCGTTGGATGATGTTGGTCTTTT--- W53 GGGGAATCCTAATGGACATO



Base edited RPE

Potential off targets of W53X BE gRNA



Gene/Region/Location							Cł	Chromosome				e s	strand			mismatches							
STK24								13				-			3								
GRCh38:133058732 Intergenic								10				-			3								
GRCh38:50530925 Intergenic								18				-			2								
PPM1K Intronic								4				+			3								
			4P2	2B1	. In	tro	nic	:				17				-			4				
TMEM117 Intronic									12	2			+			4							
		ſ	٨N	144	۱r	ntrc	onio	2					4				-			4			
G	RC	h38	8:1	13	728	305	41	ntr	oni	ic		4				+			4				
			HR	Η1	In	tro	nic					3				-			4				
G	RCł	138	8:55	535	28	15	Int	erg	gen	ic		12				-			3				
												_											
	G	С	G	С	Т	Α	G	С	G	Т	Т	G	G	Α	Т	G	Α	Т	G	Т	T	G	G
1	•	Т	•	•	•	•	•	•	С	•	•	•	•	•	•	•	Т	•	•	•	G	G	G
2	·	·	Α	·	G	·	·	G	·	·	·	·	٠	·	·	·	·	·	·	·	Т	Α	G
3	•	G	•	•	•	•	С	•	•	•	•	•	•	•	•	•	•	•	•	·	С	Α	G
4	•	·	·	Α	G	·	•	·	Т	·	·	•	•	·	·	•	•	·	•	·	Т	G	G
5	•	•	•	•	•	Т	•	•	Т	•	•	•	Т	•	•	•	•	•	•	•	G	G	G
6	•	•	т	Т	•	Т	•	•	Т	•	•	•	•	•	•	•	•	•	т	•	Т	G	G
7	Т	•	•	•	•	С	Α	Α	•	•	•	•	•	•	•	•	•	•	•	•	Α	G	G
8	•	•	•	G	•	•	•	Α	•	•	G	•	•	•	G	•	•	•	•	•	G	G	G
9	•	•	•	•	•	G	•	Α	•	•	•	•	Т	•	•	•	С	•	•	•	G	G	G
10									т	Δ				т							т	G	G



<u>hg19</u>	SGD
<u>rn4</u>	SGD
<u>sorAra1</u>	SGD
loxAfr3	SGD
<u>mm9</u>	SGD
<u>cavPor3</u>	SGD
tupBel1	SGD
ornAna1	SGD
bosTau4	SGD
anoCar1	SGD
monDom5	NG
proCap1	SGD
galGal3	SGD
taeGut1	SGD
<u>turTru1</u>	SGD



Protein ex





	_	-		_	_
expression	in	ed	ited	ce	

BE4max	
-ML P GLM- ATG-CTC - C C A-GGC-CTC-ATG	Mutar
-MLLGLM- ATG-CT T-TT A-GGC-CTC-ATG	(40.62
-MLLGLM- ATG-CTC- TT A-GGC-CTC-ATG	(8.99
-MLLGLM- ATG-CTC-C T A-GGC-CTC-ATG	(2.62 ⁹

_					-		~	~	10	~	0
73.9		76.4	71.6	73.4	92.9	92.2	91.2	89.8	83.5	94.9	SE (
91.3		92.7	92.9	92.7					92.9		SO S
66.5	93.7	72.6	71.6	70.3	90.1	88.6	89.6	82.1	78.7	89.1	78.7
С	Т	С	С	С	А	G	G	С	С	Т	C

evoCDA

-ML P GLM-	
ATG-CTC-CCA-GGC-CTC-ATG	Mutant
-M F LGLM- ATG- T T T-TT A-GGC-CTC-ATG	(46.20%)
-M F LGLM- ATG- T TC- TT A-GGC-CT T -ATG	(5.50%)
-M F LG F M- ATG- T T T-TT A-GGC- T TC-ATG	(4.42%)
-MLLGLM- ATG-C TT-TT A-GGC-CTC-ATG	(1.06%)

Is Off-targets of L144P gRNA



MAIN FINDINGS

- W53X mutation cells (25%).
- delivery.
- cells.

L144P mutation

- evoCDA mRNA.
- mutation.

CONCLUSIONS

Our results show application of CRISPR base editing for precise correction of point mutations with reduced off-targets compared to CRISPR/Cas9-mediated gene editing. Restoration of channel function in edited iPSC-RPE cells suggests potential of CRISPR BE as a treatment for childhood blindness.

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• ABE mRNA (50% editing efficiency) showed higher efficiency than RNP for W53X correction in stable

 Nanoparticle-mediated delivery of BEs in fibroblasts (47% editing) and iPSC-RPE (20% editing) established the use of CRISPR BE for in vivo BE

• On target indel mutagenesis (<3%) and deep sequencing of potential off-target sites (<0.01%) indicated high accuracy of the ABEs.

 Electrophysiology demonstrated robust rescue of channel function in the edited stable and iPSC-RPE

 BE4max mRNA showed better on-target correction efficiency (60%) and fewer off-target effects than

• The codon degeneracy of "Leucine" provides additional flexibility to correct L144P point

 Higher rate of undesired nonsynonymous editing was observed due to multiple bystander 'C' within the editing window.

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