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Antisense Oligonucleotide (AON)-based Therapy for Leber Congenital Amaurosis Caused by a Frequent Mutation in CEP290

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Leber congenital amaurosis (LCA) is the most severe form of inherited retinal degeneration, with an onset in the first year of life. The most frequent mutation that causes LCA, present in at least 10% of individuals with LCA from North-American and Northern-European descent, is an intronic mutation in CEP290 that results in the inclusion of an aberrant exon in the CEP290 mRNA. Here, we describe a genetic therapy approach that is based on antisense oligonucleotides (AONs), small RNA molecules that are able to redirect normal splicing of aberrantly processed pre-mRNA. Immortalized lymphoblastoid cells of individuals with LCA homozgyously carrying the intronic CEP290 mutation were transfected with several AONs that target the aberrant exon that is incorporated in the mutant CEP290 mRNA. Subsequent RNA isolation and reverse transcription-PCR analysis revealed that a number of AONs were capable of almost fully redirecting normal CEP290 splicing, in a dose-dependent manner. Other AONs however, displayed no effect on CEP290 splicing at all, indicating that the rescue of aberrant CEP290 splicing shows a high degree of sequence specificity. Together, our data show that AON-based therapy is a promising therapeutic approach for CEP290-associated LCA that warrants future research in animal models to develop a cure for this blinding disease.

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Introduction

Leber congenital amaurosis (LCA) is the most severe form of inherited retinal dystrophy, with an onset of disease symptoms in the first years of life1 and an estimated prevalence of ~1 in 50,000 worldwide.2,3 Genetically, LCA is a heterogeneous disease, with 15 genes identified to date in which mutations are causative for LCA.4,5 The most frequently mutated LCA gene is CEP290, accounting for ~15% of all cases.4,6,7 Severe mutations in CEP290 have been reported to cause a spectrum of systemic diseases that, besides retinal dystrophy, are characterized by brain defects, kidney malformations, polydactyly, and/or obesity.8–11 There is no clear-cut genotype–phenotype correlation between the combination of CEP290 mutations and the associated phenotypes, but individuals with LCA and early onset retinal dystrophy very often carry hypomorphic alleles.3,6,7,12,13 The by far most frequently occurring hypomorphic CEP290 mutation, especially in European countries and in the United States, is a change in intron 26 of CEP290 (c.2991+1655A>G).3,6,7,12 This mutation creates a cryptic splice donor site in intron 26 which results in the inclusion of an aberrant exon of 128 bp in the mutant CEP290 mRNA, and inserts a premature stop codon (p.C998X). Alternative splicing of the cryptic exon into the mRNA occurs in some, but not all, mRNA transcripts, explaining the hypomorphic nature of this mutation.6 LCA, and other retinal dystrophies, for long have been considered incurable diseases. However, the first phase I/II clinical trials using gene augmentation therapy have led to promising results in a selected group of adult individuals with LCA or early onset RP with mutations in the RPE65 gene.14–17 Unilateral subretinal injections of adeno-associated virus particles carrying constructs encoding the wild-type RPE65 cDNA were shown to be safe and moderately effective in some individuals, without causing any adverse effects. In a follow-up study using younger subjects, visual improvements were more sustained, especially in the children who all gained ambulatory vision.18 Together, these studies have shown the potential to treat LCA, and thereby enormously boosted the development of therapeutic strategies for other genetic subtypes of retinal dystrophies.19 However, due to the tremendous variety in gene size and technical limitations of the vehicles that are used to deliver therapeutic constructs, gene augmentation therapy may not be applicable to all genes.

An alternative therapeutic strategy depends on the use of antisense oligonucleotides (AONs) that are able to interfere with splicing, and include DNA or RNA molecules/analogues, that can be delivered either as naked oligonucleotides or

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expressed by viral vectors. Although not applicable to all mutations, AONs are ideally suited to block aberrant splice events caused by the activation of cryptic splice sites, and hence restore normal splicing. Here, we describe the use of AONs to redirect normal splicing of CEP290 in patient-derived lymphoblast cells, and show a sequence-specific and dose-dependent decrease in levels of aberrantly spliced CEP290 mRNA, thereby revealing the potential of AON-based therapy to treat CEP290-associated LCA.

Results

The intronic CEP290 mutation (c.2991+1655A>G) creates a splice donor site that results in the inclusion of an aberrant exon into the CEP290 mRNA (Figure 1a and b).

Addition of AONs directed against the aberrant exon would prevent the insertion of this exon by preventing the binding of factors that are essential for splicing such as the U1- and U2snRNP complexes, and serine-arginine rich proteins, thereby restoring normal CEP290 splicing and protein synthesis (Figure 1c). AONs can target splice sites as well as exonic sequences, although in the particular case of the Duchenne muscular dystrophy (DMD) gene, AONs targeting exonic regions tend to outperform those that target the splice sites. In addition, previous studies have suggested a positive correlation between the capability of AONs to induce exon skipping and the presence of predicted SC35 splice factor binding sites in the target sequence. To design an AON with high exon-skipping potential, the aberrant CEP290 exon (128 nucleotides exonic sequence plus 15 nucleotides of intronic sequence on each side) was scrutinized for exonic splice enhancer-binding motifs, using the ESE finder 3.0.

Figure 1  CEP290 splicing and antisense oligonucleotide (AON) function. (a) Normal CEP290 mRNA splicing of exons 26 and 27, resulting in wild-type CEP290 protein. (b) The most frequent Leber congenital amaurosis (LCA)-causing mutation is an A-to-G transition (underlined and indicated with an asterisk) in intron 26 of CEP290. This mutation creates a splice donor site, which results in the inclusion of an aberrant exon to part of the CEP290 mRNA and subsequent premature termination of the CEP290 protein. (c) Upon binding of sequence-specific AONs, factors involved in splicing will not recognize the aberrant splice donor site in intron 26, resulting in redirection of normal CEP290 splicing and synthesis of a full-length CEP290 protein.
program. At the 3′-end of the aberrant exon, two SC35-binding motifs were predicted (data not shown). Hence, the first AON was designed such that it encompassed these two motifs (designated AON-3).

To determine whether AON-3 has exon-skipping potential in vitro, immortalized lymphoblastoid cells of two unrelated individuals with LCA homozygously carrying the intronic CEP290 founder mutation c.2991+1655A>G, as well as one control individual, were cultured in the absence or presence of 1 μmol/l AON-3. As expected, in the control individual, only a band representing correctly spliced CEP290 was observed, whereas in both affected individuals two products were present, one representing correctly spliced, and one representing aberrantly spliced CEP290 mRNA. Upon addition of AON-3, a strong decrease in aberrantly spliced CEP290 was noted, in both individuals with LCA (Figure 2a). Next, the specificity of AON-3 was assessed by transfecting a sense oligonucleotide directed to the same target site (SON-3). Reverse transcription-PCR analysis showed that in the cells transfected with SON-3, both the aberrantly spliced and the correctly spliced CEP290 mRNA molecules are still present (Figure 2b, left panel), demonstrating the specificity of the antisense sequence. Using an additional pair of primers that amplifies larger products, similar results were obtained (Figure 2b, right panel). Interestingly, the decrease in aberrantly spliced CEP290 appears to coincide with an increased intensity of the product representing correctly spliced CEP290 mRNA. These data indicate that the aberrant product is not degraded, but that the AON transfection truly induces exon skipping, resulting in the synthesis of more correctly spliced wild-type CEP290 mRNA. To determine the effective dose of AON-3, cells were transfected with various concentrations of AON-3, ranging from 0.01 to 1.0 μmol/l. Even at the lowest concentration of 0.01 μmol/l, a marked reduction in aberrantly spliced CEP290 was observed. The maximum amount of exon skipping was observed at 0.05 or 0.1 μmol/l of AON, indicating that these concentrations are sufficient to convert almost all aberrantly spliced CEP290 (Figure 2c).
The effectiveness of AONs in splice modulation is thought to depend merely on the accessibility of the target mRNA molecule, and hence may differ tremendously between neighboring sequences. To determine whether this sequence specificity also applies for CEP290, several AONs were designed to target the aberrant CEP290 exon (Table 1). This exon consists of 128 base pairs, the majority of which are part of an Alu repeat, one of the most frequent repetitive elements in the human genome, covering the entire 5′-end of the aberrant exon (Figure 3a). Hence, the majority of AONs were designed to be complementary to the 3′-end of the aberrant exon or the splice donor site (Figure 3a). In total, five AONs were transfected at a final concentration of 0.1 μmol/l, which was shown to be optimal for AON-3. Besides AON-3, also AON-2 and AON-4 resulted in high levels of exon skipping. In contrast, AON-1 that targets the Alu repeat region, and AON-5 that is directed against the splice donor site, hardly showed any exon-skipping potential (Figure 3b). This sequence-specific effect is likely caused by secondary structures of the target mRNA that prevent the binding of AONs. Together, our data demonstrate the sequence specificity in AON-based exon skipping of CEP290 and highlight a small region of the aberrant CEP290 exon as a potential therapeutic target.

Discussion

In this study, we explored the therapeutic potential of AONs to correct a splice defect caused by an intronic mutation in CEP290. In immortalized lymphoblast cells of individuals with LCA homozygously carrying the intronic CEP290 mutation c.2991+1655A>G, splicing of some but not all AONs resulted in skipping of the aberrant exon, thereby almost fully restoring normal CEP290 splicing.

AONs have been the focus of therapeutic research for over a decade, for the treatment of a variety of genetic diseases. These strategies include the use of AONs to block the recognition of aberrant splice sites, to alter the ratio between two naturally occurring splice isoforms, to induce skipping of exons that contain protein-truncating mutations, or to induce the skipping of exons in order to restore the reading-frame of a transcript that is disrupted by a genomic deletion, which allows the synthesis of a (partially) functional protein. The latter approach is already being applied in phase I/II clinical trials for the treatment of individuals affected with Duchenne muscular dystrophy, with promising results.

The intronic CEP290 mutation is an ideal target for AON-based therapy, since this mutation results in the inclusion of an aberrant exon in the CEP290 mRNA which is normally not transcribed. Inducing skipping of this aberrant exon by

**Table 1** Anti-sense oligonucleotide sequences

| RNA oligonucleotide | Sequence (5′→3′) | T_m (°C) | Target in aberrant CEP290 exon (nt) |
|---------------------|-----------------|----------|-----------------------------------|
| AON-1               | TAATCCACACATTTAAGG | 58       | 72–91                             |
| AON-2               | GGGCTTCTGTCCTGAGG | 58       | 102–117                           |
| AON-3               | AACCTGGGCTAGCTGGG | 58       | 106–122                           |
| AON-4               | TACGCTTGCGCACGTG | 58       | 108–125                           |
| AON-5               | ACTGAGATTTGCTTCGAGG | 58       | 115–128+6                        |
| SON-3               | GCAGCTGCGCCCGCGTT | 58       | Nontargeting                      |

Abbreviation: AON, anti-sense oligonucleotide.

Overview of the sequences of the AONs used in this study. The right column depicts the position of the target sequence in the aberrant CEP290 exon. AON-5 is directed against the 14 most 3′-exonic nucleotides and the first six nucleotides of the splice donor site. SON-3 is complementary to AON-3 and thus does not target the aberrant CEP290 exon.

**Figure 3** Sequence specificity in anti-sense oligonucleotide (AON)-based rescue of aberrant CEP290 splicing. (a) Overview of the aberrant CEP290 exon, and the relative positions of the AONs that were selected. The 5′-end of the aberrant exon is part of an Alu repeat. (b) Reverse transcription-PCR (RT-PCR) analysis of CEP290 mRNA isolated from lymphoblastoid cells of an individual with Leber congenital amaurosis (LCA) that were cultured in the absence or presence of different AONs directed against the aberrant CEP290 exon (AON-1 to AON-5), or one sense oligonucleotide (SON-3). The AONs and SON were transfected in a final concentration of 0.1 μmol/l. The upper band represents the aberrant CEP290 splice product, whereas the lower band represents the wild-type CEP290 splice product. M, 100-bp marker. MQ, negative water control.
AONs appears to almost fully restore the normal CEP290 mRNA, allowing normal levels of CEP290 protein to be synthesized. A similar approach has been successful in individuals with Duchenne or Becker muscular dystrophy carrying intronic mutations in DMD, where addition of AONs resulted in the generation of wild-type dystrophin protein. A second major advantage is that although this AON-approach is a mutation-specific therapeutic strategy, the intronic CEP290 mutation is by far the most frequent LCA-causing mutation. Based on the estimated prevalence of LCA (1:50,000), and the observed frequency of the intronic CEP290 mutation in Northern-Europe (26%) and the United States (10%), at least one thousand and, depending on the frequency of the mutation in other populations, perhaps many more individuals worldwide have LCA due to this mutation. Finally, although the LCA phenotype associated with CEP290 mutations is severe, it appears that the photoreceptor integrity, especially in the macula, as well as the anatomical structure of the visual connections to the brain, are relatively spared in individuals with LCA carrying CEP290 mutations, which would allow a window of opportunity for therapeutic intervention.

The study described here provides a proof-of-principle of AON-based therapy for CEP290-associated LCA in vitro, using immortalized lymphoblast cells from affected individuals. In order to determine the true therapeutic potential of this method for treating LCA, additional studies are needed that include the development of therapeutic vectors, and assessment of efficacy and safety in animal models. AONs can be delivered in two ways, either as naked molecules (or conjugated to cell-penetrating peptides), or via viral vectors. A single injection of naked AONs has recently been shown to be effective for several months in a mouse model for spinal muscular atrophy. Naked AONs can be delivered to the retina by intraocular injections, although in each individual multiple injections would still be required. Alternatively, by using viral vectors, a single subretinal injection would suffice to allow a long-term expression of the therapeutic construct. Previously, others have used recombinant adeno-associated viral (rAAV) vectors carrying U1- or modified U7snRNA constructs to efficiently deliver AON sequences, in the mdx mouse model for DMD, or in myoblasts from individuals with DMD, respectively. In line with this, AONs targeting the aberrant exon of CEP290 could be cloned into such constructs, and delivered to the retina by subretinal injections of rAAV-5 or -8 serotypes that efficiently transduce photoreceptor cells where the endogenous CEP290 gene is expressed. Using rAAV-2 vectors, no deleterious immune response was evoked upon subretinal injections of these vectors in individuals with RPE65 mutations, and also for rAAV-5 and rAAV-8, immune responses appear to be benign, at least in animal models.

One final safety aspect concerns the specificity of the sequence that is used to block the splicing of the aberrant CEP290 exon. As stated before, the majority of this exon is part of an Alu repeat, and AONs directed against this repeat will likely bind at multiple sites in the human genome, increasing the chance to induce off-target effects. The AONs that were shown to be effective in this study do not fully target the Alu repeat sequence, but are also not completely unique in the human genome. However, when blasting against the EST database, no exact hits are found, indicating that at the level of expressed genes, these sequences are unlikely to induce off-target effects and deregulate normal splicing of other genes. To further study the efficacy and safety of AON-based therapy for CEP290-associated LCA in vivo, including the use of AON expression driven by viral vectors, we are currently generating a transgenic knock-in mouse model that carries part of the human CEP290 gene (exon 26 to exon 27, with and without the intronic mutation) which is exchanged with its mouse counterpart.

Compared to gene augmentation therapy, AON-based therapy has a number of advantages. First, in gene augmentation therapy, a ubiquitous or tissue-specific promoter is used to drive expression of the wild-type cDNA encoding the protein that is mutated in a certain individual. For instance in one clinical trial for RPE65 gene therapy, the chicken beta-actin promoter was used. Using either constitutive promoters or fragments of the endogenous promoters, it is difficult to precisely control the levels of expression of the therapeutic gene. In some cases, like for the RPE65 protein that has an enzymatic function, expression levels beyond those of the endogenous gene might not be harmful to the retina. For other genes however, including those that encode structural proteins like CEP290, tightly-regulated expression levels might be crucial for cell survival, and overexpression of the therapeutic protein might exert toxic effects. Using AONs, the therapeutic intervention occurs at the pre-mRNA level, and hence does not interfere with the endogenous expression levels of the target gene. A second issue is the use of the viral vector. Of a variety of different recombinant viral vectors, rAAVs are considered to be most suitable for treating retinal dystrophies, because of their relatively high transduction efficiency of retinal cells, and their limited immunogenicity. The major drawback of rAAVs however is their limited cargo size of 4.8 kb. Again, for some genes like RPE65, this is not a problem. For many other retinal genes however, including CEP290 (with an open reading frame of 7.4 kb), but also ABCA4 and USH2A, the size of their full-length cDNAs exceeds the cargo size of the currently available pool of rAAVs. One way to overcome this problem is to express cDNAs that express only partial proteins with residual activity, as has been suggested for CEP290 in two studies employing the zebrafish model, either by expressing the N-terminal region of the protein or a 299-amino acid domain of CEP290 that is deleted in the rd16 mouse. Other viral vectors, like lentivirus or adenoviruses have a higher cargo capacity than rAAVs (~8 kb), but are less efficient in transducing retinal cells, and in addition, adenovirus has a higher immunogenic potential. For AON-based therapy, the size limitations of AAV are not a problem, since the small size of the AONs and the accompanying constructs easily fit within the available rAAVs.

In conclusion, this study shows that administration of AONs to cultured cells of affected individuals almost fully corrects a splice defect that is caused by a frequent intronic mutation in CEP290 that causes LCA. These data warrant further research to determine the therapeutic potential of AON-based therapy for CEP290-associated LCA, in order to delay or cease the progression of this devastating blinding disease.
Materials and Methods

Design AONs. The 128-bp sequence of the aberrant CEP290 exon that is included into the mutant CEP290 mRNA was analyzed for the presence of exonic splice enhancer motifs using the ESE finder 3.0 program (http://rulai.cshl.edu/cgi-bin/tools/ESE3/esefinder.cgi?process=home). RNA AONs were purchased from Eurogentec, and designed with a Tm of 58°C, and modified with a 2′-O-methyl group at the sugar chain and a phosphorothioate backbone, and dissolved in phosphate-buffered saline.

Cell culture. Human B-lymphoblast cells of individuals affected with LCA and homozgyously carrying the intronic mutation in CEP290 were immortalized by transformation with the Eppstein–Barr virus, as described previously.40 Cells were cultured in RPMI1640 medium (Sigma, St Louis, MO) containing 10% (vol/vol) fetal calf serum (Sigma), 1% 10 U/μl penicillin and 10 μg/ml streptomycin (Sigma), at a density of 0.5 × 10⁶ cells/ml. Fresh medium was supplied twice a week.

Transfection of AONs. A day before transfection, 1.0 × 10⁶ cells were seeded in each well of a 6-wells plate, in a total volume of 2 ml complete medium. Transfection mixtures were prepared by combining 2.5 μl AON in a desired concentration, or distilled water, 5 μl transfection reagent (ExGen in vitro 500; Fermentas, St Leon-Rot, Germany) and 92.5 μl 150 mmol/l NaCl, and incubated at room temperature for 10 minutes, before addition to the cells. Six hours after transfection, 8 ml of low-serum medium (complete medium with only 1% fetal calf serum) was added. Forty-eight hours after transfection, cells were collected and washed with 1x phosphate-buffered saline, before directly proceeding to RNA isolation.

RNA isolation and reverse transcription-PCR. Total RNA was isolated from transfected lymphoblastoid cells using the Nucleospin RNA II isolation kit (Machery Nagel, Düren, Germany), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol. Subsequently, 1 μg of total RNA was used for cDNA synthesis using the iScript cDNA synthesis kit (Bio-Rad, Veenendaal, the Netherlands), according to manufacturer’s protocol.
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