Autosomal dominant Best disease with an unusual electrooculographic light rise and risk of angle-closure glaucoma: a clinical and molecular genetic study

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Purpose: To describe the clinical and molecular characteristics of two families with autosomal dominant Best disease and atypical electrooculography (EOG).

Methods: Four affected individuals from two families were ascertained. Detailed ophthalmic examinations, refraction, and biomey (anterior chamber depth [ACD] and axial length [AL]), gonioscopy, optical coherence tomography of the anterior segment and retina, retinal imaging, and electrophysiological assessment were performed. Arden ratios from EOG testing were calculated by direct measurement of the light peak to dark trough amplitudes. Mutations in bestrophin 1 (BEST1) were identified by bidirectional Sanger sequencing. In family 1, segregation of BEST1 alleles was performed by assaying four microsatellite markers (D11S935, D11S4102, D11S987, and D11S4162) that flank BEST1.

Results: The proband from family 1 (three of four siblings affected with Best disease) was 42 years old with bilateral macular vitelliform lesions, advanced angle closure glaucoma (ACG), a normal electroretinogram, and no EOG light rise. Her 44-year-old brother had similar fundus appearances and an EOG light rise of 170%. Their 48-year-old sister had a normal left fundus, whereas the right fundus showed a vitelliform lesion and subretinal thickening. There was no EOG light rise detectable from either eye. Mutation analysis of BEST1 showed all affected siblings to be heterozygous for a missense mutation, c.914T>C, p.Phe305Ser. Their unaffected sister had an EOG light rise of 200%, a normal fundus appearance, and did not harbor the BEST1 mutation. Haplotype analysis of family 1 showed that the affected brother with the 170% EOG light rise had inherited the same nondiseased parental BEST1 allele as his unaffected sister. The other two affected sisters with undetectable EOG light rises shared a different nondiseased parental BEST1 allele. An unrelated 53-year-old female carrying the same c.914T>C, p.Phe305Ser mutation showed all affected siblings to be heterozygous for a missense mutation, c.914T>C, p.Phe305Ser. Their unaffected sister had an EOG light rise of 200%, a normal fundus appearance, and did not harbor the BEST1 mutation. Haplotype analysis of family 1 showed that the affected brother with the 170% EOG light rise had inherited the same nondiseased parental BEST1 allele as his unaffected sister. The other two affected sisters with undetectable EOG light rises shared a different nondiseased parental BEST1 allele. An unrelated 53-year-old female carrying the same c.914T>C, p.Phe305Ser mutation showed typical features of Best disease and an EOG light rise of 180%. All four siblings from family 1 had shorter axial biometry (ACD range 2.06–2.74 mm; AL range 20.46–22.60 mm) than the normal population, contributing to their risk of ACG development. Proband 2 had deeper ACDs (2.83 mm OD and 2.85 mm OS), similar ALs (21.52 mm OD and 21.42 mm OS) compared to family 1. She had no gonioscopic evidence of angle closure.

Conclusions: A near normal EOG light rise is uncommon in molecularly confirmed Best disease, and in the present report is associated with the same mutation in two families, suggesting a specific role for this amino acid in the retinal pigment epithelium dysfunction associated with this disorder. Haplotype analysis in family 1 was consistent with an effect of the nondisease allele in mediating the presence of an EOG light rise. Clinical assessment of ACG risk is recommended for BEST1 mutation carriers and their first degree relatives.

Best disease (OMIM 153700) is an autosomal dominant macular dystrophy characterized by vitelliform macular lesions, a normal electroretinogram and reduction of the electrooculogram (EOG) light rise. Best disease was first linked to bestrophin-1 (BEST1; VMD2) in 1998 [1,2]. Mutations in BEST1 have since been found to be causative of other distinctive retinal dystrophies, including autosomal dominant vitreoretinochoroidopathy (ADVIRC; OMIM 193220) [3–7], autosomal recessive bestrophinopathy (ARB; OMIM 611809) [8–10], adult vitelliform macular dystrophy [11,12], and more recently, what was described as “concentric retinitis pigmentosa” [13]. A severely reduced EOG light rise remains the most sensitive clinical test for the diagnosis of all bestrophinopathies [14].

The BEST1 gene encodes bestrophin-1, a transmembrane protein located in the basolateral membrane of the retinal pigment epithelium (RPE) [15–18]. Current available evidence suggests that the EOG light rise results from chloride conductance across the basolateral membrane of the RPE [19]. Exogenous expression of bestrophin-1 produces a chloride ion conductance, and bestrophin-1 may function as a
calcium-sensitive chloride channel directly responsible for generating the light rise of the EOG [20]. It has been recently suggested that bestrophin-1 may indirectly modulate the light rise component of the EOG in vivo [20–24].

The clinical, electrophysiological, and molecular genetic findings in two families with Best disease are presented in this report. Both families carry the same mutation in the BEST1 gene, and each family had one individual unexpectedly showing a good EOG light rise.

METHODS
Five subjects (aged 42 to 53) from two families were recruited from clinics at Moorfields Eye Hospital. Slit-lamp examinations, including dark-room gonioscopy performed with a 1 mm slit-beam with a one-mirror Goldmann-style lens (Magnaview goniolens, Ocular Instruments, WA), applanation tonometry, and disc and fundus examinations with an aspheric lens were conducted. Autorefraction (Humphrey autorefractor; Carl Zeiss Meditec, Jena, Germany) and axial biometry measurements of anterior chamber depth (ACD) and axial length (AL) were performed (IOLMaster, Carl Zeiss Meditec, Dublin, CA). Fundus imaging included: autofluorescence (HRA 2; Heidelberg Engineering, Heidelberg, Germany), optical coherence tomography (3D-OCT; Topcon, Paramus, New Jersey), and fundus color photography (Topcon). Anterior segment OCT (AS-OCT) was performed under dark-room conditions when angle closure or secondary glaucoma was suspected (Visante; Carl Zeiss Meditec, Dublin, CA).

Standard electrophysiology was performed that incorporated the relevant ISCEV standards [25–27]. In short, EOG testing was performed with surface electrodes placed at the medial and lateral canthi of each eye. Thirty degree eye movements were recorded for 10 s each minute during 15 min dark adaptation, followed by a further 10–15 min in full-field (Ganzfeld) light adaptation (100 cd/m²). The amplitude of the dark trough and light peak were directly measured and Arden ratios calculated [25]. The EOG recordings from these two families were independently measured by three observers (SL, GEH, and CH) and average values used. Normative data were provided by 30 individuals aged between 30 and 60 years of age with no ocular abnormalities. One eye from each subject was randomly selected and used to establish the normative data.

Genomic DNA was extracted from peripheral blood with the Qiagen Blood DNA extraction kit (Qiagen, Crawley, UK). Bidirectional Sanger sequencing analysis of the entire coding regions of BEST1, including the splice donor and acceptor sites of the gene, was performed with BigDye 3.1 (Applied Biosystems, Warrington, UK). Primer sequences and annealing temperatures are shown in Table 1. The cDNA is numbered according to Ensembl transcript ID ENST00000378043, in which +1 is the A of the translation start codon.

Haplotype analysis was performed in one family by genotyping four microsatellite markers that flank the BEST1 gene: D11S935, D11S4102, D11S987, and D11S4162, available on the ABI linkage mapping set v.2.5-MD10. PCR was performed on a thermal cycler in a total volume of 9 μl containing 100 ng of genomic DNA, 0.2 μl of fluorescently labeled microsatellite markers (ABI, Foster City, CA), and equal volumes of ABsolute™ QPCR-mix (ABgene; Thermo Scientific, Epsom, UK). Reactions were performed with the standard thermocycling profile for all markers. This consisted of an initial denaturation (95 °C) for 15 min followed by 35 cycles of 94 °C for 60 s, 57 °C for 60 s, and 72 °C for 60 s, with a final extension step of 72 °C for 12 min. One microliter of each PCR product was diluted in 12 μl of the HiDi formamide containing 2.5 μl of GeneScan™-500 LIZ®.
fluorescent dye (Applied Biosystems). The samples were denatured for 5 min at 95 °C, snap-frozen on ice for 5 min, and centrifuged before loading onto the ABI Prism ® 3730 DNA Analyzer. The GeneMapper version 4.0 program (Applied Biosystems) was used to score the genotypes. All participating individuals consented to the investigation as part of an ethically approved research project that was performed in accordance with the tenets of the Declaration of Helsinki.
| Family | Individuals          | BCVA   | Refraction | IOP  | ACD  | AL  | CDR | Fundus |
|--------|----------------------|--------|------------|------|------|-----|-----|--------|
|        |                      | OD     | OS         | OD   | OS   | OD  | OS  | OD  |
|        |                      |        |            |      |      |     |     |      |
|        | Family 1             |        |            |      |      |     |     |      |
|        | Affected sister (II:1) | 6/60   | -4.00      | -4.00| 18   | 14  | 2.52| 2.43 |
|        |                      |        |            |      |      |     |     |      |
|        | Unaffected sister (II:2) | 6/6    | plano      | plano| 14   | 13  | 2.66| 2.74 |
|        |                      |        |            |      |      |     |     |      |
|        | Affected brother (II:3) | 6/36   | +0.75      | +0.75| 19   | 20  | 2.56| 2.64 |
|        |                      |        |            |      |      |     |     |      |
|        | Proband 1 (II:4)     | 6/36   | +3.50      | -3.50| 38   | 36  | 2.66| 2.66 |
|        |                      |        |            |      |      |     |     |      |
|        | Family 2             |        |            |      |      |     |     |      |
|        | Proband 2            | 6/12   | +3.00      | -2.00| 15   | 14  | 2.83| 2.83 |
|        |                      |        |            |      |      |     |     |      |

**Abbreviations:** BCVA represents best corrected visual acuity; IOP represents intraocular pressure; ACD represents anterior chamber depth; AL represents axial length; CDR represents cup: disc ratio; OD represents right eye; OS represents left eye; VL represents vitelliform lesion; SRF represents subretinal fluid.
RESULTS

The EOG Arden ratios in the normal subjects ranged from 180% to 435% (mean 260%, standard deviation [SD] 50%, n=30). An abnormal EOG typical for Best disease was defined as an Arden ratio of <120% [28,29], while 155%–185% was considered borderline or equivocal, and >185% clearly normal [30–32]. The upper limits of normal timing (mean±2.5 SD) were 15 min for the dark trough and 12 min for the light peak.

Proband 1 and family members: A 42-year-old white female (II:4) with bilateral macular scarring characteristic of Best disease was reviewed with her three older siblings. Figure 1 shows the pedigree structure. The family was of white English ancestry with no history of consanguinity. Both parents were deceased, and the only available family history was “poor sight” in the paternal grandmother. Two of the siblings of II:4 (II:1 and II:3) had clinical findings compatible with Best disease. Figure 2 shows the fundus signs of the three affected individuals. The older affected sister, II:1 (Figure 2), had asymmetric disease, with a normal left fundus appearance and macular scarring in the right eye. Their affected brother, II:3 (Figure 2), had bilateral disease, and showed a fundus appearance similar to that of the proband (Figure 2). Autofluorescence imaging demonstrated an increase in lipofuscin accumulation around the macular region with no scarring in the periphery. Posterior segment OCT imaging showed cystoid macular lesions, with thickening (hypertrophy and disruption) of the layer between RPE and the inner segment/outer segment interface. Their unaffected sister (II:2) had normal fundus examinations.

Figure 3. Anterior segment optical coherence tomography findings for family 1. A-D: Right eyes of individuals II:1 to II:4 respectively. E-H: Left eyes of individuals II:1 to II:4 respectively. The unaffected sister (II:2) shown in row 2 had closed angles on anterior segment (AS)-OCT. Slit openings were observed for individuals II:1 and II:3 on AS-OCT but their angles were closed on gonioscopy. The proband shown in row 4 had the shallowest anterior chamber depths. H: This shows a thickened cornea from aphakia and corneal decompensation from previous surgery in the proband.
A summary of the ocular characteristics is shown in Table 2. All four siblings had short axial biometry, but only the individuals affected with Best disease were found to be hypermetropic. The proband also had evidence of advanced secondary angle-closure glaucoma (ACG). Pupil-block angle closure was suspected on anterior segment OCT examination of the siblings (Figure 3), and was confirmed on dark-room gonioscopy where the convex iris configuration and iridotrabecular contact in more than 180° of the angle circumference was observed for all four siblings. Both sisters and the brother of the proband underwent laser iridotomies. Although the proband (II:4) was the youngest sibling, she had uncontrolled ACG, requiring multiple filtration and seton surgery that eventually led to corneal endothelial loss and significant corneal opacity (OS).

Electrophysiological testing showed normal electroretinograms. EOGs showed minimal dark trough and light rise in the proband (II:4) and her affected sister (II:1; Figure 4). The affected brother (II:3) showed a borderline EOG light rise of 170% and 160% in the right and left eyes (Figure 4). His unaffected sister (II:2) had an EOG light rise of 200% bilaterally. Patient II:3 had a slight delay of the light peak at 14 min, but not the dark trough at 10 min. The other two affected siblings had normal dark trough and light peak timings.

Bidirectional Sanger sequencing of BEST1 in the three affected siblings revealed a base substitution in the coding region (exon 8), c.914T>C, p.Phe305Ser, but no other variants (Figure 5). The p.Phe305Ser mutation has previously been described as segregating in a dominant fashion in another family with Best disease [1]. The unaffected sibling from this family was wild type at this allele. The haplotype carrying the mutation is illustrated in black (Figure 1). The affected brother (II:3) with a good EOG light rise had the same nondisease haplotype (yellow) as his unaffected sister (II:2). Neither parent was available for genetic analysis; however, the markers were informative enough to infer that the affected brother, II:3, had inherited a different allele from the noncarrier parent (I:2) compared to the other two siblings, II:1 and II:4 (red). See Figure 1.

**Proband 2:** An unrelated 53-year-old white female from the UK presented to the clinic with presumed Best disease after deterioration of her vision following a viral illness. She had been diagnosed with macular dystrophy at the age of 40 years. There was a family history of poor sight in her mother and maternal grandfather, but no clinical details were known. No other family members were available for clinical examination or genetic testing. Her phenotypic characteristics are presented in Table 2. Fundus and OCT examinations showed significant accumulation of subretinal fluid and central vitelliform lesions (Figure 6). Her refraction and AL readings fell within the range of all four siblings from family 1, but she had deeper ACDs of 2.83/2.85mm OD/OS, and open angles on gonioscopy. Her EOG showed a normal dark trough with a light rise of 170% right eye and 180% left eye (Figure 4). Dark trough and light peak timings were normal. Bidirectional Sanger sequencing of BEST1 revealed the patient to be heterozygous for the same missense variant in BEST1 as that present in family 1 (c.914T>C, p.Phe305Ser).

**DISCUSSION**

This report addresses the clinical, electrophysiological, and genetic findings in two families with dominant Best disease caused by the same p.Phe305Ser mutation. Very few reports of BEST1 mutation with normal or equivocal EOGs have appeared [12,33–35]. However, each of the two families herein reported contains one individual with an EOG light rise atypical for the disorder.

Hyperopia of greater than +3.00 diopters is a recognized feature of Best disease [28]. All affected patients were hyperopic; only the unaffected sister of proband 1 had a normal refraction (Table 2) with a short AL (21.98 mm), similar to all the affected subjects (range: 20.46–22.60 mm). Short axial length is a risk factor for developing angle closure,

![Figure 4](image-url)

**Figure 4.** Electrooculography tracings. There is inter- and intrafamilial variability in the electrooculographic (EOG) findings. Individual II:2 is the only unaffected subject, with no clinical evidence of Best disease, and clearly normal EOG light rises. Both individuals II:3 and proband 2 demonstrate near-normal EOG light rises, which is atypical for Best disease.

| Family 1 | Arden ratio |
|----------|-------------|
| II:1 OD  | 100µV       |
|          | 110%        |
| II:1 OS  | 100µV       |
|          | 110%        |
| II:2 OD  | 170%        |
|          | 160%        |
| II:2 OS  | 200%        |
| II:3 OD  | 170%        |
|          | 160%        |
| II:3 OS  | 200%        |
| II:4 OD  | No trace    |
|          | 110%        |
| II:4 OS  | No trace    |
shared by first degree relatives [36]. Although there are relatively few reports of Best disease and ACG [37–39], angle closure was present in all four siblings of family 1. In other bestrophinopathies, ACG is relatively common, affecting up to 50% of cases with ADVIRC [3–7] or ARB [8–10]. Proband 2 did not have angle closure, and this may be explained by her deeper ACD (Table 2).

Also of note is the completely normal left fundus of patient II:1. While marked fundus asymmetry can rarely occur in patients with Best disease [40,41], Testa et al. [35] reported an Italian family with one of three affected individuals having a completely normal fundus in one eye. That Italian family was one of the few reports of a normal EOG in Best disease; they carried a heterozygous mutation of p.Phe305Leu, the same amino acid as in this report. A normal fundus appearance in both eyes of one mutation-positive subject has been described [42] (p.Arg218Cys mutation). The Arden ratio was 175% in one eye, and 150% in the other. This subject’s affected daughter and grandchildren had findings typical of Best disease.

An abnormal Arden ratio of <120% is a characteristic finding in Best disease [28,39], with 155%–185% considered borderline [30–32]. Both patient II:3 and proband 2 had values between 160% and 180%, which is atypically high for Best disease, and which did not occur in other affected family members who had expectedly severe EOG abnormality. This inter- and intrafamilial difference in EOG findings suggests varying degrees of RPE dysfunction. A summary of the clinical and electrophysiological differences between disorders caused by BEST1 mutations is shown in Table 3.

Previously described BEST1 mutations associated with preserved EOG include: p.Phe305Leu [35], p.Asp243Val [12,34], and p.Ile295del [38]. Whole-cell patch clamp analysis in HEK-293 cells by Yu et al. has demonstrated that the p.Asp243Val mutation causes approximately a 90% reduction in chloride-specific currents generated by bestrophin-1 [43]. The researchers also showed that the p.Ile295del mutation completely abolishes the chloride channel activity of bestrophin-1 [44]. The 305 amino acid position lies within the C-terminus of BEST1, one of three mutational hotspots [45]. This is a highly conserved region of protein sequence close to transmembrane 6, lying on the outer surface of the protein, and may be involved in charge-dependent ligand binding. How the p.Phe305Ser and p.Phe305Leu mutations affect the in vitro activity of bestrophin-1 is yet to be identified and warrants further investigation.

Currently unidentified genetic mechanisms such as a single nucleotide polymorphism or a small change in the expression of the wild-type allele in the surrounding sequence may help to mitigate the EOG light rise. Only one of the three affected siblings of family 1 demonstrated a near-normal EOG light rise in the present study. To test the hypothesis that the nondisease allele was mitigating the effect, microsatellite markers flanking the BEST1 gene were genotyped. The results suggested that the nondisease allele from the noncarrier parent might determine the difference in EOG. This would be consistent with reduced penetrance of the p.Phe305Ser mutation in abolishing the EOG light rise in some cases. However, the probability of this occurring by chance alone is 25%.

The role of bestrophin-1 in ocular development, and thus its role in the development of ACG, has not been elucidated. Anterior segment changes at the cornea and lens are present in ADVIRC, and extremes of axial biometry (range: 16–25 mm) can occur, depending on whether a posterior...
| Clinical signs                  | Best disease [28,33-35,38,39] | ARB [8-10] | ADVIRC [3-7] | Concentric RP [13] | AVMD [11,12] |
|-------------------------------|-------------------------------|------------|--------------|--------------------|--------------|
| Mode of inheritance           | Autosomal dominant            | Autosomal recessive | Autosomal dominant | Autosomal dominant | Autosomal dominant |
| Fundus lesion                 | Central macula vitelliform lesions | Diffuse RPE disturbance and dispersed punctate flecks, subretinal fluid may fluctuate | Peripheral circumferential pigmentation, and peripapillary chorioretinal atrophy | Foveal deposits, prone to serous retinal detachments. Intraretinal bone spicule pigmentation - often showing an abrupt change between normal and abnormal retina | Milder phenotype characterized by RPE atrophy; small drusen-like deposits in the paracentral region |
| Lens changes                  | Not known                     | Not known | Spherophakia and cataract | Cataract | Nil |
| Refraction                    | One third ≥ +3.00 DS          | Range from +0.25 to +4.75 DS | −2.50 DS to +15.00 DS depending on axial biometry / presence of posterior staphyloma | Limited data suggest marked inter and intra-familial variability from high hyperopia to high myopia | Unknown |
| Other features                | ACG                           | ACG        | ACG, microcornea, iris dysgenesis, and posterior staphyloma | Nil | Nil |
| EOG findings of relevance to this study | Normal/ near-normal EOGs reported for p.F305S/L, p.A243V, p.I295del | No cases of affected individuals with normal EOGs to date | Marked inter and intra-familial variability for EOG findings | EOGs not tested | Mildly reduced EOG for p.A243V |

Abbreviations: ARB represents autosomal recessive bestrophinopathy; ADVIRC represents autosomal dominant vitreoretinochoroidopathy; RP represents retinitis pigmentosa; AVMD represents adult vitelliform macular dystrophy; RPE represents retinal pigment epithelium; DS represents diopters sphere; ACG represents angle-closure glaucoma; EOG represents electrooculography.
staphylocoma is present [5]. Typical fundus signs (Table 3), with hyperopia and short axial biometry are almost always present in patients with Best disease [28,37,39] and ARB [8–10]. This association between BEST1 mutations and ACG is important for clinicians.

In conclusion, this report details unusual phenotypic characteristics in two families with Best disease, both carrying the same missense p.Phe305Ser mutation. They include mutation-positive patients with a relatively well preserved EOG light rise; the presence of angle closure in all affected siblings of family 1; and a completely normal fundus in one eye of one of these affected patients. An effect of the nondisease allele is likely to contribute to the reduced penetrance of the Best disease phenotype, at least for the EOG light rise. Given the significant risk of ACG, assessment of angle-closure risk is a necessary consideration in all types of BEST1 related disease.

ACKNOWLEDGMENTS
We thank Forbes Manson, Anthony T Moore, David F Gareway-Heath and Peng T Khaw for their feedback and contribution to the ARVO presentation of this paper (Invest Ophthalmol Vis Sci 2009; 50: E-Abstract 4108); Anthony Robson and Magella Neveu for helpful discussions; James O’Sullivan for sequence analysis of proband 2; Naushin Wassem for laboratory advice; Ulrich Luhmann for translating reference [34]; and Matthew Richardson for assistance with Figure 2. Funding is acknowledged from the RD Crusaders Trust, Fight for Sight, International Glaucoma Association, and NIHR Manchester Biomedical Research Centre (BMRC). This work was supported by the National Eye Research Centre (SCIAD 051) and BMRC Ophthalmology at Moorfields Eye Hospital NHS Foundation Trust and UCL Institute of Ophthalmology.

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