Molecular genetic heterogeneity in autosomal dominant drusen

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Abstract

Objective—Autosomal dominant drusen is of particular interest because of its phenotypic similarity to age-related macular degeneration. Currently, mutation R345W of EFEMP1 and, in a single pedigree, linkage to chromosome 6q14 have been causally related to the disease. We proposed to investigate and quantify the roles of EFEMP1 and the 6q14 locus in dominant drusen patients from the UK and USA.

Design—Molecular genetic analysis.

Participants—Ten unrelated families and 17 young drusen patients.

Main outcome measures—Exons 1 and 2 of EFEMP1 were characterised by 5' rapid amplification of cDNA ends and direct sequencing. Exons 1-12 of EFEMP1 were then investigated for mutation by direct sequencing. A HpaII restriction digest test was constructed to detect the EFEMP1 R345W mutation. Marker loci spanning the two dominant drusen linked loci were used to generate haplotype data.

Results—Only seven of the 10 families (70%) and one of the 17 sporadic patients (6%) had the R345W mutation. The HpaII restriction digest test was found to be a reliable and quick method for detecting this. No other exonic or splice site mutation was identified. Of the three families without EFEMP1 mutation, two were linked to the 2p16 region.

Conclusions—EFEMP1 R345W accounts for only a proportion of the dominant drusen phenotype. Importantly, other families linked to chromosome 2p16 raise the possibility of EFEMP1 promoter sequence mutation or a second dominant drusen gene at this locus. Preliminary haplotype data suggest that the disease gene at the 6q14 locus is responsible for only a minority of dominant drusen cases.

Keywords: autosomal dominant drusen; molecular genetics

Drusen deposits in the macular region of the retina are found in an important set of inherited blinding conditions. These may be subdivided into those conditions where drusen are the earliest and principle finding occurring before 50 years of age and those conditions where drusen are a minor secondary feature, for example, Sorsby’s fundus dystrophy. All pedigrees documented to date within the former subgrouping have been reported to exhibit autosomal dominant inheritance and so are said to express a “dominant drusen” phenotype. It is not yet known whether the dominant drusen retinopathy in these different pedigrees represents one or a number of distinct disease entities. Eponymous types of dominant drusen include Doyne’s honeycomb retinal degeneration (DHRD) and malattia leventinese (ML). In DHRD, large drusen deposits have been described at the macula and around the edge of the optic nerve head. In ML, as well as macular drusen, small, discrete drusen are also seen radiating into the peripheral retina. These radial deposits are described as continuous with or internal to the basement membrane of the retinal pigment epithelium. Macular drusen are also a hallmark of age-related macular degeneration (ARMD), a complex genetic disorder that accounts for 50% of blind registration in the developed world. Characteristically, drusen are seen clinically before the sixth decade of life in dominant drusen pedigrees, but later than this in ARMD. Both ML and DHRD have been mapped to chromosome 2p16 and a single mutation

Table 1—Haplotype data in families linked to the chromosome 2p16 dominant drusen locus. Italicised area indicates common haplotype and thus common ancestry. Bar indicates EFEMP1 intragenic markers

<table>
<thead>
<tr>
<th>Pedigree</th>
<th>D2S2352</th>
<th>D2S2251</th>
<th>Intron 4</th>
<th>Intron 8</th>
<th>Intron 9</th>
<th>R345W mutation</th>
<th>322A44AT</th>
<th>D2S178</th>
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<tr>
<td>UK1</td>
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<td>U</td>
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<td>3</td>
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<tr>
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<td>10</td>
<td>5</td>
<td>11</td>
<td>3</td>
<td>1</td>
<td>U</td>
<td>Ys</td>
<td>3</td>
</tr>
<tr>
<td>UK3</td>
<td>10</td>
<td>5</td>
<td>11</td>
<td>3</td>
<td>1</td>
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<td>Ys</td>
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</tr>
<tr>
<td>UK4</td>
<td>3</td>
<td>5</td>
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<td>Ys</td>
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<td>7</td>
<td>6</td>
<td>1</td>
<td>2</td>
<td>U</td>
<td>Ys</td>
<td>3</td>
</tr>
</tbody>
</table>

U = uninformative. Families UK5 and UK6, despite linkage to the region, do not share the common haplotype or have the R345W mutation.
have the mutation. Patients 1-3, 5-7, and 10-11 are all a dominant drusen locus in a exclusion from linkage. Shaded areas show the common haplotype for the chromosome 6q14 dominant drusen phenotype. Chromosome 2 data show a recombination event suggesting HpaII and run out on agarose gels. Patients 4, 8, and 9 are una

exon 10 from patient DNA. The PCR products were digested with the restriction enzyme mutation abolishes a HpaII site. PCR was used to amplify a 240 bp fragment spanning 382

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R345W

Normal

HpaII

TGC CGG GAG

C344 R345 E346

R345W

TGC TGG GAG

C344 W345 E346

240 bp

60° GTCACC with an annealing temperature of CAGCGCTC and 1R: CATCCCAACAGAT - These were 1F: AACGCTGGGCT -

5' rapid amplification of cDNA ends (RACE) and genomic sequencing was used to characterise the region upstream of exon 3 including exon 1 (GenBank accession number 1AY027910) and exon 2 (GenBank accession number 1AY027911). Using this new information, intronic primers were designed to amplify exons 1 and 2 for mutation screening. These were 1F: AACCGTGGGCT-CAGCGCTC and 1R: CATCCCAACAGAT-GTCACC with an annealing temperature of 60°C and 2F: ACTGGAAGATTGTGCCCTCC and 2R: TCCATTTCACAGGCGG at 55°C.

Genomic DNA was extracted from peripheral blood lymphocytes from family members using the Nucleo II kit (Nucleo Biosciences). Exons 1 to 12 were then amplified by PCR using primers as listed above for exons 1-2 and using previously described primers for exons 3-12 under standard conditions. Both strands of each amplified fragment were examined for mutation by direct sequencing using standard protocols.

Since the R345W mutation removes a HpaII restriction site in exon 10, we investigated whether this could be used as an initial diagnostic test for this mutation. PCR was used to amplify a 240 bp fragment spanning exon 10 from patient DNA. The PCR products were then digested with the restriction enzyme HpaII and run out on agarose gels.

HAPLOTYPE ANALYSIS

Five microsatellite marker loci, D2S2739, D2S2352, D2S2251, D2S2153, and D2S378, spanning approximately 4 cM (Marshmed map) of the chromosome 2p16 region linked to dominant drusen, were used to generate haplotype data. Six further marker loci were also used in the chromosome 2p16 analysis, 133018CA, 322AA4AAAT, and four intragenic polymorphisms derived from introns 4, 8, 9, and 11 of the EFEMP1 gene. Six microsatel-
Results
Mutation screening established that seven of the 10 families (70%, four British, three American) and one of the 17 simplex cases (6%, one British patient) had the EFEMP1 R345W mutation. This was further established using the HpaII restriction enzyme digestion assay (fig 1). Haplotype data generated at marker loci spanning the 4 cM linked interval of chromosome 2p16 showed that these patients all shared a common genetic haplotype across the 1 cM region D2S2251 to D2S378, including intragenic EFEMP1 polymorphisms (table 1). This suggests a founder mutation. It was of particular note that the intragenic marker loci were often uninformative, for example, marker locus intron 11 was uninformative in all families studied.

Three of the 10 families and 16 of the simplex cases were found to be negative for the R345W mutation by HpaII restriction enzyme analysis and direct sequencing of exon 10 (fig 1). Subsequent sequencing of exons 1-9, 11, and 12 in these cases did not identify any other mutation in any exons or at splice site junctions of the EFEMP1 gene. It was noteworthy that each of the three families without the R345W mutation also had different haplotypes at the 2p16 linked locus, both from each other and from the R345W founder population. This suggests that these families are unrelated to the original common ancestor who had the EFEMP1 mutation (table 1). Interestingly, two of these families, UK5 and UK6, have previously been linked to the 2p16 disease associated locus. The other family, UK7, was too small for statistically significant linkage analysis. However, recombination events observed in family UK7 show convincing exclusion of the 2p16 locus (fig 2). Haplotype data for the chromosome 6q14 dominant drusen locus generated in family UK7 is presented in fig 2. Recombination events in families UK5 and UK6 excluded linkage to this locus (data not shown).

Clinical photographs of the retina of dominant drusen patients who do not have EFEMP1 R345W mutation are presented in fig 3. Typically, soft macular drusen were noted in each case. It was noteworthy that clinically, in each case, these deposits were confined to the macular region and were neither juxtapapillary (abutting the optic nerve head) nor extended into the periphery as has been described in many dominant drusen pedigrees with the R345W mutation.341

Discussion
It is clear from the work presented here that EFEMP1 mutation including R345W accounts for a large but not an overwhelming proportion of cases of dominant drusen. Only 70% of families and more strikingly only 6% of sporadic cases showed EFEMP1 mutation. Therefore, although an EFEMP1 mutation screen should be the initial test in the molecular diagnosis of a case of retinal drusen in a patient under 50 years of age, a negative result does not exclude this clinical diagnosis. Abolition of the HpaII restriction site in exon 10, as

Figure 3 Fundus photographs of patients affected by dominant drusen. (A) A 44 year old patient from pedigree US1 with R345W EFEMP1 mutation. (B) A 63 year old patient (drusen noted from 45 years of age) from pedigree UK6, linked to chromosome 2p16 but without EFEMP1 mutation. (C) A 39 year old sporadic drusen patient who does not have EFEMP1 mutation.
described here for the first time, can be used to enhance the efficiency of EFEMP1 screening for the common R345W mutation (fig 1). In addition, information on untranslated exons 1 and 2 now allows for a more complete assessment of the role of this gene in subjects expressing a drusen phenotype.

It is of particular interest that two pedigrees UK5 and UK6, although showing linkage to chromosome 2p16, did not have an EFEMP1 mutation. This may be interpreted as evidence to suggest a second dominant drusen gene at this locus. Alternatively, these pedigrees may express mutations of the EFEMP1 promoter sequence. No such promoter sequence mutation has yet been associated with outer retinal dystrophy, although RBL1 promoter sequence mutations have been associated with retinoblastoma.16

Another striking feature of this study was the phenotype seen in dominant drusen cases that did not have EFEMP1 mutation. All had soft macular drusen, but none seemed to exhibit juxtapapillary or hard radial drusen (fig 3B, C). This latter feature is a cardinal sign in ML.16 In DHRD, juxtapapillary drusen are seen unless there is juxtapapillary atrophy and radial drusen are seen in some cases but not others.11 It is of interest that these ML and DHRD pedigrees have all had R345W EFEMP1 mutation.8 It is possible that the juxtapapillary drusen and radial drusen are features specific to R345W EFEMP1 although the pedigree recently mapped to 6q also had members with radial drusen.16 This needs to be investigated in further studies.

Family UK7 also did not exhibit EFEMP1 mutation and, significantly, haplotype analysis excluded the chromosome 2p16 locus. Chromosome 6q haplotype data, however, may suggest that the dominant drusen phenotype in UK7 is the result of mutation at this locus. The evidence for this is, however, not conclusive and other loci may be relevant. Drusen are a minor feature of a number of other mapped retinal dystrophies including Sorsby’s fundus dystrophy (chromosome 22q31),17 North Carolina macular dystrophy (chromosome 6q16),18 and autosomal dominant age related macular degeneration (1q).19 Each of these loci should be included in any secondary genome search for the disease gene leading to a retinal drusen phenotype.

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14 Genetic map. http://www.marshmed.org/genetics/