Congenital progressive polymorphic cataract caused by a mutation in the major intrinsic protein of the lens, MIP (AQP0)

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Abstract

Background—Congenital cataract, when inherited as an isolated abnormality, is phenotypically and genetically heterogeneous. Although there is no agreed nomenclature for the patterns of cataract observed, a recent study identified eight readily identifiable phenotypes.

Methods—The Moorfields Eye Hospital genetic eye clinic database was used to identify a four generation family with isolated autosomal dominant congenital cataracts. All individuals (affected and unaffected) underwent a full ophthalmic assessment.

Results—The results of the molecular linkage study identifying a missense mutation in the gene encoding the major intrinsic protein of the lens (MIP) have been published elsewhere. Affected individuals had bilateral discrete progressive punctate lens opacities limited to mid and peripheral lamellae with additional asymmetric polar opacification. One young female had predominantly cortical cataract and another had serpiginous nuclear opacities.

Conclusions—This phenotype has not been recorded in human families before and has been termed polymorphic. The pattern of opacification appears to reflect the distribution of MIP in the lens.

Furthermore, this is the first clear evidence of allelic heterogeneity in this condition following the identification of a family with lamellar cataracts who have a different mutation within the MIP gene. (Br J Ophthalmol 2000;84:1376–1379)

Inherited cataract is the most common treatable cause of visual loss in children. When it occurs in isolation, it is most often transmitted as an autosomal dominant trait. Many different phenotypes are recognised but as yet no agreed classification exists. A recent study of families with isolated non-syndromic human inherited cataract recorded eight clearly distinguishable phenotypes—antarior polar, posterior polar, nuclear, lamellar, blue dot, coralliform, cortical, and pulverulent.

Inherited cataract is also genetically heterogeneous. Independent chromosomal loci have been mapped to 1p36, 1q21–25, 2q33–35, 13q, 16q22.1, 17p, 17q11–12, 17q24, 21q, and 22q. A recessive form has been linked with the I-blood group locus and characterisation of balanced chromosomal translocations has identified further loci on 2p22.3, 14q24, and 15q (Table 1a). Underlying mutations are now known in the crystallin genes at the loci on 2q, 13q, 19q, and 22q, the connexin genes on 1q and 13q and the developmental regulator gene PITX3 on 10q (Table 1b).

We have identified a family with autosomal dominant progressive lamellar opacification of the lens associated with anterior and posterior polar cataract. This “polymorphic” phenotype has not previously been recorded in human pedigrees. We have genetically linked this family to the long arm of chromosome 12, to the locus 12q14, and have shown that in this and another genetically unrelated family, a mutation in the MIP gene underlies cataractogenesis. In this paper, we describe the clinical spectrum of the disease.

Spontaneously occurring dominant mutations in major intrinsic protein (MIP) have already been shown to produce heritable cataract traits in mice. The Catmouse has a splice site mutation that leads to cataract and wrinkling of the capsule. The top mouse (lens opacity) has a missense mutation which leads to mistargeting of the protein and accumulation in the endoplasmic reticulum of the lens fibre cell. The underlying mechanisms by which each results in cataractogenesis remain to be elucidated.
Discussion

In this paper, we document a new inherited cataract phenotype resulting from a mutation in the gene that encodes the major intrinsic protein of the lens (MIP), the most abundant membrane protein in the mature lens fibre cell.

A number of roles have been suggested for MIP but it is now known to be one of a number of sequence related proteins known as aquaporins, which form channels to selectively transport water molecules across cell membranes. The missense mutation we have described substitutes an amino acid thought critical for this specialised function.

Ten mammalian aquaporins are now known. Often more than one is expressed in a single tissue. The proteins are suggested to have important functions in the eye, being involved in aqueous humour dynamics and lacrimation. Aquaporins also have significant roles in renal water reabsorption, cerebrospinal fluid secretion, and the generation of pulmonary secretions have been suggested.

To date, only aquaporin-2 has been implicated in human disease. It is found abundantly in kidney collecting duct epithelium, where its function is regulated by ADH (antidiuretic hormone). Several missense mutations (recessive and dominant) have been identified that result in the development of nephrogenic diabetes insipidus. Interestingly, polymorphisms of aquaporin-1 (present on the red blood cell membrane, the Colton blood group antigens) have been documented that produce a non-functional protein (the null phenotype) but whose effects are subclinical.

Such evidence has suggested that other mechanisms are able to compensate for aquaporin dysfunction. Our evidence that mutations in aquaporin-0 underlie cataract formation confirm the critical role of these proteins in certain tissues.

The phenotype of the cataract in this family has not previously been observed as an inherited trait and to reflect the variable appearance between eyes and among individuals has been termed “polymorphic”.

The discrete punctate opacities are similar to the pulverulent phenotype, which is characterised by fine dust-like opacification. However, the opacities in this pedigree are larger and, critically, their position within the lens is consistent contrasting markedly with the variable distribution of pulverulent opacities. Polar opacification is also not a feature of the pulverulent phenotype.

The phenotype observed in our family is also clearly distinct from the incompletely penetrant non-progressive polymorphic cataract mapped to chromosome 2q33–35 by Rogaev et al in the Turkmen populations of the former.
Soviet Union. In this cataract opacities resembled lumps of grapes or cotton anywhere from the fetal nucleus to the equator. Polar opacification was also not observed.

Although the mature lens fibre cell is metabolically inert, aquaporin water transport would be expected to continue as it is not energy dependent. Thus, the progressive nature of the cataract might well be explained as the cumulative effect of cellular dysfunction over time. The presence of polar cataract is less easily explained but parallels the distribution observed in the Catfr mouse.

Screening our panel of other families with isolated inherited congenital cataract identified a second pedigree with a different dominant
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missense mutation in the MIP gene.\textsuperscript{10} Lens opacification in this family was non-progressive and confirmed a perinuclear lamella. Such an observation is intriguing because it is not clear why two missense mutations in similar parts of the gene would produce such strikingly different phenotypes. Furthermore, this provides the first confirmation of allelic heterogeneity in this condition.

In conclusion, we have reported the identification of a new congenital cataract phenotype that results from a missense mutation in the major intrinsic protein of the lens. Studies of the implications for the function of the protein will provide further understanding of how the underlying genotype relates to the phenotype observed.

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Table 2

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