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## Alport syndromes: phenotypic heterogeneity of progressive hereditary nephritis

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**Abstract** Alport syndrome is a primary genetic disease of basement membranes, manifested clinically as a progressive nephropathy variably associated with sensorineural deafness and a plethora of ocular abnormalities. The long-recognized phenotypic heterogeneity of Alport syndrome may be considered on several levels, including basement membrane biochemistry, basement membrane ultrastructure, the natural history of the nephropathy, and the occurrence of extrarenal abnormalities. This review discusses the possible molecular bases for the heterogeneity. The discussion draws upon recent insights into the molecular genetics of Alport syndrome, and the biochemistry of normal and Alport syndrome basement membranes, in order to provide a framework for understanding the variable renal and extrarenal manifestations of the disease.

**Key words** Alport syndrome · Molecular genetics · Heterogeneity · Extrarenal disease

### Introduction

Alport syndrome is a primary genetic disease of basement membranes, manifested clinically as a progressive nephropathy variably associated with sensorineural deafness and a plethora of ocular abnormalities. It has long been recognized that Alport syndrome is a phenotypically heterogeneous disorder. The phenotypic heterogeneity of Alport syndrome can be considered on several levels, including basement membrane biochemistry, basement membrane ultrastructure, the natural history of the neph-

ropathy, and the occurrence of extrarenal abnormalities. The purpose of this review is to discuss the possible molecular bases for this heterogeneity. This discussion will draw upon recent insights into the molecular genetics of Alport syndrome, and the biochemistry of normal and Alport basement membranes, in order to provide a framework for understanding the variable manifestations of the disease.

Epithelial and endothelial cells rest on structures known as basement membranes. These sheet-like structures are comprised of a collagenous scaffolding consisting primarily of type IV collagen that interacts with other extracellular matrix glycoproteins, such as laminin, entactin, and proteoglycans. The type IV collagen protein family includes six isomeric chains, designated  $\alpha 1(\text{IV})$ – $\alpha 6(\text{IV})$  [1]. Each chain is encoded by a distinct gene, *COL4A1*–*COL4A6*. The six genes are arranged in pairs on three chromosomes: *COL4A1*/*COL4A2* on chromosome 13, *COL4A3*/*COL4A4* on chromosome 2, and *COL4A5*/*COL4A6* on the X chromosome. The shared features of type IV collagen  $\alpha$  chains include a collagenous domain of about 1,400 residues containing the repetitive triplet sequence glycine (Gly)-X-Y, in which X and Y represent a variety of other amino acids; a carboxy-terminal noncollagenous (NC1) domain of about 230 residues and a noncollagenous amino-terminal sequence of 15–20 residues. Approximately 20 interruptions of the collagenous triplet sequence are present in the collagenous domain. The NC1 domains each contain 12 completely conserved cysteine residues, which participate in intrachain and interchain disulfide bonds.

Type IV collagen  $\alpha$  chains form trimers through associations between their carboxy-terminal NC1 domains, accompanied by folding of the collagenous domains into triple helices [2]. These trimers form networks through several types of intermolecular interaction, including end-to-end linkages between the carboxy-terminal domains of two trimers, covalent interactions between four trimers at their amino-terminal ends, and lateral associations between trimers via binding of the carboxy-terminal domains to sites along the collagenous region of

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the trimer [3, 4]. Disulfide bonds involving conserved cysteine residues are critical to the interactions between NC1 domains. The various linkages between type IV collagen molecules produce a nonfibrillar polygonal assembly that serves as scaffolding for the deposition of other matrix glycoproteins and for cell attachment.

## Molecular genetics of Alport syndrome

Alport syndrome arises from mutations of type IV collagen, the predominant collagenous constituent of basement membranes. Alport syndrome is a genetically heterogeneous disorder (Fig. 1). About 80%–85% of patients have the X-linked form of Alport syndrome, resulting from mutations in the *COL4A5* gene [5]. Most of the remaining patients have autosomal recessive Alport syndrome due to mutations in either *COL4A3* or *COL4A4* [5]. A small minority of families exhibits autosomal dominant disease, which may also arise from mutations in *COL4A3* or *COL4A4* [6].

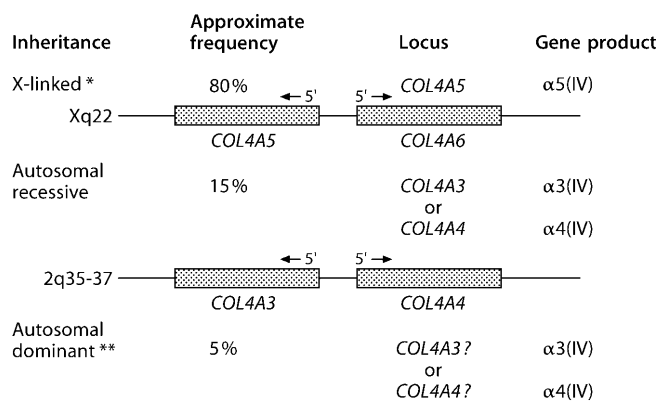
### X-linked Alport syndrome

Several hundred mutations in the *COL4A5* gene causing Alport syndrome have been identified to date [5]. These mutations are distributed throughout the gene, with no apparent hot spots, and with few exceptions each family carries a unique mutation. Approximately 10%–15% of *COL4A5* mutations are de novo, having occurred in the gamete of a parent; 5%–15% of *COL4A5* mutations consist of major rearrangements of the gene, such as large deletions. Other reported types of mutation in *COL4A5* include missense mutations causing amino acid substitutions (approximately 35%), mutations resulting in pre-

mature stop codons (nonsense mutations, small frame-shifting deletions, or insertions, splice site mutations – approximately 40%), small in-frame deletions, and splicing mutations that result in skipping of one or more exons. Mutations in the promoter of the *COL4A5* gene have not been reported.

The most-common type of *COL4A5* mutation is a missense substitution involving replacement of a guanine in the first or second position of a glycine codon, resulting in the substitution of a glycine residue in the collagenous domain of  $\alpha5(\text{IV})$  by another amino acid. Such mutations are thought to interfere with the normal folding of the mutant  $\alpha5(\text{IV})$  chain into triple helices with other type IV collagen  $\alpha$  chains. Glycine lacks a side chain, making it the least bulky of amino acids, and is sufficiently small so that three glycine residues can fit into the interior of a tightly wound triple helix. The presence of a bulkier amino acid in a glycine position presumably creates a kink or an unfolding in the triple helix. Glycine substitutions account for a large proportion of disease-causing mutations in collagens I, II, III, IX, X, and XI [7]. Abnormally folded collagen triple helices exhibit increased susceptibility to proteolytic degradation, potentially resulting in the destruction of the mutant chain, as well as the normal chains with which it has formed triple helices. The position of the substituted glycine, or the substituting amino acid itself, may influence the effect of the mutation on triple helical folding, and ultimately the impact of the mutation on the severity of the clinical phenotype.

Rare missense mutations in the *COL4A5* gene involve critical residues in the carboxy-terminal noncollagenous (NC1) domain of the  $\alpha5(\text{IV})$  chain, such as 1 of the 12 conserved cysteine moieties. The loss of 1 of these cysteines would eliminate a disulfide bond, which could interfere with the formation of triple helices, or with the construction of networks involving  $\alpha5(\text{IV})$  chains.



**Fig. 1** Genomic organization of *COL4A3–COL4A6* genes, and genetic forms of Alport syndrome. \*The Alport syndrome-diffuse leiomyomatosis complex arises from deletions that encompass some portion of the 5'-end of *COL4A5* and terminate within the second intron of *COL4A6*. \*\*Autosomal dominant Alport syndrome (ADAS) has been mapped to 2q35–37 in at least one family [5]. A specific mutation in *COL4A3* or *COL4A4* causing ADAS has yet to be reported. Heterozygous carriers of *COL4A3* and *COL4A4* mutations may have asymptomatic hematuria [9, 12, 13]

### Autosomal recessive Alport syndrome

To date, mutations causing autosomal recessive Alport syndrome (ARAS) have been reported in the *COL4A3* gene in 6 patients [8–11], and in the *COL4A4* gene in 12 patients [11, 12]. Some of these patients are homozygous for their mutations, some are compound heterozygotes, and others are heterozygotes in whom only one of the mutant alleles has been identified. Reported *COL4A3* and *COL4A4* mutations include nonsense, frame-shift, splicing, and missense alterations. As with *COL4A5*, there appear to be no mutation hot spots in *COL4A3* or *COL4A4*. Individuals who are heterozygous for *COL4A3* or *COL4A4* mutations may display hematuria [9, 12], and mutations of *COL4A4* have been implicated in autosomal dominant benign familial hematuria [13].

### Autosomal dominant Alport syndrome

Autosomal dominant Alport syndrome (ADAS) has been mapped in a single family to chromosome 2, in proximity

ty to *COL4A3* and *COL4A4* [6]. A specific mutation of either gene in this family has yet to be reported.

## Heterogeneity of the Alport phenotype

### Heterogeneity of basement membrane biochemistry

The availability of monospecific antibodies against each of the six type IV collagen  $\alpha$  chains has made it possible to characterize the changes in type IV collagen expression that occur as a result of mutations in the *COL4A3*, *COL4A4*, or *COL4A5* genes [14–20]. These changes are diagnostically useful and have been extensively illustrated in recent reviews [17, 21, 22].

Normally, the  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , and  $\alpha5(\text{IV})$  chains are highly expressed in basement membranes that are definitively, or in some cases possibly, involved in Alport syndrome: glomerular basement membrane (GBM), anterior lens capsule, Descemet's membrane, Bruch's membrane, and several basement membranes of the cochlea, including the basilar membrane and the basement membranes of the stria vascularis, spiral limbus, and spiral prominence [15, 23–30]. In 70%–80% of males with X-linked Alport syndrome (XLAS), the GBM, distal tubular basement membrane (TBM), and Bowman's capsules fail to stain for the  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , and  $\alpha5(\text{IV})$  chains, but expression of the  $\alpha1(\text{IV})$  and  $\alpha2(\text{IV})$  chains is preserved and is increased [18, 31]. Basement membranes of some males with XLAS exhibit normal, or reduced but positive, staining for the  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , and  $\alpha5(\text{IV})$  chains [16]. The  $\alpha6(\text{IV})$  chain is not expressed in Bowman's capsule or distal TBM of XLAS males whose basement membranes lack  $\alpha5(\text{IV})$  expression. Epidermal basement membranes (EBM) normally express the  $\alpha1(\text{IV})$ ,  $\alpha2(\text{IV})$ ,  $\alpha5(\text{IV})$ , and  $\alpha6(\text{IV})$  chains, but not the  $\alpha3(\text{IV})$  or  $\alpha4(\text{IV})$  chains. Most males with XLAS show no EBM expression of  $\alpha5(\text{IV})$  or  $\alpha6(\text{IV})$ . Lens capsules of some males with XLAS do not express the  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , or  $\alpha5(\text{IV})$  chains, while expression of these chains appears normal in other patients [32]. The expression of type IV collagen chains in the cochleae of human Alport patients has not been studied.

Women who are heterozygous for XLAS mutations frequently exhibit mosaicism of GBM and distal TBM expression of the  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , and  $\alpha5(\text{IV})$  chains, while expression of the  $\alpha1(\text{IV})$  and  $\alpha2(\text{IV})$  chains is preserved [16, 21, 26]. Female heterozygotes frequently also display mosaicism of EBM staining for  $\alpha5(\text{IV})$ .

In patients with ARAS, GBMs usually show no expression of the  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , or  $\alpha5(\text{IV})$  chains, but  $\alpha5(\text{IV})$  and  $\alpha6(\text{IV})$  are strongly expressed in Bowman's capsule, distal TBM, and EBM [20, 33, 34]. Therefore, XLAS and ARAS may be distinguished by immunohistochemical analysis of renal biopsy specimens. It should be noted that occasional patients with *COL4A5* mutations may show weak expression of  $\alpha5(\text{IV})$  and  $\alpha6(\text{IV})$  in Bowman's capsule or distal TBM, and no expression of the  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , or  $\alpha5(\text{IV})$  chains in GBM [35].

As in XLAS, the absence of  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , and  $\alpha5(\text{IV})$  chains from GBM is associated with a marked increase in the expression of  $\alpha1(\text{IV})$  and  $\alpha2(\text{IV})$  chains. The expression of type IV collagen chains in basement membranes of patients with ADAS has not been studied, but is likely to be normal.

These observations, along with immunochemical studies of extracted normal and Alport basement membranes [36–38], strongly suggest that basement membranes contain several distinct type IV collagen networks. Normal GBM appears to contain at least two networks: a major network composed of  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , and  $\alpha5(\text{IV})$  chains, and a minor network consisting of the  $\alpha1(\text{IV})$  and  $\alpha2(\text{IV})$  chains. In Bowman's capsule, distal TBM, and EBM the  $\alpha6(\text{IV})$  chain is available as a partner for the  $\alpha5(\text{IV})$  chain, explaining why in ARAS patients the  $\alpha5(\text{IV})$  chain persists in these basement membranes but is absent from GBM.

The abnormalities of type IV collagen expression observed in XLAS and ARAS patients indicate that a mutation affecting one of the chains involved in the putative  $\alpha3$ - $\alpha4$ - $\alpha5(\text{IV})$  network can prevent basement membrane expression not only of that chain but of the other two chains as well. Similarly, a mutation involving the  $\alpha5(\text{IV})$  chain can interfere with basement membrane expression of  $\alpha6(\text{IV})$ . The mechanisms that produce these effects remain under investigation. It is likely that at least some mutations interfere with the formation of trimeric type IV collagen molecules, leading to degradation of normal chains that have been prevented from forming trimers, or that have formed abnormal trimers. This kind of process accounts for abnormal type I collagen deposition in bone in osteogenesis imperfecta [39]. In some instances, a mutation at one of the type IV collagen loci may result in reduced transcription of other type IV collagen genes, or may accelerate degradation of mRNA transcribed from these genes. Thorner et al. [40] found that kidneys of male dogs with Samoyed hereditary nephropathy, a canine form of Alport syndrome that arises from a *COL4A5* mutation, contained levels of mRNA for the  $\alpha3(\text{IV})$  and  $\alpha4(\text{IV})$  chains that were substantially less than in unaffected males. Thus far, this observation has not been supported by other studies. Nakanishi et al. [41] found no differences in mRNA levels for  $\alpha3(\text{IV})$  and  $\alpha4(\text{IV})$  chains, measured by competitive reverse transcription-polymerase chain reaction, in kidneys of men with XLAS compared with normal male kidneys. Sasaki et al. [42] observed that dermal fibroblasts of males with XLAS express normal levels of  $\alpha6(\text{IV})$  mRNA, despite the absence of  $\alpha6(\text{IV})$  protein in their EBMs. In transgenic mice with *COL4A3* mutations, renal mRNA levels for the  $\alpha4(\text{IV})$  and  $\alpha5(\text{IV})$  chains are not different from levels in normal mice [43, 44]. The results of these studies suggest that post-transcriptional events account for the ability of a mutation affecting one of the type IV collagen genes to prevent tissue expression of normal type IV collagen chains.

There is evidence to suggest that *COL4A5* mutations that are associated with preservation of GBM expression

**Table 1** Hypothetical relationships between the mutation type, basement membrane (BM) expression of the  $\alpha 3$ - $\alpha 4$ - $\alpha 5$ (IV) network, and clinical phenotype (ESRD end-stage renal disease)

Type of <i>COL4A5</i> mutation	Deletion, nonsense	Missense	Splicing (reading frame maintained), some missense mutations
Effect on triple helices involving $\alpha 5$ (IV)	↓ Triple helices involving $\alpha 5$ (IV) do not form	↓ Triple helices involving $\alpha 5$ (IV) fold abnormally and undergo rapid degradation	↓ Triple helices involving $\alpha 5$ (IV) fold abnormally but degradation is slow
Effect on $\alpha 3$ - $\alpha 4$ - $\alpha 5$ network	↓ $\alpha 3$ - $\alpha 4$ - $\alpha 5$ network is absent from BM	↓ $\alpha 3$ - $\alpha 4$ - $\alpha 5$ network is absent from BM	↓ $\alpha 3$ - $\alpha 4$ - $\alpha 5$ network present in BM in reduced amount, or forms abnormal networks
Phenotype	↓ Juvenile ESRD, deafness	↓ Juvenile ESRD, deafness	↓ Adult ESRD, hearing may be normal or deteriorate slowly

of  $\alpha 3$ (IV),  $\alpha 4$ (IV), and  $\alpha 5$ (IV) chains may result in a less-severe phenotype [16, 35, 45]. Information about the effects of individual *COL4A5* mutations on basement membrane expression of these chains, and the relationship of chain expression to phenotype, is still being accumulated; hypothetical relationships between the mutation type, basement membrane expression of the  $\alpha 3$ - $\alpha 4$ - $\alpha 5$ (IV) network, and clinical phenotype are presented in Table 1. Naito et al. [35] observed absence of renal basement membrane  $\alpha 3$ (IV),  $\alpha 4$ (IV), and  $\alpha 5$ (IV) chains in two males with *COL4A5* deletions, but these chains were detectable in four of six males with glycine substitutions in  $\alpha 5$ (IV). Knebelmann et al. [46] observed absence of these chains from renal basement membranes in eight of nine males with glycine substitutions in  $\alpha 5$ (IV).

#### Heterogeneity of basement membrane ultrastructure

The pathognomonic ultrastructural feature of the Alport kidney is a thickened GBM, in which the lamina densa has been transformed into a heterogeneous network of interwoven lamellae enclosing clear electron-lucent areas; these may contain round granules of variable density measuring 20–90 nm in diameter [47–49]. These changes can be seen regardless of inheritance pattern or the presence or absence of sensorineural deafness or ocular abnormalities.

This lesion is found in most, but not all, patients with Alport syndrome. Affected young males, heterozygous females at any age, and affected adult males on occasion, may have diffusely attenuated GBM measuring 100 nm or less, rather than the pathognomonic lesion. Studies of males with human or canine Alport syndrome have shown that the earliest manifestation of the GBM lesion is attenuation, and that the extent and severity of thickening and multilamellation increase with age [50, 51]. Heterozygous females may have GBM of normal appearance or, at the other end of the spectrum, diffuse GBM thickening and multilamellation, but most will display a mixture of normal, thin and thick, lamellated GBM [52].

Although diffuse attenuation of GBM has been considered the hallmark of benign familial hematuria, some patients with GBM attenuation have progressive renal

disease and a *COL4A5* mutation [46, 53]. These cases illustrate the fact that “thin GBM” is a descriptive term, rather than a specific disease entity.

#### The influence of gender on the expression of the Alport phenotype

About 80% of people with Alport syndrome have the X-linked form of the disease. As expected for an X-linked condition, all affected males exhibit the disease phenotype, although the natural history of the renal, cochlear, and ocular aspects of the disease varies from family to family. Thus, it can be predicted that an affected male in an XLAS kindred will inevitably develop kidney failure at some time in his life and, if deafness is a feature of the phenotype in that kindred, that he will eventually exhibit hearing loss. In contrast, affected females in XLAS kindreds typically display mild clinical involvement, particularly during childhood and young adulthood. At least 90% of heterozygous females exhibit microhematuria. However, the incidence of chronic renal failure before 40–50 years of age is probably no greater than 10%–15% in heterozygous females.

The lesser severity of disease in heterozygous females most likely reflects the presence of a normal *COL4A5* allele. A random pattern of X chromosome inactivation would be expected to result, in most heterozygotes, in an approximate 1:1 ratio between cells expressing the normal *COL4A5* allele and cells expressing the mutant allele. A small percentage of heterozygotes would lie at either end of the spectrum, with predominant inactivation of either the normal or the mutant *COL4A5* allele. Results of studies of the skin basement membrane expression of the  $\alpha 5$ (IV) chain in females who are heterozygous for XLAS support these predictions. The basement membrane underlying the epidermis (EBM) normally expresses the  $\alpha 5$ (IV) chain, but in most males with XLAS, EBM expression of the  $\alpha 5$ (IV) chain is completely lacking [14, 17]. Most heterozygous females exhibit a mosaic pattern of  $\alpha 5$ (IV) expression in the EBM [16]. In a study of 25 females heterozygous for XLAS, Nakanishi et al. [54] determined an  $\alpha 5$ (IV) expression ratio, i.e., the fraction of total EBM expressing the  $\alpha 5$ (IV) chain.

The mean (SD) ratio was 56% (27%), with a range of 8%–94%, and the ratios were normally distributed. We have obtained similar results in female dogs that are heterozygous for XLAS [55]: the mean  $\alpha 5(\text{IV})$  expression ratio in EBM was 61% (16%), with a range of 21%–100%, and the ratios were normally distributed (C. Kashtan, G. Lees, unpublished observations). These results are consistent with the results one would predict on the basis of random X inactivation in basement membrane-producing cells of the epidermis.

While we intuitively would predict that heterozygous females with renal insufficiency would exhibit skewed inactivation patterns favoring the X chromosome carrying the mutant *COL4A5* allele, this relationship has not been clearly established. Guo et al. [56] described an XLAS female with a severe phenotype in whom 90% of the *COL4A5* mRNA in white blood cells and kidney was derived from the mutant allele. Vetrie et al. [57], studying X inactivation patterns in white blood cells of XLAS females, found a symmetrical pattern in most subjects and occasional subjects with extreme skewing of inactivation. However, these authors were unable to demonstrate a correlation between the X inactivation pattern and disease severity in females with XLAS [57]. While Nakanishi et al. [54] found an inverse correlation between the EBM  $\alpha 5(\text{IV})$  expression ratio, an indirect indicator of the X inactivation pattern, and urinary protein excretion in heterozygous females, we have been unable to confirm this relationship in a dog model of XLAS (C. Kashtan, G. Lees, unpublished observations).

These various observations support the notion that the presence in heterozygous females of a normal *COL4A5* allele, and consequently some level of  $\alpha 5(\text{IV})$  expression in basement membranes, is indeed protective of renal function. However, it is not yet clear whether or not a threshold protective level of  $\alpha 5(\text{IV})$  expression exists, or what this threshold level might be. Although there is currently no evidence that modifying genes affect the natural history of Alport syndrome in affected males, this issue has yet to be addressed in heterozygous females.

While some heterozygous females with severe manifestations of XLAS would be expected simply on the basis of random X inactivation, nonrandom events favoring expression of the mutant *COL4A5* allele may also occur. For example, Kapoor and Dasgupta [58] described a 20-year-old woman with anterior lenticonus and other features of a severe Alport phenotype, who had a 45,XO karyotype.

#### Heterogeneity of the natural history of the Alport nephropathy

##### *Native kidney disease*

End-stage renal disease (ESRD) develops in virtually all affected males with XLAS, but the rate of progression shows significant interkindred variability. A bimodal distribution of age at ESRD has been observed among fami-

lies with XLAS [59]. In families with so-called juvenile Alport syndrome, the mean age at ESRD in affected males is less than 31 years, while in adult Alport syndrome the mean age at ESRD is greater than 31 years. Because the standard deviation around the mean age at ESRD is about 5–7 years, the timing of ESRD in an affected male can be estimated if information about related affected males is available. However, marked intrakindred variability in the rate of progression to renal failure of affected males has occasionally been reported in families with missense *COL4A5* mutations [60].

Compared with affected males, the renal prognosis in affected females with XLAS is generally benign, with most surviving into old age with clinically mild renal disease. Approximately 15% of female heterozygotes develop renal insufficiency during adolescence, young adulthood, or middle age. Many women with progressive nephritis maintain adequate renal function until late in life; the true incidence of renal failure in elderly heterozygotes remains to be determined. Gross hematuria in childhood, nephrotic syndrome, and diffuse GBM thickening by electron microscopy are features suggestive of a progressive course in affected females [61]. Sensorineural deafness and anterior lenticonus are also indicative of an unfavorable renal outcome in affected women.

Male patients with *COL4A5* mutations that result in an absent or truncated  $\alpha 5(\text{IV})$  chain, such as deletions and nonsense mutations, consistently exhibit juvenile ESRD, usually associated with deafness [5, 53]. Most of the missense and splicing mutations of *COL4A5* described thus far are also associated with juvenile ESRD and deafness. Several missense mutations of *COL4A5* have been associated with adult ESRD and late development of deafness [5, 53, 62]. With regard to missense mutations affecting glycine residues in the collagenous domain of the  $\alpha 5(\text{IV})$  chain, there is at present no clear correlation between the position of the substituted glycine, or the substituting amino acid, and the resulting clinical phenotype. Splicing mutations that cause skipping of an exon but maintain the *COL4A5* reading frame may also be associated with adult ESRD [46].

Patients with ARAS consistently exhibit juvenile ESRD, regardless of gender [8, 10–12, 63]. Patients with ADAS appear to exhibit a slower rate of progression to ESRD than most patients with XLAS [64].

With regard to the progressive nature of the Alport nephropathy, it is worth noting that a mutation in the *COL4A3*, *COL4A4*, or *COL4A5* gene results in renal failure indirectly. In the normal developing kidney,  $\alpha 1(\text{IV})$  and  $\alpha 2(\text{IV})$  chains predominate in the primordial GBM of immature glomeruli [30, 31, 65]. The formation of capillary loops within the maturing glomeruli is associated with the appearance of  $\alpha 3$ ,  $\alpha 4$ , and  $\alpha 5(\text{IV})$  chains in the GBM. As glomerular maturation progresses, the  $\alpha 3$ ,  $\alpha 4$ , and  $\alpha 5(\text{IV})$  chains become the predominant type IV collagen chains in GBM. This process has been referred to as “isotype switching” [30]. Although this isotype switch does not occur in Alport syndrome [30, 31, 65], glomerular development otherwise pro-

ceeds normally, and the GBM of young animals and children with Alport syndrome exhibits a normal trilaminar appearance by electron microscopy [43, 44, 50, 51]. These glomeruli exhibit normal capacities for filtration and for selective permeability, as demonstrated by the normal glomerular filtration rates and absence of overt proteinuria that are characteristic of early Alport syndrome in both humans and animals. Hearing is likewise normal early in life, with deafness becoming apparent and progressing with increasing age. Therefore it appears that proteinuria and renal insufficiency, as well as sensorineural deafness, result from processes that are initiated by the absence of the  $\alpha3$ - $\alpha4$ - $\alpha5$ (IV) network, rather than arising directly from the absence of this network. These processes probably include, but may not be limited to, overexpression in the GBM of the  $\alpha1$ (IV) and  $\alpha2$ (IV) chains, type V collagen, and type VI collagen [18, 20, 31, 44, 65–67].

Although most research on Alport syndrome focuses on the glomerulus, it is important to note that, as in other chronic glomerulopathies, expansion of the renal interstitial compartment shows a strong inverse correlation with glomerular filtration rate in males with Alport syndrome [68]. It is possible that independent genetic, dietary, or environmental factors influence the rapidity of renal interstitial expansion that occurs as a downstream effect of *COL4A3*, *COL4A4*, and *COL4A5* mutations. In this regard, the provocative report of Callis et al. [69], describing diminished proteinuria and stabilization of renal function in a small group of Alport males treated chronically with cyclosporine, raises several questions. First, of course, is the question of whether these effects can be replicated in other people and in animals with Alport syndrome. Other questions concern the mechanism of the effect of cyclosporine on protein excretion in Alport patients, and whether stabilization of renal function is a consequence of the reduced proteinuria or an independent effect of cyclosporine.

### *Transplant outcome*

At present, renal transplantation is the only available treatment for Alport syndrome. The data of the North American Pediatric Renal Transplant Cooperative Study (NAPRTCS) document equivalent allograft survival rates in patients with familial nephritis and patients with other diagnoses [70]. Anti-GBM nephritis involving the renal allograft is a rare, but dramatic, manifestation of Alport syndrome, occurring in 3%–4% of transplanted male Alport patients [71–75]. Alport patients who develop post-transplant anti-GBM nephritis are usually male, always deaf, and likely to have reached ESRD before age 30 years [22]. This profile describes the majority of Alport patients presenting for renal transplantation, limiting its predictive value. However, Alport patients with normal hearing or late progression to ESRD are at very low risk for the development of post-transplant anti-GBM nephritis. Females with XLAS also appear to be at low risk for this complication.

The pathogenesis of post-transplant anti-GBM nephritis in Alport syndrome patients is presumably based upon exposure to antigens present in the donor GBM, for which the recipient has not established immune tolerance [76]. The target(s) of anti-GBM antibodies in some of these patients has been determined, with variable results. Most of those with XLAS exhibit antibodies against the NC1 domain of the  $\alpha5$ (IV) chain, but antibodies against  $\alpha3$ (IV) NC1 have also been described [77–79]. In ARAS patients with anti-GBM nephritis, antibodies appear to target the  $\alpha3$ (IV) NC1 domain [77].

Females who are heterozygous for *COL4A5* mutations would not be expected to be at risk for the development of post-transplant anti-GBM nephritis, since the product of the normal *COL4A5* allele would allow establishment of immunological tolerance for  $\alpha5$ (IV). Nevertheless, post-transplant anti-GBM nephritis has been reported in two females with Alport syndrome, both of whom proved to have ARAS, due to *COL4A3* mutations [8, 10, 80].

There is evidence to suggest that mutations in the *COL4A5* gene that prevent expression of an immunogenic gene product, thereby preventing the establishment of tolerance for  $\alpha5$ (IV), are associated with an increased risk for the development of post-transplant anti-GBM nephritis [81]. For example, a recent review of the genetics of Alport syndrome included seven patients with XLAS and post-transplant anti-GBM nephritis; six had large deletions of *COL4A5* and the other had a splicing mutation [5]. Even if certain types of *COL4A5* mutation confer a higher risk of developing post-transplant anti-GBM nephritis, such data are currently of limited value in planning transplantation. It is clear that Alport patients with *COL4A5* deletions can undergo renal transplantation without developing anti-GBM nephritis, indicating that other factors, presently unknown, must influence the initiation and elaboration of the immune response to the allograft [5, 82]. Patients with ARAS can also be transplanted successfully [83].

### Heterogeneity of extrarenal disease in Alport syndrome

#### *Leiomyomatosis*

The association of Alport syndrome with leiomyomatosis of the esophagus and tracheobronchial tree has been reported in approximately 20 families [84]. Affected females in these kindreds typically also exhibit genital leiomyomas, causing clitoral hypertrophy with variable involvement of the labia majora and uterus. Bilateral posterior subcapsular cataracts also occur frequently in affected individuals in these kindreds. Symptoms usually appear in late childhood and include dysphagia, postprandial vomiting, retrosternal or epigastric pain, recurrent bronchitis, dyspnea, cough, and stridor.

All families in which XLAS cosegregates with diffuse leiomyomatosis exhibit large deletions that span the adjacent 5' ends of the *COL4A5* and *COL4A6* genes [85,

86]. The deletions involve varying lengths of *COL4A5*, but the *COL4A6* breakpoint is always located in the second intron of the gene [87, 88]. These deletions appear to arise as a result of recombination events involving repetitive LINE-1 elements, at least in some cases [89, 90]. Leiomyomatosis does not occur in patients with deletions of *COL4A5* and *COL4A6* that extend beyond intron 2 of *COL4A6*. Mutations of *COL4A6* alone do not appear to cause Alport syndrome, consistent with the absence of the  $\alpha 6(\text{IV})$  chain from normal GBM [86, 91]. The fact that leiomyomatosis is so rare among patients with XLAS, most of whom lack tissue expression of the  $\alpha 6(\text{IV})$  chain, indicates that these tumors do not develop simply from absence of the  $\alpha 6(\text{IV})$  chain in smooth muscle. The pathogenesis of these tumors remains under investigation.

### *Deafness*

High-frequency, sensorineural hearing loss is frequently but not universally associated with the Alport renal lesion, occurring in an estimated 55% of males and 45% of females with the disease [92]. The true incidence of deafness may be higher, since patients are not always evaluated with audiograms, and the prevalence of deafness increases with age. Males with XLAS exhibit deafness earlier in life, and develop more severe hearing deficits, than heterozygous females. There are no gender differences in the occurrence or progression of deafness in ARAS. In some families with XLAS and apparently normal hearing, deafness may be a late and very slowly progressive phenomenon [62].

Male patients with *COL4A5* mutations that result in an absent or truncated  $\alpha 5(\text{IV})$  chain, such as deletions and nonsense mutations, usually exhibit deafness that is detectable in the first 2 decades of life [53]. Most of the missense and splicing mutations of *COL4A5* described thus far are also associated with juvenile onset of deafness. Several missense mutations of *COL4A5* that are associated with adult ESRD are also characterized by late development of deafness [5, 62].

### *Ocular abnormalities*

Ocular defects are common in patients with Alport syndrome. The types of ocular lesions exhibited by XLAS and ARAS patients are similar [93, 94]. Anterior lenticonus, in which the central portion of the lens protrudes into the anterior chamber, is pathognomonic of Alport syndrome [95], and appears to be almost entirely restricted to Alport families exhibiting juvenile-type nephropathy and deafness [59]. In XLAS families anterior lenticonus is far more common in affected males, but can occur in females. Anterior lenticonus appears to arise as a result of mechanical weakness of the anterior lens capsule, which exhibits attenuation and fracturing by light and electron microscopy [96–98]. This fragility of the anterior

or lens capsule presumably reflects absence or deficiency of the  $\alpha 3\text{-}\alpha 4\text{-}\alpha 5(\text{IV})$  network [32].

A variety of other ocular lesions have been reported in patients with Alport syndrome. The most-common abnormalities are pigmentary changes in the perimacular region, consisting of whitish or yellowish granulations, or flecks, surrounding the foveal area [99–101]. These lesions are frequently accompanied by anterior lenticonus, but may occur in the absence of lenticonus. The occurrence of flecks is correlated with deafness, and the incidence appears to increase with age [99, 102]. Retinal flecks may represent abnormalities of Bruch's membrane, the basement membrane supporting the retinal pigment epithelium.

Corneal endothelial vesicles (posterior polymorphous dystrophy) observed in some Alport patients [103–105] may arise from defects in Descemet's membrane, the basement membrane underlying the corneal endothelium. Recurrent corneal erosion in Alport patients has been attributed to alterations of the corneal epithelial basement membrane [106, 107]. At present there do not appear to be clear correlations between the type of *COL4A5* mutation and the occurrence or nature of ocular abnormalities in individuals with XLAS [102].

### *Mental retardation*

Jonsson et al. [108] recently described the co-occurrence of Alport syndrome, mental retardation, midface hypoplasia, and elliptocytosis in two brothers (AMME complex), who were shown to have a microdeletion involving the entire *COL4A5* gene, and extending beyond its 3' end. To date, two new genes have been identified in the deleted region downstream of the *COL4A5* gene: *FACLA*, which encodes a long-chain acyl-CoA synthetase, and *AMMECR1*, a gene that is evolutionarily conserved and encodes a protein with as yet unknown functions [109, 110]. The association of hereditary nephritis with mental retardation is a rare occurrence [111].

### *Hematological abnormalities*

In 1972, a family was described in which hereditary nephritis segregated with deafness and megathrombocytopenia, and reports of several similar families have subsequently appeared [112–118]. In most of the families described, the disorder appears to have been transmitted as an autosomal dominant trait. GBM thickening and lamellation were found in two of the reported patients.

The association of these platelet defects, and in some families granulocyte abnormalities [119], with hereditary nephritis remains unexplained. There have been few reports of gene localization or mutation analysis in these families, except for negative reports regarding *COL4A5* involvement, so the genetic locus or loci involved remains unknown. Basement membranes of these patients show normal expression of type IV collagen  $\alpha$  chains

[120]. As noted above, the association of Alport syndrome and elliptocytosis has been described in a single family [108].

## Summary

It is now evident that the phenotypic features of Alport syndrome arise from mutations in the *COL4A3*, *COL4A4*, or *COL4A5* genes that interfere with the incorporation into basement membranes of a type IV collagen network composed of  $\alpha3(\text{IV})$ ,  $\alpha4(\text{IV})$ , and  $\alpha5(\text{IV})$  chains. Absence or deficiency of this network triggers molecular processes that gradually produce severe alterations in the architecture and function of the basement membranes of the glomerulus, cochlea, and eye, resulting in progressive glomerulopathy, high-frequency sensorineural deafness, and acquired ocular anomalies. Certain correlations between mutation and phenotype have been established, such as the precise nature of the deletion mutations associated with the Alport syndrome/diffuse leiomyomatosis complex, and the consistent association of deletion and nonsense mutations with the development of ESRD and deafness during the first several decades of life, at least in affected males. The rules governing the phenotypic consequences of missense *COL4A5* mutations have yet to be determined. Also, it is not yet possible to define a simple relationship between X inactivation patterns and the outcome of females who are heterozygous for *COL4A5* mutations. Ongoing efforts to correlate genotype and phenotype in Alport patients, and to elucidate the pathogenesis of chronic renal failure and deafness, should eventually refine our understanding of the factors that determine the fate of an individual with a mutation in the *COL4A3*, *COL4A4*, or *COL4A5* gene.

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## LITERATURE ABSTRACT

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### Familial clustering of IgA nephropathy: further evidence in an Italian population

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Several lines of evidence suggest that genetic factors have an important role in the pathogenesis of immunoglobulin A (IgA) nephropathy. We report the prevalence of familial IgA nephropathy in a referral center in northern Italy and present the data on HLA genotypes in the families identified. Twenty-six of 185 patients (14%) with IgA nephropathy investigated in Brescia, Italy, were related to at least one other patient with the disease. Restriction fragment length polymorphism (RFLP) analysis of HLA-DR beta and HLA-DQ alpha and beta genes, as well as polymerase chain reaction-

based oligonucleotide typing, was performed in family members. The 26 patients with IgA nephropathy belonged to 10 families. Familial relationships between the patients varied greatly, ranging from parent-child to sib-pair to more distant familial relationships. No common nephrotoxic factor was identified in the families. The intervals separating the apparent onset of disease in relatives with IgA nephropathy varied from 8 months to 13 years. In patients with a family history of IgA nephropathy, there was an increased incidence of HLA-DRB1\*08 compared with those with sporadic IgA nephropathy. The study shows that a significant number of the patients with IgA nephropathy followed up in Brescia had a family history of disease. The fact that the Italian population, an ethnic group not previously examined, also presents an increased familial susceptibility to IgA nephropathy suggests that familial predisposition is a very common finding for IgA nephropathy. Thus, clinicians should become aware that IgA nephropathy may aggregate within families in a substantial number of cases. In addition, this subgroup of patients with IgA nephropathy offers an ideal opportunity to elucidate the molecular genetics of this disease.