Mapping and cloning hereditary deafness genes
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In the past two years, considerable progress has been made in the mapping and cloning of human deafness genes. Highlights are the chromosomal localization of at least five genes for autosomal forms of non-syndromic deafness and, more recently, the cloning of an X-linked deafness gene, DFN3, and the Usher syndrome type IB gene. This last gene encodes a myosin-like protein and was identified as the human homolog of the mouse shaker-1 gene. The DFN3 gene Brain 4 encodes a POU domain containing transcription factor that is involved in the development of the inner ear.

Introduction

Deafness is the most common inherited human sensory defect, affecting one in 2000 children [1]. In 70% of cases, the deafness is non-syndromic, i.e. not associated with other clinical features [2]. Progress in mapping deafness genes has been relatively slow for several reasons. Firstly, ~75% of cases are of the recessive type [3] which, because of the inherently small pedigree sizes, renders linkage analysis difficult. Secondly, several forms of hearing loss are age-dependent; in others, disease manifestation and clinical course depend on environmental factors. Thirdly, the nosologic classification of hearing loss is complicated by the inaccessibility of the inner ear for clinical examination. Fourthly, our understanding of the auditory signal transduction cascade in the sensory hair cells of the organ of Corti is still in its infancy, so we know of only a few candidate genes for hereditary forms of sensorineural deafness that can be tested for mutations. Fifthly, only recently have inner ear specific cDNA libraries been established [4,5,6]. Finally, when compared to the funding of eye research, financial support for research into genetic forms of deafness has been relatively meager. Still, remarkable progress has been made in this field during the past few months. Molecular studies have recently shed more light on the etiology and pathogenesis of various syndromes in which deafness is an inconsistent or minor symptom.

In this review, we have chosen, somewhat arbitrarily, to confine ourselves to two syndromes in which early-onset deafness is a major symptom, Usher syndrome (USH) and Waardenburg syndrome (WS). The central focus of the review will be the human genes involved in non-syndromic deafness that have been mapped and cloned recently, and on the nosologic implications of this work. In another review, Steel and Brown [7] have dealt with various forms of mammalian deafness on the basis of their pathologic features.

Usher syndrome

USH comprises a group of autosomal recessive disorders associated with congenital sensorineural deafness and progressive visual loss caused by retinitis pigmentosa. Clinically, at least three types of Usher syndrome (USH1–3) can be distinguished. Patients with USH1 have congenital, severe to profound hearing loss and absence of vestibular function, whereas in USH2, the hearing loss is congenital but moderate to severe and the vestibular function is normal.

Linkage studies suggest the presence of causal genes for USH1 at 14q32.1–q32.3 (USH1A), 11q13.5 (USH1B), and 11p15.1–p14 (USH1C) [8–12]. Recently, a novel type VII myosin gene at 11q13.5 has been shown to be homologous to the murine deafness gene shaker-1 and is responsible for USH1B [13**,14**]. The phenotypes of the original shaker-1 mutant and five other shaker-1 mutants seem to be different from that of USH1 patients in that no retinal degeneration has so far been reported in these mouse mutants. In another study, the autosomal recessive deafness gene DFN2 has been localized to the same interval of chromosome 11 [15]. A major locus for USH2 (USH2A) is situated at 1q41 [16–18], but evidence exists for a further USH2 locus, as one large USH2 family does not show linkage to 1q [19]. The choroideremia-like gene CHML is a candidate for USH2A because it maps to the same chromosomal in-
terval, but the search for CHML mutations in USH2A patients has been unsuccessful [20,21].

The third type of Usher syndrome (USH3) differs from USH2 by the progressive nature of its hearing loss. Linkage studies have assigned the underlying gene to 3q21–q25 [22]. A clear clinical distinction between USH2A and USH3 is difficult, as exemplified by the observed linkage of one ‘USH3’ family to 1q41 [22] and the linkage of five ‘USH2A’ families to 3q21–q25 (WS Kimberling, personal communication).

Waardenburg syndrome

Waardenburg syndrome (WS) is an auditory pigmentary syndrome in which hearing loss is associated with abnormal pigmentation of hair, skin and eyes. Clinically, WS has been divided into two types, WS1 and WS2, which are distinguished by the presence or absence of mild facial dysmorphic features such as dystopia canthorum, a lateral displacement of the inner canthi of the eyes, which is defined by the W index. Redefinition of the W index now allows a better classification of WS families. Patients with WS1 have been shown to have mutations in the PAX3 gene [23,24], whereas WS2 patients have mutations in other genes. In a putative mouse model for WS, mutations were found in the mitrophathalhia gene, encoding a novel basic helix-loop-helix zipper protein [25]. Subsequently, the human homologue of this gene, MITF, and a locus for WS2 were mapped at 3p14.1–p12.3 [26,27], and mutations were found in the MITF gene in two families with WS2 [28]. As a result of improved clinical classification, families can now be reliably defined as WS1 or WS2 and mutations sought in the appropriate genes.

Mitochondrially inherited deafness

In recent years, mutations in the mitochondrial genome have been reported to be associated with a variety of multisystem disorders [29], many of which include sensorineural deafness as a symptom. In four unrelated families, a maternally transmitted susceptibility to non-syndromic sensorineural hearing loss was associated with a mitochondrial DNA mutation at nucleotide 1555 in the 12S rRNA gene [30*]. In three of these families, the disease became manifest after aminoglycoside antibiotic treatment; in the fourth family, it was associated with a mutation in an (as yet) unknown nuclear gene. Early-onset sensorineural hearing loss in another maternal pedigree has been found to be associated with a mutation at nucleotide 7445, converting the 3′ terminal thymine residue of tRNA-ser(UCN) to a cytosine [31].

Autosomal recessive deafness

Non-syndromic autosomal recessive deafness is extremely heterogeneous, as documented by the fact that most marriages between unrelated deaf individuals do not result in affected offspring. Estimates of the number of genes involved in recessive deafness do not include the possibility that affected individuals are non-complementary double heterozygotes, as shown recently in retinitis pigmentosa [32**]. After a systematic genome–wide search using highly polymorphic microsatellite repeats, the first gene for autosomal recessive deafness (DFNB1) was localized to the pericentromeric region of chromosome 13. In this study, homozygosity by descent was observed in affected individuals from consanguineous Tunisian families for two genetic markers [33]. The DFNB1 locus may also be involved in other populations, as homozygosity for this region has also been found in a consanguineous family of Pakistani origin [34]. Using the same approach, a second locus for autosomal recessive deafness (DFNB2) was mapped to chromosome 11q13.5 [15], a region which also harbours the human USH1B gene [14**] (see above). A third autosomal recessive gene (DFNB3) was assigned to the pericentromeric region of chromosome 17 by a strategy termed allele frequency dependent homozygosity mapping [35*]. Evolutionary conserved synteny with other markers indicates that the murine deafness gene shaker-2 may be the homologue of DFNB3 [36].

Autosomal dominant deafness

In isolated populations, a single or very few deafness genes may prevail. This was illustrated in a Costa Rican and an Indonesian pedigree in which genes for non-syndromic autosomal dominant deafness mapped to 5q31 (DFNA1) and 1p (DFNA2), respectively [37,38]. In the latter study, the locus on 1p was confirmed in an American family. Using a large French family, a third locus for autosomal dominant deafness has been localized recently to human chromosome 13 [39]. Possibly the same locus is involved as in DFNB1, the recessive form of deafness described above. As this region has now been implicated in families from three different populations, it may be a major locus for deafness. Dominant and recessive forms of deafness may result from different mutations in the same gene, as shown recently for mutations in the COL11A2 gene which can be associated with autosomal dominant and recessive forms of Stickler syndrome, a syndromic form of sensorineural deafness [40**].
X-linked deafness

The most frequent form of X-linked deafness, DFN3 (X-linked deafness with perilymphatic gusher during stapes surgery), has been mapped to the Xq13–q22 region by linkage studies [41–43]. In patients with DFN3, computerized tomography has revealed specific structural defects in the temporal bone resulting in an abnormal wide communication between the cerebrospinal fluid and the perilymph, which appears to account for the 'gusher' observed during stapes surgery. In families with X-linked sensorineural deafness without the bony defect, linkage studies suggest the association of one locus at or near Xq21 and another at Xp21 [44,45]. Detailed analysis of Xq21 deletions associated with DFN3, choroideremia and mental retardation, and others found in patients with non-syndromic DFN3, has localized the underlying gene to a 500 kb segment of Xq21.1 [46–50].

These data, and the assignment of the mouse POU domain encoding gene Brain 4 to the murine X-chromosome in a region homologous to human Xq13–q22 [51], have been instrumental in the recent isolation of the human DFN3 gene [52**]. The human homologue of Brain 4, POU3F4, could be mapped to the physical interval carrying the DFN3 locus, and POU3F4 mutations were found in five unrelated DFN3 patients [52**]. Although these observations demonstrate that mutations in the POU3F4 gene cause DFN3, they do not explain the association of DFN3 with four microdeletions and a duplication that map up to 400 kb proximal to POU3F4. Although the involvement of a second DFN3 gene in different parts of the rat cochlea [54]. In the light of our data [52**], it is now tempting to speculate that these genes are implicated in other forms of deafness. In the mouse genome, several POU domain genes have been mapped [55], and the precise chromosomal localization of their human counterparts is eagerly awaited.

POU3F4 is a member of a multigene family encoding transcription factors (with >25 members) [53]. At least five POU domain genes have been found to be expressed in different parts of the rat cochlea [54]. In the light of our data [52**], it is now tempting to speculate that these genes are implicated in other forms of deafness. In the mouse genome, several POU domain genes have been mapped [55], and the precise chromosomal localization of their human counterparts is eagerly awaited.

Conclusions

Hereditary deafness is extremely heterogeneous. Most cases show an autosomal recessive mode of inheritance. Through the widespread use of a dense array of microsatellite markers, the introduction of novel genetic mapping techniques and improved clinical classification, several deafness genes have been mapped in the human genome. Although in man, precise regional assignment of the underlying gene defects is frequently hampered by small family sizes, comparison of their map locations with those of corresponding defects in the mouse will greatly facilitate their isolation. Recently, this has been illustrated by the identification of the human USH1B gene on the basis of its murine homologue, shaker-1. Positional cloning and candidate gene approaches have led to the identification of the gene for X-linked deafness, DFN3. Future efforts in cloning deafness genes will benefit from the availability of an increasing number of candidate genes which are being isolated from inner ear specific cDNA libraries.

Acknowledgements

The authors thank SDM Brown, WS Kimberling and C Petit for providing unpublished data, SM van der Maarel and ECM Marinain for helpful suggestions, and I Goossens for assistance in preparing the manuscript.

References and recommended reading

Papers of particular interest, published within the annual period of review, have been highlighted as:
• of special interest
•• of outstanding interest


A human fetal cochlear (membranous labyrinth) cDNA library was constructed using subtractive hybridization and differential screening. Analysis of a subset of cDNAs yielded several known genes that serve structural or regulatory functions in the inner ear and some novel cochlear genes.

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