## Abstract DGA 2005

## Molecular genetics of hearing impairment

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The molecular mechanisms underlying the development and the functioning of the inner ear sensory hair cells, has escaped characterisation for a long time owing to the small number of these cells in the cochlea. Thus, the study of hereditary deafness provides a unique approach to gaining relevant insights into the understanding of these processes. Indeed, most early onset forms of hereditary deafness, whether in humans or in mice, are caused by monogenic defects affecting the cochlea, whilst (i) about a hundred genes are considered to be underlying the early onset forms of isolated deafness, and (ii) mutations in another 300 additional genes may also be accountable for syndromic forms of deafness in humans. The difficulties encountered in order to analyse isolated forms of deafness over the previous decade have now been settled and 36 genes involved in the isolated forms of deafness have been identified.

The analysis of the phenotypic abnormalities resulting from the inactivation of the corresponding genes, mostly in mice and for some of them in zebrafish too, have enabled us to identify genes likely to provide entry points into the understanding of the following aspects of the hair bundle development, i.e. the control of (i) the growth of the stereocilia composing the hair bundle, (ii) the cohesion of the hair bundle, (iii) the orientation of this structure and (iv) the neurotransmitter exocytosis. Notably, among their encoded hair bundle proteins, several unconventional myosins (myosin VIIa, VI, XV), cadherins (cadherin23 and protocadherin15) and PDZ domain-containing proteins (whirlin, harmonin) have been found. The analysis of the localisation of these proteins in wild-type and mutant mice combined with the characterisation of the interaction protein networks into which those proteins are integrated, has been performed. The role played by several of these molecules in the developing hair bundle or in the synapse will be discussed.