pseudogene were found to be arranged in a head-to-tail orientation, clustered within 40kb of human DNA. To determine whether the other members of the family are also syntenic with this cluster, we have examined the chromosomal location of these genes by gel blot-hybridization analysis of DNA derived from human-rodent cell hybrids containing different subsets of human chromosomes. By correlating the presence and absence of gamma-crystallin gene sequences with segregation of a particular chromosome, it was possible to assign at least six of the human gamma-crystallin genes to chromosome 2 in man. By using additional cell lines carrying human chromosome 2 with various rearrangements, we were able to further map these genes to the long arm of chromosome 2, suggesting that all the human gamma-crystallin genes are located within the same chromosomal region. The regional assignment of this gamma-crystallin gene cluster to region q33-q35 was subsequently confirmed by in situ hybridization analysis. Moreover, we have detected several TaqI RFLPs associated with these genes, providing an opportunity for testing whether any of the inherited cataract diseases are resulted from mutations within the gamma-crystallin locus.

Identification of a polymorphic DNA marker pDL32B (D12S7) and its localization to the long arm of chromosome 12, region q14.3-qter

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Random human DNA fragments have been isolated from a small human genomic library prepared for the identification of RFLPs useful for mapping the human genome. The library was constructed by ligating HindIII-digested total human DNA to plasmid vector pBR322. One clone, designated as pDL32B, which contains a 3.2 HindIII insert, detects a TaqI RFLP of moderately high frequency. The four alleles are observed as fragments of (a) 6.8, (b) 5.1+0.28, (c) 4.1+2.7, and (d) 2.7+2.4kb. The allelic frequency of each is 0.09, 0.28, 0.61 and 0.02, respectively, yielding a PIC value of 0.47. Results of further analyses suggested that these RFLPs are probably due to single site mutations at the TaqI recognition sites. Subsequent experiments showed that pDL32B also detects a high frequency polymorphism with PstI. The chromosomal location of this polymorphic DNA segment was then examined by gel blot-hybridization analysis of DNA prepared from human-rodent cell hybrids. The result has allowed us to assign pDL32B to chromosome 12. Regional assignment was achieved by using a series of human-hamster cell hybrids each containing a whole or part of human chromosome 12. The marker was absent in a hybrid with a deletion of 12q14.3-qter, suggesting that pDL32B maps to the long arm of chromosome 12, region q14.3-qter.

Cystic Fibrosis: Progress on mapping of the disease locus by conventional chromosomal markers

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With a frequency of approximately one in 2000 births, Cystic Fibrosis (CF) is the most common autosomal recessive disorder in the Caucasian population. Although the basic biochemical defect in this disease remains unknown, CF is likely the result of mutation in a single gene. As a means to discover the basic defect of the disease, we have begun to search for a genetic marker closely linked to the "CF gene" by genetic linkage studies using polymorphic DNA and protein markers. Here we present our data to date for a number of the serum protein and cell surface markers tested using a panel of 26 CF families each with at least two affected children. Using the LIPED analysis program, linkage was excluded (lod(-2.0) for: ACP1 (2p23 or 2p25)at θ=0.05, AHSG (3q) at θ=0.05, AK1 (9q34) at θ=0.10, GC (4q11-q13) at θ=0.10, C3 (19pter-q13.2) at $\hat{\theta}$=0.10, GM (14q32.3) at θ=0.05, GPT (8q13-qter or 16pter-p11) at θ=0.05, PGM1 (1p22.1)