

A HyperCard-shell for the Human Genome Mapping database (HGM) including a stand-alone reference database

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The HGM-database contains over 5000 entries at present and is the standard database for human genome mapping. The Yale-Human Gene Mapping Library offers distribution of the HGM database for IBM and Macintosh computer systems and for the latter ASCII text or Microsoft-Excel formatted data is available. ASCII files do not offer any retrieval routines and rely on the capabilities of a database management program. Microsoft-Excel is a commercial spreadsheet/database program offering some retrieval options and allowing field specific searches. However, presentation and retrieval based on Microsoft-Excel is somewhat cumbersome and awkward to manage for scientists who are not regular users of Excel. I took advantage of the Macintosh HyperCard programming tool licensed to Macintosh computers to develop a HyperCard-shell that will provide all desired database retrieval functions at no extra costs. It automatically loads both HGM-data and references into HyperCard stacks linked during loading. Updating with further HGM-data or references requires a simple mouse click upon which the new information will be added to the existing HGM-HyperBase.

Data is presented on a single card divided into two sections providing information on mapping (left section) and relevant clones and probes (right section; see figure HGM-HyperBase data card). Guided search routines support retrieval based on individual or all fields according to the original HGM-field definitions. Automatic scanning of the whole genome is easily achieved, requiring only about 20 seconds on a Macintosh IIx. The references are kept in separate stacks for each chromosome and are available by simply clicking one of the reference buttons of the data-card. The reference stacks feature search and retrieval routines of their own. Furthermore they can be used as stand-alone databases for management of a personal literature database, including easy retrieval of reference lists for publications. HGM-HyperBase allows import and export of formatted text files, ensuring compatibility with any word processor and most other reference databases.

HGM-HyperBase is designed to be a user-friendly tool featuring self-explanatory buttons as well as complete on-line help. It requires a Macintosh computer running HyperCard Version ≥ 1.2 , the HGM database in field and record delimited text format and about 5 MB on a hard disk. The database is available on request from Yale-Howard Hughes Medical Institute (HHMI), Human Gene Mapping Library, 25 Science Park, New Haven, CT 06511, USA, at a charge of US\$ 20.00. In order to avoid copyright infringements the data should be ordered by the user. HGM-HyperBase ready for downloading including

the reference-database program and a brief guide is available free for nonprofit institutions from the author. To get a copy please send a *formatted* 800KB or 1.44 MB Macintosh diskette to the above address.