Overview of HGM10.5

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Human gene mapping came of age at the HGM 9.5 and HGM10 meetings in Yale, where the dependency of the mapping community on extensive computing support with literature and gene localization databases became firmly established. The challenge for the future was to build on these foundations and to work towards a system that could be readily established at a wide variety of centres. Such a system should provide flexibility and the potential to accept additional modules capable of integrating information from physical and genetic mapping. HGM10.5 provided the opportunity to evaluate and test the new relational database, GDB (Genome Data Base) developed by the Howard Hughes Medical Institute in collaboration with The Johns Hopkins University School of Medicine and the William H. Welch Medical Library, Baltimore. The HGM11 computing team at the ICRF in London worked closely with the GDB group and were responsible for the interim gene mapping data collection from committee chairs on diskettes, for all aspects of HGM10.5 networking and for production of the report. One particularly pleasing aspect of the meeting was the increased role played by committee assistants. This reflected a considerable investment of their own time, that of the organizers and the UK computing team in extensive preparation and training. The universal comment of the Chairs in the final review session was "Thanks to my assistant – without whom etc.". Preliminary discussions involving a wide range of groups who had interests in the identification of a range of useful markers for each chromosome led to joint proposals from the Linkage and DNA committees to the effect that each chromosome committee report should carry recommendations for "reference markers". This term was chosen to embrace the concepts of several previous recommendations. Such markers should be valuable for both linkage and physical mapping and conform to the essential characteristics described in the DNA committee report. Most committees were unable, at HGM10.5, to provide a complete range of reference markers. However, the exercise was beneficial in identifying where future effort should be concentrated and what goals should be achieved by HGM11. A decision concerning the referencing of mapping data made during the Helsinki meeting was also reaffirmed; the important aspect being that "personal communication", unless drawing attention to an article in press, should not provide the basis for a mapping entry (other than as a D number).

The great advantage of assembling interest groups covering the whole range of human gene mapping activities and which could discuss issues varying from nomenclature, to the integration of physical and sequence data into the gene mapping data base, was evident to all attendees. Such benefits should not be lost sight of in the inevitable move towards chromosome specific workshops.

Finally, while we are anticipating widely available on-line access to the database with the potential for remote editing for committee chairs, the requirement for hard copy, of at least a core of the information, will remain. HGM10.5 saw increasing implementation of graphic support and most committees made use of idiograms in preparing their reports. Comparative Mapping, in particular, appeared to derive particular benefit from the services available and we would like to record our thanks to all those in the support teams who employed considerable skill and most of the hours in the day in assisting the committees.

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