Physical Mapper is designed to draw various physical maps including contig map, restriction map, and STS map; to coordinate these various maps in the same window with a common scale; to assemble map objects into groups and combine them with relative distances; and to manage a wide range of scale from plasmid size (~5kb) to the chromosome size (~250 Mb). Fig.2 shows a representative physical map of the IGL region. Many cosmid clones, restriction sites and genes are shown and mapped objects within an object group are connected each other.

These softwares will be demonstrated at workstation session.

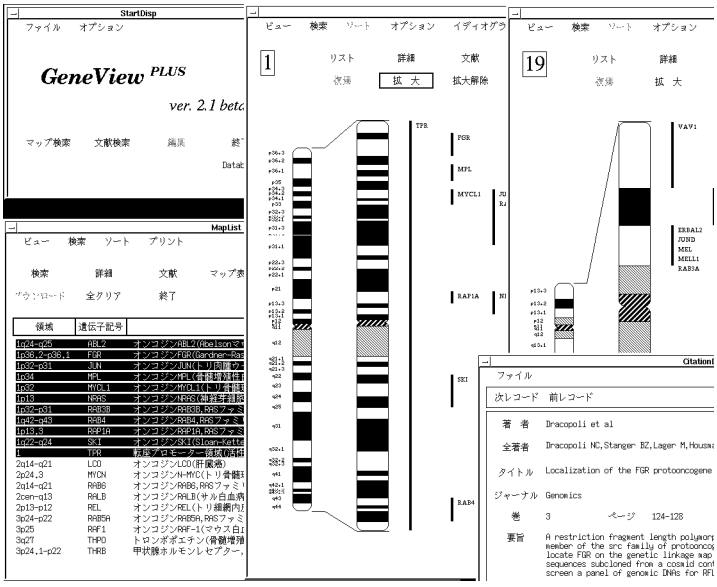

Fig.1

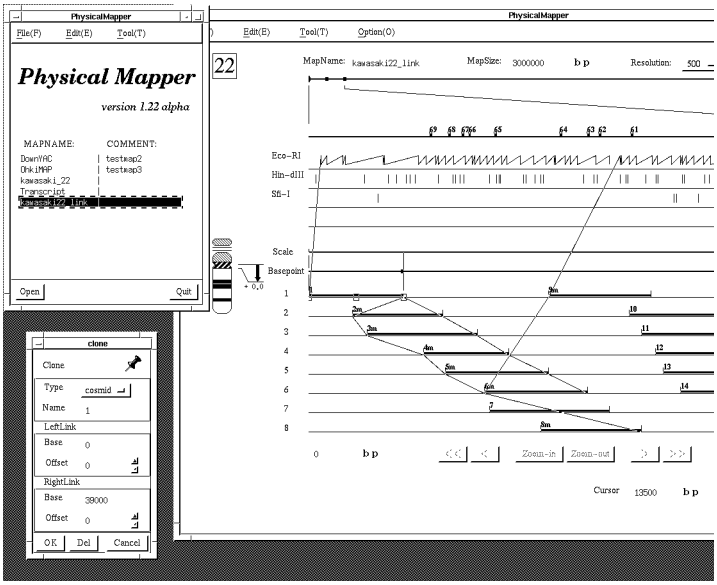

Fig.2

GeneView^{PLUS}, **Locus-in** and **Physical Mapper** : The GUI-softwares for genome mapping data management

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The final goal of human genome project is to identify and sequence all the genes in human body for complete understanding of their structure and function. Towards this challenging goal, it is essential to construct the detailed genome map and to prepare ordered DNA clones for the entire genome. Mapping data have been compiled into GDB (Genome Data Base) with international collaborative efforts. Search queries to GDB at JICST can be carried out with various protocols including WWW (http://gdb.gdbnet.ad.jp), X access (gdb.gdbnet.ad.jp) and GDB accessor. Now, GDB has become an indispensable international resource for the human genome analysis. It is yet necessary to develop user friendly softwares for more efficient access to GDB data.

We have developed three softwares, **GeneView**^{PLUS}, **Locus-in** and **Physical Mapper** . These were designed for input of raw mapping data, integration of various genome maps, and efficient use of GDB data. These systems have smooth graphical user interfaces (GUI) and operate on a workstation with X-window. The characteristics of each software are as follows.

GeneView^{PLUS}is able to quickly search GDB data; to accept both English and Japanese; to show search results on graphical chromosome ideograms; to zoom-in to an interested region; and to show supplementary information such as literatures with abstracts of each map object. Fig.1 shows a representative display in which search with a keyword 'oncogene' (**オンコジン**) was done. The locations of oncogenes on chromosomes 1 and 19 were graphically shown in a Citation Detail window.

Locus-in is able to graphically display a specific region of interest on the chromosome ideograms (800-band level); to generate sub-windows within a specific region for display of current GDB data through SQL access; to open new sub-windows by creating arbitrary boundaries; to construct database by filling mapped objects into sub-windows; to show detailed information of each map object; and to manage the ownership of data.

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