cally linked to *XRCC*3. The second human repair gene, *HHR*23A, maps to 19p13.2. Sequence analysis of 110,000 bases containing *HHR*23A identified six other genes, five of which are new genes with similarity to proteins from mouse, human, yeast, and *Caenorhabditis elegans*.

- Complete sequencing of full-length cDNAs for three new DNA repair genes (*XRCC*2, *XRCC*3, and *XRCC*9) in collaboration with the LLNL DNA repair group.
- Generation of a metric physical map of chromosome 19 spanning at least 95% of the chromosome. This unique map incorporates a metric scale to estimate the distance between genes or other markers of interest to the genetics community.
- Assembly of nearly 45 million bases of *Eco*R I restriction-mapped cosmid contigs for human chromosome 19 using a combination of fingerprinting and cosmid walking. Small gaps in cosmid continuity have been spanned by BAC, PAC, and P1 clones, which are then integrated into the restriction maps. The high depth of coverage of these maps (average redundancy, 4.3-fold) permits selection of a minimum overlapping set of clones for DNA sequencing.
- Placement of more than 400 genes, genetic markers, and other loci on the chromosome 19 cosmid map. Also, 165 new STSs associated with premapped cosmid contigs were generated and added to the physical map.
- Collaborations to identify the gene (*COMP*) responsible for two allelic genetic diseases, pseudoachondroplasia and multiple epiphyseal dysplasia, and the identification of specific mutations causing each condition.
- Through sequence analysis of the 2A subfamily of the human cytochrome P450 enzymes, identification of a new variant that exists in 10% to 20% of individuals and results in reduced ability to metabolize nicotine and the antiblood-clotting drug Coumadin.
- Location of a zinc finger gene that encodes a transcription factor regulating blood-cell development adjacent to telomere repeat sequences, possibly the gene nearest one end of chromosome 19.
- Completion of the genomic and cDNA sequence of the gene for the human Rieske Fe-S protein involved in mitochondrial respiration.
- Expansion of the mouse-human comparative genomics collaboration with ORNL to include study of new groups of clustered transcription factors found on human chromosome 19q and as syntenic homologs on mouse chromosome 7.
- Numerous collaborations (in particular, with Washington University and Merck) continuing to expand the LLNL-based IMAGE Consortium, an effort to characterize the transcribed human genome. The IMAGE clone collection is now the largest public collection of sequenced cDNA clones, with more than 500,000 arrayed clones, 500,000 sequences in public databases, and 10,000 mapped cDNAs.
- Development and deployment of a comprehensive system to handle sample tracking needs of production DNA sequencing. The system combines databases and graphical interfaces running on both Mac and Sun platforms and scales easily to handle large-scale production sequencing.
- Expansion of the LLNL genome center's World Wide Web site to include tables that link to each gene being sequenced, to the quality scores and assembled bases collected each night during the sequencing process, and to the submitted GenBank sequence when a clone is completed. [*http://bbrp.llnl.gov/test-bin/projqcsummary*]
- Implementation of a new database to support sequencing and mapping work on multiple chromosomes and species. Web-based automated tools were developed to facilitate construction of this database, the loading of over 100 million bytes of chromosome 19 data from the existing LLNL database, and automated generation of Web-based input interfaces.
- Significant enhancement of the LLNL Genome Graphical Database Browser software to display and link information obtained at a subcosmid resolution from both restriction map hybridization and sequence feature data. Features, such as genes linked to diseases, allow tracking to fragments as small as 500 base pairs of DNA.
- Development of advanced microfabrication technologies to produce electrophoresis microchannels in large glass substrates for use in DNA sequencing.
- Installation of a new filter-spotting robot that routinely produces $6 \times 6 \times 384$ filters. A $16 \times 16 \times 384$ pattern has been achieved.
- Upgrade of the Lawrence Berkeley National Laboratory colony picker using a second computer so that imaging and picking can occur simultaneously.

Future Plans

Genomic sequencing currently is the dominant function of Livermore's Human Genome Center. The physical mapping effort will ensure an ample supply of sequence-ready clones. For sequencing targets on chromosome 19, this