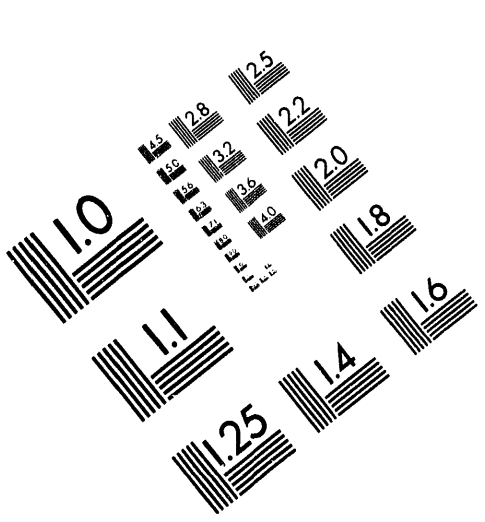

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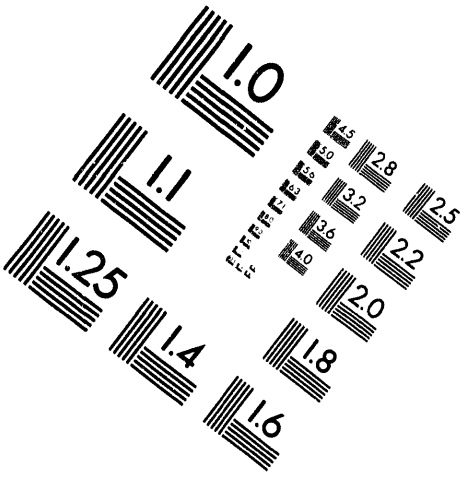

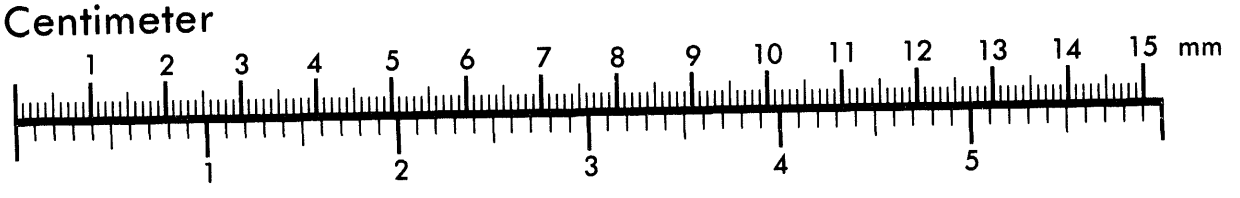

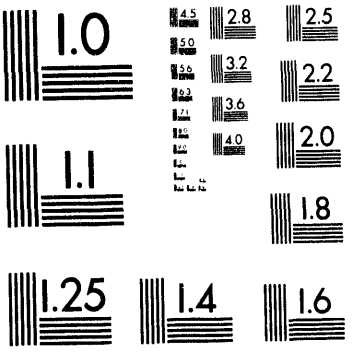

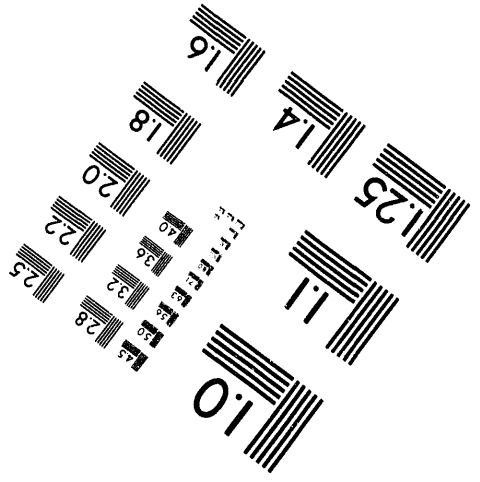

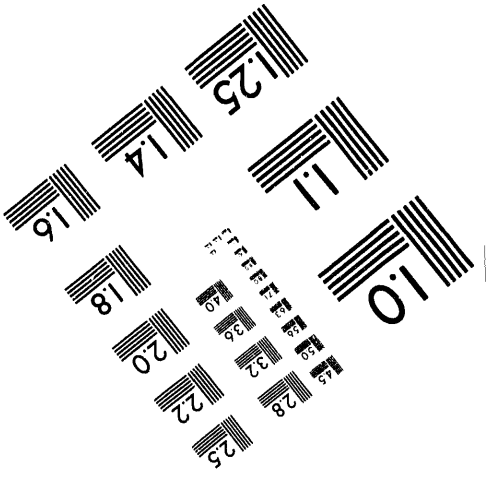

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CONF-9209464--Summ.

Genome Sequencing and Analysis Conference IV

J. Craig Venter (The Institute for Genomic Research—[TIGR]) and C. Thomas Caskey (Baylor) co-chaired Genome Sequencing and Analysis Conference IV held at Hilton Head, South Carolina from September 26-30, 1992. Venter opened the conference by noting that approximately 400 researchers from 16 nations were present—four times as many participants as at Genome Sequencing Conference I in 1989. Venter also introduced the Data Fair, a new component of the conference allowing exchange and on-site computer analysis of unpublished sequence data.

In his keynote speech, the Honorable Senator Pete Domenici (R—New Mexico), stated that "health care in America is undergoing revolutionary change as we speed toward the new century propelled by incredible research advances in biotechnology." Senator Domenici, author of the Technology Transfer Act of 1986 and a major supporter of the genome project from its inception, predicted that human genome research will provide the technology to create a nearly disease free society within 50 years.

Plenary Conference sessions largely focused on new sequencing results and technology development. George Church (Harvard), Doug Smith (Collaborative Research Inc.) and Robert Weiss (U. Utah) presented a substantial amount of data from *E. coli*, *M. leprae* and humans obtained by multiplex sequencing. These results prove that multiplexing is now a viable technique. Fred Blattner (U. Wisconsin), Karen Thomas (Medical Research Council) and Chris Martin (Lawrence Berkeley Laboratory) presented new genomic sequences from *E. coli*,

C. elegans and *Drosophila*. The *Drosophila* sequence, a 90 kb P1 insert from the *Bithorax* region, is the first sequencing result from the new *Drosophila* genome center.

Daniel Cohen (Centre D'Etudes Du Polymorphisme Humain) provided an update on whole-genome physical mapping using mega YACs. Mark Adams (TIGR), Charles Auffray (Génethon) and Kousaku Okubo (Osaka U.) discussed the approximately 13,000 human ESTs now available, many of which have been identified by sequence similarity. Lee Rowen (U. Washington), Richard Gibbs (Baylor) and Chris Fields (TIGR) demonstrated that sequencing and analysis of large regions of anonymous human DNA is now reasonably straightforward. Matches between ESTs and genomic sequences, several of which were found during the Data Fair, have identified new genes in bacteria, yeast, *C. elegans* and humans.

The technology development sessions presented new or improved methods for mapping, sequencing and functional characterization, many of which were expanded upon in the posters or workshops. Julie Korenberg (Cedars-Sinai Medical Center) described methods for single-band resolution fluorescence in-situ hybridization (FISH) and showed that this method could be used to map cDNA fragments less than one kilobase in length. F. William Studier (Brookhaven National Laboratory) presented new results showing that tandem hexamers could be used as primers for walking without ligation. Data from Edwin Southern (Oxford) and Mitch Eggers (Houston Advanced Research Center) made it clear that sequencing by hybridization (SBH) is nearing the stage where it will be a useful, and potentially very fast and inexpensive, method for fingerprinting cDNAs and

genomic fragments. Ronald Plasterk (Netherlands Cancer Center) described a collection of transposon-insertion mutants that make reverse genetics straightforward for many genes in *C. elegans*.

A total of 94 posters were presented in two afternoon sessions, covering new technologies, sequencing and mapping results, and informatics. Advances in automation of all stages of a sequencing project was a major theme of the poster sessions. Several groups demonstrated software packages for sequence analysis and project support at the Data Fair.

Workshops and discussion groups were popular afternoon and evening sessions. In an exceptionally well attended workshop chaired by Charles Cantor (Boston U.) and F. William Studier, scientists discussed new sequencing technologies, including multiplexing and hybridization using high-density filters. During the workshop chaired by Tony Kerlavage (TIGR) and Jean-Michel Claverie (NIH), participants presented database designs for tracking sequencing and mapping information from genomic and EST projects.

The Data Fair was a highlight of the conference. Scientists from the United States, Europe and Japan brought previously unpublished sequences for comparison and analysis on computers ranging from PCs to supercomputers. Data Fair participants analyzed approximately 20,000 EST sequences (6,200,000 nucleotides) from human brain, lymphocyte and liver, mouse testis, *C. elegans* and *P. falciparum*, and 438 kb of new genomic sequences from *D. melanogaster*, *C. elegans*, *M. leprae* and *E. coli*. Comparison of ESTs and genomic sequences identified several new genes, especially in *E.*

coli, providing further evidence that genome projects in all organisms will complement each other.

Beyond the number and types of matches found, Data Fair coordinator Tony Kerlavage cited "two other important results. First, scientists from around the world have been able to overcome the sociological barrier of bringing unpublished data to a public meeting and, second, the data, software and hardware generated much interest among the (Conference) attendees. This was truly a working meeting, with groups of scientists exploring new avenues of sequence analysis."

Reported by Alison Hay Tinsley, Science Writer
The Institute for Genomic Research

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