

RESEARCH NEWS

chromosomes—probably chromosome 21 and X chromosome—of the human genome.

Most of the sequencing of the yeast chromosome has been done 'by hand', and though hereafter automatic sequencing machines will undoubtedly be used, this gives hopes to Indian laboratories, which are not richly equipped, to participate in future sequencing programmes. On the other hand, these long sequences will have to be stored in computers and searched automatically. As Maddox points out in *Nature*, the sequence of the smallest of the yeast chromosomes would have occupied 45 pages of *Nature*.

The results of sequencing *C. elegans* genome and yeast chromosome reveal some unexpected information. With both there are more genes in the regions sequenced than had been expected. In

C. elegans, for example, the number of predicted genes in the three cosmids sequenced is higher than that would have been expected on the basis of genetic estimates of essential gene numbers and on a previous transcript analysis around the vitellogenin gene. The high gene density (one over 3–4 kb) may arise in part because the sample comes from the gene-rich cluster on chromosome 3. But each chromosome contains a central gene-rich cluster, and the physical map shows that about half the genome is contained in such clusters. Extrapolations indicate that *C. elegans* will have about 15,000 genes in the clusters alone. The other half of the DNA is not devoid of genes, but there is no accurate estimate of the gene density there.

Chromosome III of yeast is also replete with previously unknown genes,

or at least with open reading frames from which mRNA molecules can be transcribed when there are appropriately placed regulatory elements to turn them on. Indeed, the genetic map of the chromosome contained only 34 genes before the complete sequence was assembled, but now there are 182, not counting tRNA genes, transposable elements and genes with fewer than 300 bases. Allowing for a small handful of genes previously sequenced but not mapped, the result is that chromosome III has now 145 new genes, or that its gene content is five times greater than previously believed.

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Erratum

Seismotectonics of Himalaya

Umesh Chandra

(*Curr. Sci.*, 1992, 62, 40)

In Figure 1 on page 59, the boundary of the NW parts of India was wrongly indicated. The correct map is given below.

