-Applications and advances of sequencing technologies on human genome research

The landmark of sequencing of human genome was accomplished by two groups,the publicy funded Human Genome Group (HGP) and Celera Groups. Both groups utilized different strategies. The HGP group produced a working draft of the human genome by a map-based strategy, while Celera, to sequence the human genome by the whole – genome shotgun(WGS) approach . the availability of sequence material

Obtained through different approaches greatly facilitated the ability of the entire scientific community to interpret the data.

The strategy of HGP originally established by the publicly funded effort and was based on the localizing bacterial artificial

Chromosomes (BACs) containing large fragments of human DNA within the framework of a Landmark-based physical map.

Ideally, sequencing would have been done on a clone-by-clone

basis, with clones selected from the minimum BAC tiling path.

The key to the HGP's strategy was the subsequent "mapping"

Step in which the BACs were each positioned on the genome's

Chromosomes by looking for distinctive marker sequences, called sequence tagged sites (STSs), whose location had already been pinpointed. In this way, the BACs provided a high-resolution map of the entire genome. The working draft, although containing some gaps and ambigu-ities in order, is extremely useful in such efforts as identifying disease-associated genes. Simultaneously, the idealized start-egy of Celera was to avoid the up-front mapping phase by subcloning random fragments of the human genome directly. Sequencing of both ends of fragments in libraries of different sizes facilitated ordering. While saving time and effort at the beginning, the Celera approach made the assembly process much more dependent on algorithms and computer time. In their effort to reach their goals, the idealized strategies evolved into hybrids in which the HGP selected more clones arbitrarily

And Celera made use of BAC maps and sequence generated by the HGP.