Resolution Encyclopedia Article

Resolution

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Resolution

The amount or degree of detail that can be expressed on a physical genetic map of **DNA** is referred to as the resolution of the map or the resolution of study.

The greater the resolution on a physical map the more readily identifiable are the genetic elements designated on the map. Of course, such resolution reflects the precision of the studies used to characterize the section of DNA in question and of the ability of researchers to identify genetic landmarks (e.g., intergenic nitrogenous base sequences, genes, bands, markers, **cutting sites**, etc) within the region of interest.

The degree of resolution is often express in terms of base pairs (bp). The maximum resolution obtainable is the goal of the Human **Genome** Project--the complete and accurate **sequencing** of all the nucleotides comprising the human genome.

There are low and high resolution genetic maps (physical maps). Low resolution chromosomal maps carry an average resolution of about 10-12 Mb (1 MB =1,000,000 base pairs). The resolution may be increased depending on the tightness of DNA binding. Accordingly, DNA extracted from loose chromatin-like chromosomal DNA at interphase may be resolve down to 100,000 to 200,000 base pairs.

Higher resolution maps (e.g., connoting and macrorestriction maps) can be generated using restriction **enzymes**, **polymerase chain reaction** (PCR), and **protein electrophoresis** techniques. With macrorestriction maps (top- down mapping) **restriction enzymes** cut chromosomes into large pieces a single **chromosome** is cut (with rare- cutter restriction enzymes) into large pieces, which are ordered, further subdivided, and studied often yield resolutions of 100,000 bp to 1Mb. Contig maps (bottom-up maps) result from the cutting of chromosomes that are then cloned and ordered into contiguous blocks (hence a contig map). Such contig maps provide higher resolution usually from 1Mb down to 10,000 bp.