30 nm Chromatin fibre Structure -

Electron microscopic studies of chromatin fibres in interphase nuclei and mitotic chromosomes have revealed a thick fibril of a diameter that ~~revealed~~ varies from 20 to 30 nm and which probably represents the structure of inactive chromatin. The 20 or 30 nm fibril consist of closely packed nucleosomes.

The 20 nm to 30 nm fiber arises from the folding of the nucleosomes chain into a solenoidal structure having six nucleosomes per turn. The histone H1 is located in the central hole of the solenoid, and the whole structure is stabilized by interactions between different H1 molecules. DNA of a 30 nm fibre has a packing that is about 40 fold. However in metaphase stage it is packed between 5000 and 10,000 times.

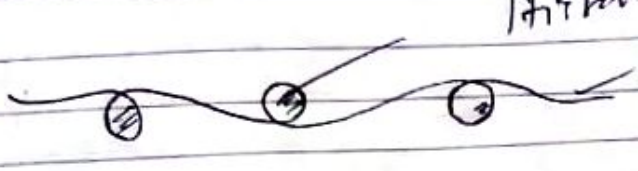
With addition of H1, the beads on a string structure in turn will into a 30 nm diameter helical structure known as a 30 nm fibre or filament. The Precise structure of the chromatin fibre in the cell is not known in detail, and there is still some debate over this.

This level of chromatin structure is thought to be the form of heterochromatin which contains mostly transcriptionally silent genes. Electron microscopic studies have demonstrated that the 30 nm fibre is highly dynamic such that it unfolds into a 10 nm fibre (beads on a string structure) when traversed by an RNA Polymerase engages in transcription.

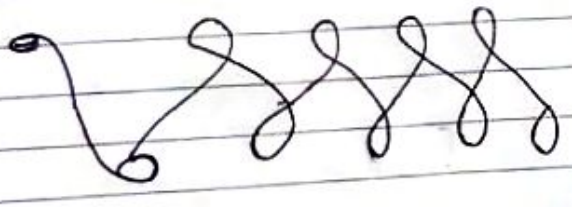
The existing models commonly accept that the nucleosome lie perpendicular to the axis of the fibre with linker histones arranged internally. A stable 30 nm fibre relies on a regular positioning of nucleosome along DNA. Linker DNA is relatively resistant to bending and rotation. This makes the length of linker DNA critical to the stability of the fibre requiring nucleosomes to be seperated by lengths that permit rotation and folding into the required orientation with excessive stress to the DNA. In this view different lengths of linker DNA should produce different folding topologies of chromatin fibre.

Chromatin undergoes various structural changes during a cell cycle Histone proteins are the basic packer and arranger of chromatin and can be modified by various post translational modifications to alter chromatin packing (Histone modification) Most of the modifications occur on the histone tail. The consequences in terms of chromatin accessibility and compaction depend both on the amino acid that is modified and the type of modification. For example, Histone acetylation results in loosening and increased accessibility of chromatin for replication and transcription. Lysine 9- methylation can either be correlated with transcriptional activity and chromatin compaction.

Polycomb group proteins play a role in regulating genes through modulation of chromatin structure.



Beads on a string nucleosome structure.



Basic units of chromatin fibre.

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