The 30 nm filament: facts, fictions and speculations

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The story of the low resolution structure of chromatin is a long one marked by quite unnecessary controversies, which are essentially based on speculations and an infelicitous choice of words for the description of what is a structure with short range order constrained by the fibrous nature of the material. This situation results from the absence of reliable high resolution imaging methods for native non-crystalline biological materials.

During the past decade progress in atomic force microscopy [1] and cryoelectron microscopy [2] have largely confirmed previous studies on the folding of the uncondensed fiber at low ionic strength where X-ray and neutron scattering played a significant role. Most of the different models, which still existed at the end of the eighties have been abandoned and the remaining ones fall into two broad classes: solenoids and models where the linker crosses the central part of the fiber (for reviews see [3-6]).

Some of the more recent indirect experimental and theoretical evidence in favor of one or the other class of models will be critically reviewed.

These recent developments and the high resolution structure of the nucleosome [7] have, however, not sufficed to unambiguously determine the path of the linker in isolated chromatin fibers, nor allowed to clearly establish the relationship between the structures in vivo and in vitro.

Recent suggestions that the 30 nm fiber may have a physiological significance other than the packing of untranscribed DNA, have produced a rebound in interest for the path of the linker. Whether X-rays can be useful in solving the problem remains as much an open question as the path of the linker itself.

References

[1] - J. Zlatanova, S.H. Leuba, G. Yang, C. Bustamante, K. Van Holde, Proc. Natl. Acad. Sci. USA 91, 5277-5280 (1994)

[2] - J. Bednar, R.A. Horowitz, S. Grigoryev, L.M. Carruthers, J.C. Hansen, A.J. Koster, C.L. Woodcock, Proc. Natl. Acad. Sci. USA 95, 14173-14178 (1998)

[3] - M.H.J. Koch The structure of chromatin and its condensation mechanism in Protein-Nucleic Acid Interaction. Eds U. Heinemann and W. Saenger. McMillan: London pp 163-204 (1989)

- [4] V. Ramakrishan, Annu. Rev. Biophys. Biomol. Struct. 26, 83-112 (1997)
- [5] J. Widom, Annu. Rev. Biophys. Biomol. Struct. 27, 285-327 (1998)
- [6] J.C. Hansen, Annu Rev Biophys Biomol Struct 31, 361-392 (2002)

[7] - C.A. Davey, D.F. Sargent, K. Luger, A.W. Maeder, T.J. Richmond, J. Mol. Biol. 319, 1097-1113 (2002)