Chromatin dynamics resolved with force spectroscopy

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Propositions

accompanying the thesis
"Chromatin dynamics resolved with force spectroscopy"
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1. A fully folded chromatin fiber, representing the first level of chromatin condensation, behaves like a Hookean spring.
   [*Chapter 2 of this thesis.*]

2. The difference in stiffness between chromatin fibers with a linker length of 20 base pairs and chromatin fibers with a linker length of 50 base pairs reflects the difference between a solenoid and a zigzag structure.
   [*Chapter 2 of this thesis.*]

3. The plateau in the force-extension relation of chromatin fibers that is observed between 3 and 4 piconewton indicates the exposure of both the linker DNA and the first turn of nucleosomal DNA.
   [*Chapter 3 of this thesis.*]

4. Nucleosome unstacking and DNA unwrapping cannot be distinguished in force spectroscopy experiments on chromatin fibers; this may indicate that some of the nucleosomal DNA is permanently unwrapped in the folded fiber.
   [*Chapter 3 of this thesis.*]

5. The lifetime of the open state, which represents an unstacked and partially unwrapped nucleosome, increases by six orders of magnitude when a small force of 4 piconewton is applied.
   [*Chapter 4 of this thesis.*]

6. Purified chromatin fibers are too heterogeneous to determine the strength of nucleosome-nucleosome interactions and to gain a detailed understanding of the mechanical properties of chromatin fibers.
   [Cui and Bustamante *Proc. Natl. Acad. Sci. U.S.A.* **97**: 127–132 (2000)]

7. A better control of buffer conditions during the manipulation of chromatin fibers *in vitro* is required to fully understand the compaction of genomic DNA *in vivo*.
   [Claudet *et al. J. Biol. Chem.* **280**: 19958–19965 (2005) and Cui and Bustamante *Proc. Natl. Acad. Sci. U.S.A.* **97**: 127–132 (2000)]

8. A physical characterization of the dynamics of mononucleosomes under torsional stress is required to interpret the structural plasticity of torsionally constrained chromatin fibers.
   [Bancaud *et al. Nat. Struct. Mol. Biol.* **13**: 444–450 (2006)]

9. The mechanism of nucleosome remodeling enzymes is more complex than what single-molecule measurements on bare DNA have revealed.
   [Lia *et al. Mol. Cell* **21**: 417–425 (2006) and Zhang *et al. Mol. Cell* **24**: 559–568 (2006)]