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The centers of premeltons signal the beginning and ends of genes

Premeltons are examples of emergent structures (i.e. structural solitons) that arise spontaneously in DNA due to the presence of non-linear excitations in its structure. They are of two kinds, B-B or A-A premeltons form at specific DNA-regions to nucleate site-specific DNA melting. These are stationary and being globally non-topological, undergo breather motions that allow drugs and dyes to intercalate into DNA. B-A or A-B premeltons, on the other hand, are mobile and being globally topological, act as phase-boundaries transforming B- into A- DNA during the structural phase-transition. They are not expected to undergo breather-motions. A key feature of both types of premeltons is the presence of an intermediate structural-form in their central regions (proposed as being a transition-state intermediate in DNA-melting and in the B- to A- transition), which differs from either A- or B- DNA. Called beta-DNA, this is both metastable and hyperflexible-and contains an alternating sugar-puckering pattern along the polymer-backbone combined with the partial-unstacking (in its lower energy-forms) of every other base-pair. Beta-DNA is connected to either B- or to A- DNA on either side by boundaries possessing a gradation of non-linear structural-change, these being called the kink and the antikink regions. The presence of premeltons in DNA leads to a unifying theory to understand much of DNA physical-chemistry and molecular-biology. Premeltons are predicted to define the 5' and 3' ends of genes in naked-DNA and DNA in active chromatin, this having important implications for understanding physical aspects of the initiation, elongation and termination of RNA synthesis during transcription. For these and other reasons, the model will be of broader interest to the general audience working in these areas. The model explains a wide variety of data and carries within it several experimental predictions all readily testable as will be described.

Biography

Henry M Sobell has completed his studies at Brooklyn Technical High School, Columbia College and the University of Virginia School of Medicine. He went to the Massachusetts Institute of Technology (MIT) to join Professor Alexander Rich in the Department of Biology where, as a Helen Hay Whitney Postdoctoral Fellow, he learned the technique of single crystal X-ray analysis. He has then joined the Chemistry Department at the University of Rochester, having been subsequently jointly appointed to both the Chemistry and Molecular Biophysics departments becoming a full tenured Professor in both departments.

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