Abstract

With almost no consensus promoter sequence in prokaryotes, recruitment of RNA polymerase (RNAP) to precise transcriptional start sites (TSSs) has remained an unsolved puzzle. Uncovering the underlying mechanism is critical for understanding the principle of gene regulation. We attempted to search the hidden code in ~16500 promoters, of twelve prokaryotes representing two kingdoms, in their structure and energetics. Twenty eight fundamental parameters of DNA structure including backbone angles, base pair axis, inter base pair and intra base pair parameters were used and information was extracted from X-ray crystallography (XRC) data. Three parameters (solvation energy, hydrogen bond energy and stacking energy) were selected for creating energetics profiles using in-house programs. DNA was found to be inherently designed to undergo a change in every parameter undertaken, from some distance upstream of TSSs to adopt a signature state at these locations in all prokaryotes. These signature states might be the universal hidden codes recognised by RNAP. This observation was reiterated when randomly selected promoter sequences (with little sequence conservation) were subjected to structure generation; all developed into very similar three dimensional structures, quite distinct from those of conventional B-DNA and coding sequences. Fine structural details at important motifs (viz. -11, -35, -75 positions relative to TSS) of promoters reveal novel and pointed insights for RNAP interaction at these locations; it could be correlated that how some particular structural changes at -11 region may allow insertion of RNAP amino acids in inter-base pair space as well as facilitate the flipping out of bases from DNA duplex.