

High affinity binding of proteins HMG1 and HMG2 to semicatenated DNA loops

ABSTRACT

Our research has revealed that Form X, which is a DNA loop with semicatenated DNA junction at its base, has the highest affinity among all known DNA structures. This implies that if these structures are present in the cell nucleus, one of their functions may be related to the unique yet reversible property of DNA chaperones, specifically for linking two remote regions of the genome.

INTRODUCTION

'In this work, we have developed a novel approach to the direct binding of HMG1 and HMG2 to DNA by using the HMG1-HMG2 heterodimer in a DNA-binding assay'.

The HMG1-HMG2 heterodimer is a protein-protein complex containing the HMG1 and HMG2 subunits, and is responsible for the binding of the HMG1 subunit to the DNA of the *S. cerevisiae* genome. The HMG1-HMG2 heterodimer is also present in the host genome, and is a major determinant of the host's susceptibility to infection with *H. pylori*.

'We have developed a novel approach to the direct binding of HMG1 and HMG2 to DNA by HMG1 and HMG2, two of the most prevalent non histone proteins, are known for their homology with many other proteins that play a role in development or differentiation. Recent research has focused on their molecular partners and their interactions with various other DNA types, including flattening of nuclear complexes, assembly of complex structures, and the identification of molecular sites. During our study of CA microsatellites, we discovered that a protein present in nuclear extracts of cultured monkey cells formed specific delayed complexes with PCR-poly(CA) Poly(TG) sequence. Two proteins, HMG1 and HMG2, were identified as the proteins responsible for this process (Fig. 1A), and the DNA-binding activity was found to be lower than that of the regular double-stranded fragment ("Form X"), which has been identified by scientists as having semicatenated DNA loops. The interactions between HMG1/2 and Form X were investigated, and it was discovered that these proteins bind more strongly to semicatenated DNA junctions than any other known DNA substrate.'

CONCLUSION

Remarkable conclusions We have identified Form X, a DNA loop with essentially the same semicatenated DNA junction at its base as one of the few known examples of such interacting DNA. This suggests that higher order chromatin structures may exist within the cell nucleus and that the HMG domain is likely to play clerical or structural roles in this process.