

## Elastic Deformation Patterns of Microsatellite DNA Sequences

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### Abstract

In DNA sequences, regions where 3-5 nucleotide repeats themselves is often found in the non-coding areas. These sequences are called microsatellites (MS). Recent studies attribute the presence of MS to diverse diseases. Using Molecular Dynamics simulations, we studied how specific MS affect the DNA mechanical properties. Our results show that the presence of MS tend to make the DNA 'softer' to mechanical elongation. Further studies are needed to clarify the biological implications of this behavior.

### Key words:

Deoxyribonucleic Acid, Microsatellites, Molecular Dynamics.

### Introduction

DNA is a macromolecule composed of long chains of nucleotides. Nucleotides consist of 3 functional groups: a phosphate, a sugar molecule and a nitrogenized base. The information in the DNA is represented by 4 different bases: adenine (A), cytosine (C), thymine (T) and guanine (G), with the constraint that A can only be paired with T and C with G.

It is known that in certain areas of the DNA occurs the repetition of 2-5 base pairs. These sections are called microsatellites and recent studies show [1] that their presence correlates to certain diseases and increase in severity or earlier age of manifestation after each generation.

In this work we created a 1800 base pair long random DNA sequence, and used it to compare its properties with other DNA sequences. By changing the order of the base pairs, but having the same total number of bases, we created different MS sequences, from 5 up to 200 repetitions. The used repetitions were AAG, CAG and CGG.

We investigated through fully atomistic molecular dynamics the elastic behavior of different MS sequences while being stretched with constant force.

### Results and Discussion

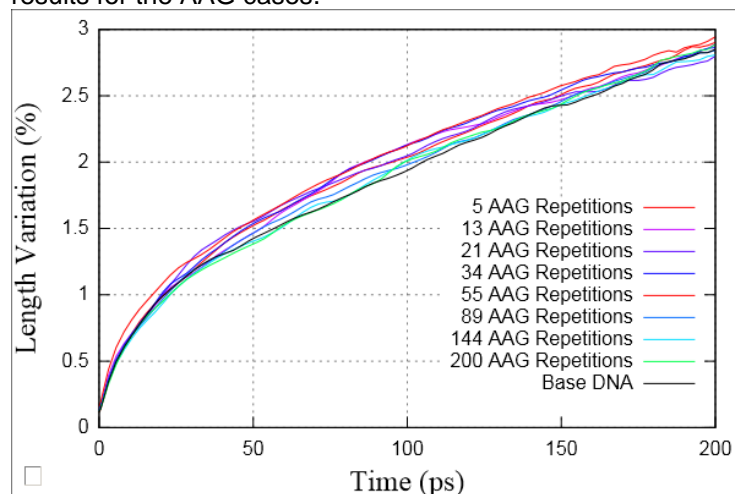
This study was divided into 2 parts. The first one was to minimize the DNA sequences and contrast their energy against random sequences (Table 1).

**Table 1** – Minimized total energy (kcal/mol) of different sizes and type of the MS compared a reference sequence.

MS Size	AAG	CAG	CGG
5	-6	-6	-29
8	-15	-24	-30
13	13	40	-48
21	9	31	-42
34	27	120	45
55	1	174	67
89	-8	333	118
144	-105	637	306
200	-176	887	389

The energy reference configuration was a random DNA sequence. As we can see from the table, some configurations increase the mechanical stability while others have the opposite effect, without a clear pattern.

In the second part of the study we stretched the DNA structures during 200 ps and analyzed their elastic behavior. The MD simulations were carried out using the well-known NAMD [2] code. In Figure 1 we present the results for the AAG cases.



**Figure 1** – DNA length variation (%) as a function of the MD simulation time while been stretched by a constant force.

### Conclusions

Our results show that the general trends of the MS presence are to make the DNA 'softer' to elastic elongations, although this is not a common feature for all configurations and also it does not happen for all the length variation percentages. Further studies are needed to clarify the biological implications of this behavior.

### Acknowledgement

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[1] R. D. Wells, J. Biol. Chem. 271, 2875 (1996).  
 [2] S. Plimpton, J. Comp. Phys. 117, 1 (1995).