Dynamics of siRNAs: Comparison of Force Fields Reliability

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INTRODUCTION: Nucleic acids, including DNA (deoxyribonucleic acid) and RNA (ribonucleic acid), are central molecules in the transmission, expression, and conservation of genetic information. Among this class of molecules are small interfering RNA (siRNA), small pieces of double-stranded RNA functioning to silence the expression of specific genes at the post-transcriptional level by a pathway known as RNA interference. While such molecules constitute an important target for several proteins and drugs, their computational simulations are still impaired by the reliability of the available force fields. In this context, the current work intends to compare AMBER, CHARMM and GROMOS force fields on the conformation and structure description of siRNAs under molecular dynamics simulations.

MATERIAL AND METHODS: The simulations employed GROMACS package with AMBER 99sb-ildn, CHARMM 27 and GROMOS 53a6 force fields for comparison. Both unbounded, protein bounded siRNAs were selected for simulations under TIP3P and SPC water models.

RESULTS AND DISCUSSION: Analyzing the main parameters of nucleic acids structure and conformation in AMBER and CHARMM force fields, such as propeller, opening, tilt, and roll both force fields were observed to behave similarity to the expected parameters, previously established in the literature. CONCLUSIONS: So, these data could indicate a reliability of force fields AMBER and CHARMM for simulation of DNA and RNA, supporting a precise conformational and structural characterization of these molecules in solution. On the other hand, the GROMOS force field shows many problems with conformation and structure of siRNA such as opening of double-stranded and loss of base pairing indicating a force field not reliable for simulation of nucleic acids.

Keys Words: nucleic acids, siRNA, DNA, force fields, molecular dynamics
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