On Periodicity of Adenine-Adenine Dinucleotides in Bacterial Genomes

Masahiko Wada [12] **Yukihiro Kawashima** [13] **Masaru Tomita** [13]
wadari@sfc.keio.ac.jp t95270yk@sfc.keio.ac.jp mt@sfc.keio.ac.jp

[1] Laboratory for Bioinformatics
[2] Graduate School of Media and Governance
[3] Department of Environmental Information
Keio University, 5322 Endo, Fujisawa, 252 Japan

1 Introduction

Computer analyses of various bacterial genome sequences revealed that there exist certain periodical patterns of adenine-adenine dinucleotides (ApA). For each ApA dinucleotides in the genome sequences, we counted other ApA's at each downstream position within 100bps, in order to detect positional correlations of ApA frequencies.

2 Results

We found that the complete genomes of three archaebacteria, *Archaeoglobus fulgidus*, *Methanococcus jannaschii*, and *Methanobacterium thermoautotrophicum*, have the ApA periodicity of about 10bps (Fig. 1). Four eubacteria, *Mycoplasma genitalium*, *Helicobacter pylori*, *Synechocystis* sp. and *Haemophilus influenzae*, on the other hand, are found to have the ApA periodicity of about 11bps (Fig. 2). Three other eubacteria, *Escherichia coli*, *Bacillus subtilis*, and *Treponema pallidum*, show weaker periodic pattern (Fig. 3). Both coding and non-coding regions show the periodic patterns (Fig. 4).

3 Discussion

Nucleosome sequences of prokaryote Chicken are known to have ApA periodicity of about 10.15bps [1] and it is believed to be due to DNA bending pattern for the formation of the nucleosome structure. However, our results with the bacterial genomes show the similar periodic patterns, indicating that the ApA periodicity might contribute to the bending of prokaryotic chromosomes.

Acknowledgements

This work is supported in part by a Grant-in-Aid for Scientific Research on Priority Areas, "Genome Informatics", from The Ministry of Education, Science, Sports and Culture in Japan.

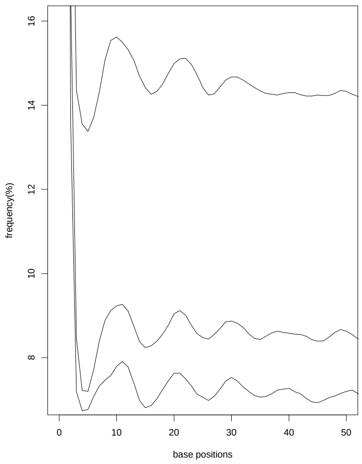

Figure 1

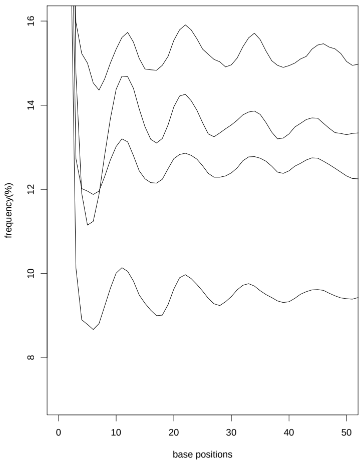

Figure 2

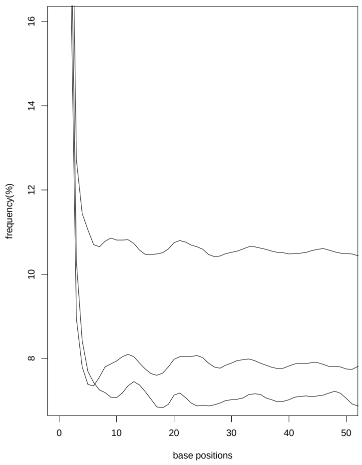

Figure 3

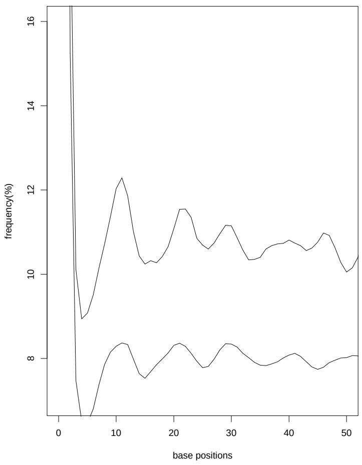

Figure 4

Figure 1: *Archaeoglobus fulgidus*, *Methanococcus jannaschii*, and *Methanobacterium thermoautotrophicum* (from top to bottom).
Figure 2: *Mycoplasma genitalium*, *Helicobacter pylori*, *Synechocystis* sp. and *Haemophilus influenzae* (from top to bottom).
Figure 3: *Escherichia coli*, *Bacillus subtilis*, and *Treponema pallidum* (from top to bottom).
Figure 4: Non-coding region (top) , Coding region (bottom) (*Archaeoglobus fulgidus*).

References

[1] Bolshoy, A., Shapiro, K., Trifonov, E.N., and Ioshikhes, I., Enhancement of the nucleosomal pattern in sequences of lower complexity, *Nucleic Acid Res.*, 25:3248–3254, 1997.