Noda Institute for Scientific Research GRANT
2012 Research Grant

Study of *Aspergillus* nucleosome positioning

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Research aims

Eukaryotic genomic DNA is packaged with histones to form chromatin. The most fundamental repeating unit of chromatin is the nucleosome. Nucleosome positioning is not only related to genomic DNA compaction but also to other biological functions, such as gene transcription.

Nucleosome positioning differs even among phylogenetically close ascomycetous yeasts.[1] To date, fungal nucleosome positioning data has been reported only for ascomycetous yeasts. Thus, we sequenced and mapped the pair ends of nucleosomal DNA fragments of the filamentous ascomycete *Aspergillus fumigatus*.[2]

It has been reported that the GC content of the exons is higher than that of the introns in the genes of *Arabidopsis thaliana*, *Homo sapiens*, and *Oryza sativa*.[3] In addition, GC content and nucleosome positioning are related to the structure of the exons and introns.[4]

In this study, we mapped the *Aspergillus nidulans* and *A. oryzae* nucleosomal DNA fragments and compared the nucleosome density in the exons and introns of their genes.

Methods

A. nidulans A4 and *A. oryzae* RIB40 were used in this study. Micrococcal nuclease digestions were performed, and the resulting cleavage products were analyzed using agarose gel electrophoresis. The nucleosomal DNA fragments were excised from the gel. Both ends (each 101 bp long) of the DNA fragments were sequenced using an Illumina GAIIx, and only the uniquely mapped read-pairs were used in the subsequent analyses. The midpoint of the region mapped in each nucleosomal DNA fragment was used as the nucleosome position. In this study, nucleosome density is defined as the number of the nucleosome positions per exon or intron.

Results

We examined the positions of 36,871,528 and 43,690,293 nucleosomes in the genomes of *A. nidulans* and *A. oryzae*, respectively. The means of the exon GC content in the *A. nidulans* and *A. oryzae* genomes were 51.6% (sd=5.33) and 50.0% (sd=5.21), respectively. The means of the intron GC content in the *A. nidulans* and *A. oryzae* genomes were 46.6% (sd=6.54) and 44.3% (sd=5.92), respectively. Figure 1 shows scatter plots of GC content vs. nucleosome density for the protein-coding regions in the genomes of *A. nidulans* and *A. oryzae*, comparing 9,616 orthologous genes from *A. nidulans* and *A. oryzae*. The Spearman's rank correlation coefficient was 0.084 for *A. nidulans* and 0.15 for *A. oryzae*. Figure 2 shows scatter plots comparing the genomes of *A. nidulans* and *A. oryzae* with respect to the GC content of protein-coding regions and exon nucleosome density. The Spearman's rank correlation coefficient was 0.51 for GC content and 0.31 for nucleosome density.

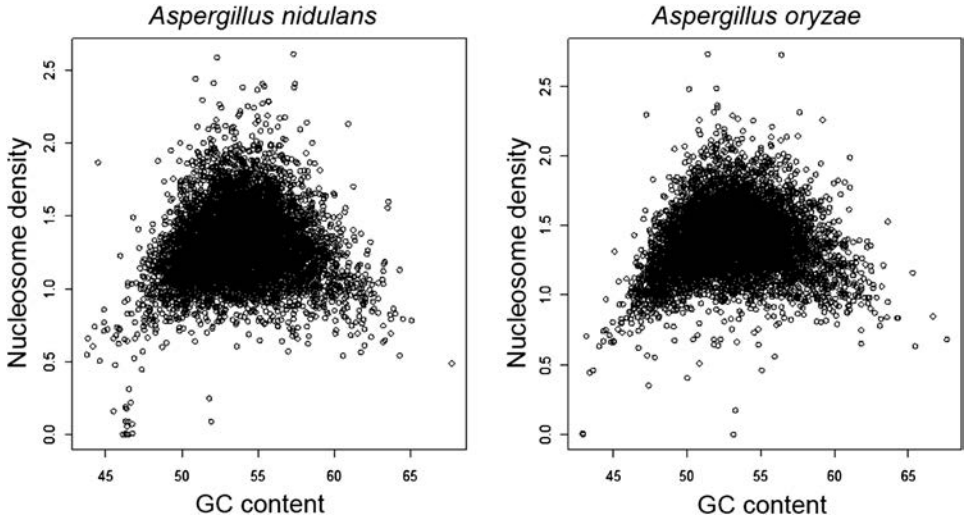

Fig. 1. Scatter plots of the GC content vs. nucleosome density of protein-coding regions in orthologous genes of *A. nidulans* and *A. oryzae*.

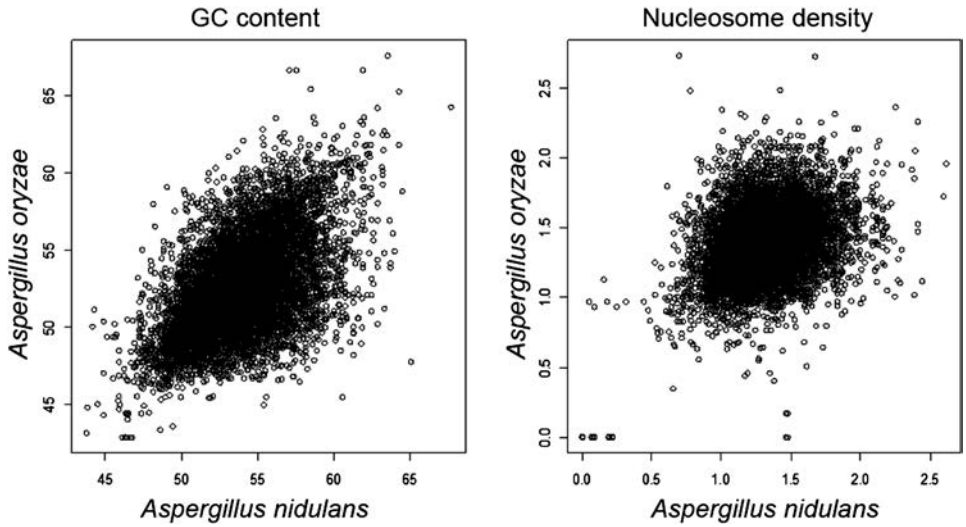

Fig. 2. Scatter plots of the GC content of protein-coding regions and the nucleosome density in exons in *A. nidulans* vs. those in *A. oryzae*.

Conclusion

The highest nucleosome density in the *A. nidulans* and *A. oryzae* genomes was found to be in areas with a GC content of 54%. The GC content and nucleosome density in exons are higher than in introns. However, the conservation level of the GC content is higher than that of the nucleosome density in the exons, suggesting that the variation in the location of the nucleosome may be species-specific.

References

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