

THESIS INFORMATION

Title: STUDY ON THE DNA OLIGOMER ARRANGEMENT IN THE BACTERIAL AND YEAST CHROMOSOMES

Major: Biotechnology

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Abstract:

Aims to get deep knowledge about the distribution of nucleotides in the chromosomes of bacteria and yeast, and to establish a method for classifying the closely related bacteria below genus level, this thesis has made two main research contents, as follows:

Content 1: Study on the oligomer arrangement in the bacterial and yeast chromosomes. Initial study includes the investigation on the relationship between the oligomer size and the chromosomal strand symmetry, the consideration of the monomer asymmetry of local sequences in the chromosome, and the determination of the presence of individual oligomers along the length of the single strand of chromosomal DNA molecules. The results showed that the larger the oligomer size, the less symmetric the chromosomes were, and that while the whole chromosome was symmetric, the local sequences of the chromosomes were asymmetric. At the chromosomal level, the distribution of oligomers and their respective reverse complements in the sequences that carried the information to encode proteins and that in the protein non-coding sequences contributed equivalently to the chromosomal strand symmetry. In the sequences carrying information for encoding the proteins, the trimers were distributed according to a rule that exhibited the equivalence in their frequencies on the basis of the position of the nucleotides in a codon and thus shaping the codon usage, contributing to the chromosomal strand symmetry. Deeper investigation results showed that the distribution of the codon encoding trimers in the sense sequences of

each chromosome had a very close relationship with that in the antisense sequences. The distribution of codon encoding trimers in the sense and antisense sequences along the length of the bacterial chromosomes on the basis of this relationship clearly shaped two replichores. Densities of codon encoding trimers in the sense and antisense sequences on the replichores of the bacterial chromosome showed that the codon encoding trimers and their respective reverse complements on the basis of this relationship were distributed in the sense and antisense sequences to balance the two replichores, thus contributing to the bacterial chromosomal strand symmetry. In the protein non-coding sequences, the distribution of trimers was different in comparison with that in the sequences that carried the information for encoding the proteins.

Content 2: Based on the species-specificity of the codon usage shaped by the trimer arrangement in the sequences that carried the information for encoding the proteins at the chromosomal level, the species-specificity of the trimer densities in genomes was determined and was applied in the classification of closely related bacteria belonging to the *Enterobacteriaceae*, *Burkholderiaceae* and *Pseudomonadaceae* families. The results of this research content showed that the trimer densities in genomes could be used to classify the bacteria below genus level.

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