Séminaire

CONFÉRENCIER INTERNE

Vendredi 20 Mai 2022 à 11h

Salle des séminaires

Institut de biologie structurale - 71 avenue des Martyrs CS 10090 38044 Grenoble Cedex 9 - T.+33 (0)4 57 42 85 00

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Structural basis for the origin and evolution of the genetic code

The genetic code (GC) was deciphered in 1966 by Nirenberg and co-workers. These authors found that the four DNA nucleobases, A, T, C, G, were combined in three-letter words (codons) generating 64 (4^3) codes for the 20 amino acids. Each gene in the DNA molecule contains a series of codons that are transcribed into a corresponding messenger RNA molecule. Other nucleic acid molecules called transfer RNAs are adaptors, each specifically charged with one of the 20 amino acids. These tRNAs also carry a three-letter code, called anticodon, that is complementary to the corresponding codon. Charged tRNA molecules and the mRNA bind to the ribosome active site where the former use their anticodons to bind to the corresponding codons of the latter. In this way amino acids are sequentially added to a nascent peptide chain and a protein is synthetized. The obvious question after the GC elucidation was whether there was a chemical connection between a given amino acid and its codon or anticodon. Francis Crick, one of the discoverers of the DNA double helix, believed that the GC was a “frozen accident” and that there was no relationship between a codon and its amino acid. However, both SELEX oligonucleotide directed evolution and the crystal structure of the ribosome have shown that bulky amino acid side chains can preferentially bind to their anticodons. Based on this observation many authors think that the GC evolved through “template”-based interactions between peptides and oligonucleotides. The evolution of tRNAs and the analysis of their 3D structures have also shed significant light on the origin of the GC. Still, there is no consensus on this subject. These issues will be discussed during the seminar.

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