特別講演

High brilliance synchrotron radiation and origin of life

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Constant development of macromolecular crystallography by synchrotron radiation enabled the determination of the high resolution structure of the ribosome, the universal cellular machine that translates the genetic code into proteins in all organisms with high efficiency. They posses spectacular architecture accompanied by inherent mobility that allow for their smooth performance

The ribosome's active site, resides within a highly conserved symmetrical region, and is composed solely of ribosomal RNA. Structural analysis supported by comprehensive mutagenesis and quantum mechanical calculations, led to the identification of an internal architectural element that facilitates the ribosome's main catalytic function: peptide bond formation and amino acid polymerization. This architectural element guides the motions required for poly peptide elongation, for the succession of this reaction and for the direction of the nascent protein into its exit tunnel.

The universality of the symmetrical region implies its existence irrespective of environmental conditions. Hence, this region appears to be the remnant of the ancient version of a biosynthetic machine, the proto-ribosome. The stunning architecture of this region and its dynamic properties enable all activities involved in non-coded peptide bond formation and the production of short oligopeptides. A substantial increase in catalytic performance of the proto-ribosome and the eventual progress towards programmed decoding seem to result from further mutagenesis. The inclusion of peripheral elements, some of which could be the products of the non-coded amino acid polymerization, followed. These ideas are consistent with results of structural analysis performed independently elsewhere, based on categorizing the nature of interactions within the contemporary ribosome. Supporting experimental results alongside conceptual issues will be presented.