Decoding the genetic information on the riboosme at close to atomic resolution. A. Yonath. *Weizmann Inst. Rehovot and Max Planck Research Unit, Hamburg.*
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Ribosomes are the universal ribonucleoprotein organelles performing the translation of the genetic code into proteins. The ribosomes are built of two subunits that associate upon the initiation of protein biosynthesis. The large subunit ctalyzes the foramtion of the peptide bond and protects the newly born proteins. The small subunit is involved in the initiation of the process, controls its fidelity, provides the decoding site and govern the mRNA and tRNA translocation.

Crystallography of ribosomes met with severe technical and conceptual difficulties, owing to their large size (mw of 2.3 million daltons in bacterial ribosomes), their complex structurure (58 proteins and three RNA chains of 4500 nucleotides), the lack of internal symmetry, their high inherent flexibility, their weak diffraction power and their extreme beam sensitivity. Nevertheless, gradual improvement of crystal quality, the implementation of cryo-bio-crystallography and the stabilization of the riboosmal particles by functional or chemical means, led to crystals diffracting to relatively high resolution.

Over 1400, of the total 1518 nucleotides, were traced in the 3.6 A MIRAS map of the small ribosomal subunit. All the proteins of this particle were localized, some of which by heavy atom markers bound to their exposed cysteines prior to crystallization. Most of them were traced fully or partially.

The image emerged shows that the small ribosomal subunit is of a precisely engineered machine, capable of transmitting information over long distances in order to create a defined sequence of events at the decoding center. It indicates that the decoding of the genetic information is accomplished solely by ribosomal RNA and that the ribosomal proteins are essential for maintaining the correct conformation and for directing the progression of the mRNA chain.

A latch-like connection at the entrance of the mRNA channel enables accurate mRNA threading and provides the special geometry that guarantees processivity and ensures fidelity. Ratchet-like mechanism controls the directionality of the mRNA progession and head-platform correlated movements facilitates the tRNA/mRNA co-translocation.

Docking of an mRNA chain together with three tRNA moleculares, led to a striking fit between the outer contour of the decoding center and the mRNA chain, inducig a double-kink conformation that facilitates simultaneous binding of two acylated tRNA molecules. A heavily mercurated mRNA analouge, contaning the trigger sequence and co-crystlas with antibiotics that bind specifically to the decoding center, illuminated the path taken by the mRNA once being translated. Co-crystals with initiation factor 3 indicate its location and its possible contribution to the formation of the initiation complex.

Notes