INVITED SPEAKER

TRANSLATION INITIATION IN ARCHAEA

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Translation initiation (TI) allows accurate selection of the initiation codon on a messenger RNA (mRNA) and defines the reading frame. In all domains of life, translation initiation generally occurs within a macromolecular complex made up of the small ribosomal subunit, the mRNA, a specialized methionylated initiator tRNA, and translation initiation factors (IFs). Once the start codon is selected at the P site of the ribosome and the large subunit is associated, the IFs are released and a ribosome competent for elongation is formed. However, even if the general principles are the same in the three domains of life, the molecular mechanisms are different in bacteria, eukaryotes, and archaea and may also vary depending on the mRNA.

In archaea, there is no long-range scanning because mRNAs have Shine-Dalgarno sequences or very short 5' UTR. However, genomic analyses have shown that initiation factors homologous to their eukaryotic counterparts, aIF1, aIF1A, aIF2 and aIF5B are found. Using biochemistry, X-ray crystallography and cryo-EM, we previously studied two steps illustrating start codon selection in the Archaea Pyrococcus abyssi. Recently, we determined the cryo-EM structure of the 30S:mRNA:aIF5B-GDPNP-tRNA:aIF1A complex at 3 Å resolution. This complex corresponds to the last step of translation initiation on the small ribosomal subunit. The structure highlights for the first time the interaction of aIF5B with the initiator tRNA on the small ribosomal subunit and shows how aIF5B interacts with aIF1A. All available data allow us to understand how the initiator tRNA goes from aIF2 to aIF5B and how the large ribosomal subunit is recruited.

Because, the late steps of translation initiation are controlled by initiation factors conserved in the three domains of life, IF1-e/aIF1A, and IF2-e/aIF5B, molecular evolution of translation initiation mechanisms will be discussed.