Cryo-electron microscopy (cryo-EM) studies of ribonucleoprotein complexes: the group II intron and ribosomes

Prem Singh Kaushal

NYS-Department of Health, Wadsworth Center, Albany, NY, 12201 USA

Abstract

Single-particle cryo-electron microscopy (cryo-EM) is an emerging technique in the field of structural biology. With the recent advancement in electron detection technology and improved image processing algorithms, it is now possible to achieve near-atomic resolution structure of macromolecular complexes. We have been applying cryo-EM to illustrate the architecture of ribonucleoprotein complexes, such as bacterial introns and ribosomes. Recently, a 3.8 Å resolution cryo-EM structure of *Lactococcus lactis* group IIA intron, in complex with an intron-encoded protein, was resolved. Bacterial group II introns are large catalytic RNAs related to nuclear spliceosomal introns and eukaryotic retrotransposons. Molecular analysis of the cryo-EM structure of the group II intron reveals functional coordination of the intron RNA with the protein. In the second set of studies, cryo-EM structures of the mammalian mitochondrial ribosome (mitoribosome) have yielded the architecture of small subunit of the mitoribosome and existence of the previously eluded E-site within the mitoribosome. In addition, the structures of *Mycobacterium smegmatis* (Ms) ribosome in different conformational states provide insights into some of the unique conformations of the Ms ribosome. I will summarize the results of these studies that I have been involved in, and will outline my future research plan that I would like to pursue as an independent investigator.