Nature Reviews Molecular Cell Biology | AOP, published online 2 February 2011; doi:10.1038/nrm3061

Journal club

THE 'RNP BRIDGE' BETWEEN TWO WORLDS

I believe that the genetic code was the greatest discovery of the twentieth century. When I saw the recent paper by Reiter *et al*. on the crystal structure of the tRNA–RNase P complex, my thoughts went to the origin of the genetic code and to the path from the RNA world to the protein world. As reviewed by Kazantsev and Pace, RNase P is an ancient universal ribozyme that cleaves the 5′-leader sequence of newly synthesized tRNAs, which harbour the nucleotide triplets of the genetic code, to generate mature tRNAs. Although the discovery of RNA catalysis made plausible the idea of an early RNA era, much of modern biology emanates from protein catalysts.

> “RNA–protein catalysts might, at one time, have been common.”

However, somewhere between the RNA world and the contemporary theatre of proteins, a transition through ribonucleoprotein (RNP) catalysts, which include RNase P, can be imagined.

The aminoacylations of tRNAs establish the rules of the genetic code. Because Xiao *et al*., among others, have demonstrated that tRNA-specific aminoacylations can be generated by laboratory-created ribozymes, RNAs could in principle provide the origins of a code for peptide synthesis. Advantageously, peptides can coat and protect RNA structures that are vulnerable to hydrolysis and unfolding. Indeed, RNase P has long been known as a catalytic RNA that is covered, in part, by a small protein cofactor. But the identity and interactions of the RNA's active site, and the particulars of the protein's role, were not clear. The wonder of seeing the active site of this ribozyme contacting the bound tRNA in a universally conserved way, and of the protein fitting onto and protecting a conserved structural motif in the catalytic RNA, reinforces the possibility that RNA–protein catalysts might, at one time, have been common. My guess is that this structure is a prototype from that transitional world.

Paul Schimmel
The Skaggs Institute for Chemical Biology, The Scripps Research Institute, Beckman Center, BCC379, 10550 North Torrey Pines Road, La Jolla, California 92037, USA.
e-mail: schimmel@scripps.edu

The author declares no competing financial interests.

ORIGINAL RESEARCH PAPERS Reiter, N. J. *et al*. Structure of a bacterial ribonuclease P holoenzyme in complex with tRNA. *Nature* **468**, 784–789 (2010) | Xiao, H. *et al*. Structural basis of specific tRNA aminoacylation by a small *in vitro* selected ribozyme. *Nature* **454**, 358–361 (2008)
FURTHER READING Kazantsev, A. V. & Pace, N. R. Bacterial RNase P: a new view of an ancient enzyme. *Nature Rev. Microbiol.* **4**, 729–740 (2006)