FOUND IN TRANSLATION. A. S. Petrov and L. D. Williams, School of Chemistry and Biochemistry, Georgia Institute of Technology, 315 Ferst Dr., Atlanta, GA 30332, anton.petrov@biology.gatech.edu, loren.williams@chemistry.gatech.edu.

Ribosomes exist in every cell and are responsible for translation of mRNA to protein. The origins and evolution of the ribosome remain imprinted in the biochemistry of extant life and in the ribosomal structure, just as the history of a tree is recorded in growth rings. The information contained within the ribosome connects us to the history of biology.

The ribosome is one of the most conserved elements in the cell. Nevertheless, the size of ribosomal RNAs (rRNAs), in general, tends to increase proportionally with the complexity of the species. Ribosomal RNA expansion can be 'observed' by comparing three-dimensional rRNA structures of bacteria and archaea (small), protists (medium) and metazoans (large). Analysis of the ribosomal structures reveals that rRNA expansion segments have been added to rRNAs without perturbing the pre-existing core [1].

rRNA growth occurs by a limited number of processes that include inserting a branch helix onto a pre-existing trunk helix, and elongation of a helix. rRNA expansions can leave distinctive atomic resolution fingerprints, which we call *insertion fingerprints*. Observation of insertion fingerprints throughout the ribosomal common core, the aboriginal assembly of all biological systems, allows us to construct well-grounded and fine-grained models outlining the origins and evolution of the ribosome.

This approach provides insight to the structure of common core rRNA, which preceded the Last Universal Common Ancestor. Conceptually reversing these expansions allows extrapolation backwards in time to generate evolutionary models of primordial ribosomes and to assign the functions to the expansion segments. Ancestral insertion fingerprints point to locations and temporal sequence of addition of ancestral expansion segments.

A correlated molecular level model of the evolution of the large ribosomal subunit, the small ribosomal subunit, tRNA and mRNA is presented. This model can be presented in eight phases. In each phase, the size of the ribosome increases by the addition of rRNA expansion segments.

Phase 1. RNA Stem-loops. The ancestral rRNAs fold to stable stem loops, which protect against chemical degradation.

Phase 2. Primitive Function: Condensation and single-stranded RNA binding. The LSU is a crude ribozyme, catalyzing non-specific, non-coded condensation by a simple proximity and orientation effects. Charged minihelices deliver activated substrates to the PTC. SSU function may involve association with single-stranded RNA.

Phase 3. The LSU, SSU, tRNA and proto-mRNA Meet-up. The end of this phase marks the association of the subunits, mediated by proto-mRNA and tRNA, which has been expanded from a minihelix to form the modern L-shape. The tRNA on one end associates with the PTC and on the other end binds to the proto-mRNA, which in turn form base pairs with the exposed single-stranded 3' terminus of the SSU.

Phase 4. Efficient Non-coded Peptidyl Transfer. At end of this phase the ribosome is an efficient, non-coding diffusive ribozyme. Along with single-stranded RNA cofactors (proto-mRNA), new SSU arms precisely position the A- and P-site tRNAs. The subunit interface is well-developed, with numerous RNA-RNA interactions.

Phase 5. Coding and Translocation. The ribosome achieves primitive decoding ability. In the LSU, binding sites for elongation factors G and Tu are finalized. The translocation function of mRNA is achieved by the acquisition a SSU pseudoknot that interacts with mRNA and assists in translocation and decoding.

Phase 6. Maturation of the Common Core. In this phase, the ribosomal rRNA common core is finalized.

Phase 7. Encasing the Common Core in Eukaryotes. The ribosome undergoes expansion in eukaryotes. rRNA develops eukaryotic-specific expansions that are stabilized by eukaryotic-specific proteins to form a secondary shell.

Phase 8. Surface Elaboration in Complex Eukaryotes. The beginning of this phase marks the origin of metazoa, in which ribosomes are decorated with "tentacle-like" rRNA elements that extend well beyond the subunit surfaces.

References:

[1] Petrov A. S., Bernier, C. R. *et al.* (2014) *PNAS, 111 ,* 10251–10256.