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In vitro RNA-peptide co-evolution system for screening ATP-binding RNP

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Introduction: The advent of biological polymers was a key step for the emergence of life. Modern organisms use proteins to achieve energy harvest and transfer in various ways to sustain structural organization through reproduction of molecules. Whereas "evolvability" of the biological system is maintained by replicable nucleotide polymers that undergo Darwinian evolution. Here Functional RNA-protein complexes (RNPs) represent perhaps the oldest conserved molecular assemblies in cells, such as ribosome carring out transfer of information from RNA to protein.

In order to answer questions regarding the emergence and historical trajectories of the co-evolution of RNA and proteins leading to RNPs, we established an *in vitro* system using a synthetic DNA library consist of both random 60 mer non-coding RNA and a random 42 aa amino acid peptide region. We performed used an mRNA-display method along with in vitro translation system to display both random RNA and random peptides to screen for a potential ATP-binding RNA/peptide/RNP candidates. High-throughput sequencing and bioinformatics analysis of the first round screened RNP library present demonstrated minimal enrichment at the RNA sequence level. with no significant concensus RNA secondary structure. However at the peptide level, the coding region have showed the enrichment of lysine, asparagine, and methionine among the over-represented clusters of coding sequences. Further investigation will involve optimizing the yield of RNA-peptide conjugates during mRNA-display, performing further enrichment on the RNP population, and comparing the results to those of RNA- and peptide-only trajectories.