

July 16-21, 2017 at UC San Diego, CA, USA

Elucidating signatures of the genetic code with binding assays

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Introduction: What defined specific assignment of amino acids to their cognate codons during the emergence of the genetic code? According to the stereochemical theory, the assignments were established based on affinity interactions between amino acids and their codons/anticodons. In the structure of the modern tRNA molecule, the acceptor stem with the amino acid and the anticodon loop with the anticodon triplet are separated by 6 nm in space, making direct interaction impossible. However, two alternative primal tRNA structures have been proposed that bring together in space the amino acid and the codon determinant [1, 2]. Both structures contain tetraloop-like geometries – simple structures that were recently shown to possess enzymatic activity such as ligation, cleavage, and terminal recombination [3].

In this project, we experimentally study the binding of stable AMP activated amino acid analogs to RNA motifs of AMP-binding aptamers as a testbed or to the above mentioned tetraloop-like structures containing corresponding coding triplets using microscale thermophoresis. We aim to elucidate patterns of anticodon-amino acid correlations for the emergence of the genetic code.

[1] Hopfield JJ (1978) *Proceedings of the National Academy of Sciences* 75, 4334–8. [2] Rodin AS et al. (2009) *Biology Direct* 4, 4. [3] Stadlbauer P et al. (2015) *Chemistry* 21, 3596–604.