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Understanding Increase in Complexity in The RNA World Using a Two Enzyme System

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Introduction: The dynamics of the emergence of complexity in an RNA World is an important problem in the quest towards understanding the origins of life. We address this problem using a dynamic combinatorial chemistry (DCC) approach [1,2] on the premises that when subject to a persistent equilibrium of ligation and cleavage, RNAs will naturally increase in complexity while gaining resistance to degradation over time. It will be of immense interest to see if this equilibrium or the pathways towards increasing complexity are strongly affected by the presence of amino acids or peptides. To obtain such equilibrium, we are using a two enzyme system. The cleavage enzyme is Benzonase which cleaves RNA, including circular forms, to produce products with a 3' hydroxyl and 5' phosphate [3]. The cleavage products are ideal for ligation by T4 RNA ligase, while utilizing ATP as a source of energy [4]. Population changes are monitored by determining millions of individual RNA sequences from reaction samples using RNA-seq technology on an Illumina NextSeq 500 system [5]. The results from initial experiments using both enzymes in a mutually compatible buffer system will be presented.

References:

[1] Benner SA et al.(1996) *Acta Chem. Scand* 50(3):243-248. [2] Tuerk C and Gold L (1990) *Science*, 249:505-510. [3] Olszewski M and Filipkowski P (2009) *Postepy Biochem* 55:21-24. [4] Tessier DC et al. (1986) *Anal Biochem* 158:171-178. [5] http://support.illumina.com/downloads/nextseq-500-user-guide-15046563.html