Posters will be on Display for the Entire Week. Presenters are Requested to be Present at Their Poster the Last Half-Hour Break of the Evening.

POSTER SESSION: GENETIC INFORMATION AND FUNCTION IN THE EARLY STAGES OF LIFE Price Center Ballroom East

Zamudio G. S. José M. V.

Information Analysis is Used to Determine the Identity Elements of the Operational tRNA Code [#4015]

We obtained the identity elements (IE) of the 20 tRNAS of the 20 canonical amino acids from about 53,000 sequences. We use the variation of information along the 76 nucleotides of each tRNA molecule. We expand the current catalogue of IE.

Edeleva E. V. Schwintek P. J. Braun D.

Elucidating Signatures of the Genetic Code with Binding Assays [#4036]

What defined specific assignment of amino acids to their cognate codons during the emergence of the genetic code? In this project, we develop experimental strategies to test the stereochemical theory of the genetic code origin.

Ying J. X. Liu Y. Xu P. X. Zhao Y. F.

Synergistic Effects of Nucleosides on Amino Acid Dipeptide Yields in Aqueous Conditions [#4041]

Our concern is the synergistic effect of codon and anti-codon (A/U, C/G) on the forming peptide of amino acid. Experimental results reveal that the yield of dipeptide formation (Phe-Phe) is indeed affected by the double nucleoside synergistic effect.

Maurel M.-C.

From Viroids and Ribozymes RNA Back and Forth [#4063]

We recently demonstrated that viroids replicate in non-specific hosts, emphasizing their adaptability to different environments. These results exemplify the plasticity and efficiency of small RNAs, viroïds and ribozymes.

Tihung K. F. Joyce G. F.

Advancing Polymerase Ribozymes Towards Self-Replication [#4126]

Autocatalytic replication and evolution in vitro by (i) a cross-chiral RNA polymerase catalyzing polymerization of mononucleotides of the opposite handedness; (ii) non-covalent assembly of component fragments of an existing RNA polymerase ribozyme.

Wei C. Pohorille A. Popovic M. Ditzler M.

Exploring Connectivity in Sequence Space of Functional RNA [#4137]

Connectivity between clusters on the sequence space of RNA ligase ribozymes selected through in vitro evolution is investigated to shred light on evolution paths. Common motifs for activity are shown with increased complexity for longer molecules.

Takeuchi N. Hogeweg P. Kaneko K.

<u>The Origin of a Genome Through Spontaneous Symmetry Breaking: A Computational Modeling Study</u> [#4139] Differentiation between templates and catalysts is a fundamental property of life. We use individual-based modeling to show that such differentiation could first emerge in primitive cells owing to an evolutionary conflict between molecules and cells.

Popovi? M. Wei C. Pohorille A. Ditzler M. A.

Modular Growth and Structural Remodeling in Early RNA Evolution [#4164]

By combining exhaustive mapping of fitness landscapes for short RNAs with structure guided mapping for long RNAs, we investigated RNA fitness landscapes as a function of polymer length.

Plebanek A. J. Ditzler M. A.

Sequence Duplication as an Evolutionary Mechanism in Functional RNAs [#4190]

Understanding the adaptive mechanisms available to RNA is useful when reconstructing the early evolutionary history of life, especially in an "RNA World" context. This study explores how a duplication event can enable new functions to evolve in RNA.

Biondi E. Yang Z. Zhang L. Dasgupta S. Piccirilli J. A. Leal N. A. Benner S. A. <u>Developing a Molecular Biology for Alternative Biopolymers in Early Evolution</u> [#4191]

We report the further development and applications of a molecular biology for an artificial genetic system composed of nucleic acid-like biopolymers made from six different building blocks (Artificially Expanded Genetic Alphabet, or AEGIS).

Neme R. Landweber L. F.

Molecular Innovation in Ciliates with Complex Genome Rearrangements [#4194]

We study molecular innovation in several ciliate species with unique massive genome rearrangements to understand how a radically distinct genome architecture can shape the process of acquiring new functions, genes and structures.

José M. V. Morgado E. R.

The Total Number of Possible Genetic Codes with 64 Triplets, 20 Amino Acids, and One Stop Signal [#4121]

Given the recent discovery of several exo-planets which may show conditions for the existence of life, we count all the possible genetic codes with some property in common with our current genetic code.

Horning D. P. Joyce G. F.

Amplification of RNA by an RNA Polymerase Ribozyme [#4024]

An RNA polymerase ribozyme can synthesize structured, functional RNAs, transcribe RNA into nucleic acid analogs, and amplify RNA via a protein-free form of the polymerase chain reaction. Directed evolution towards a general RNA replicase is underway.

Cai H. H. Lin R. C. Xu P. X. Liu Y. Zhao Y. F. A New Method to Verify of the Triplet Code [#4058]

This protocol chose the DNA chain and dipeptide to prove the genetic code reflected by the synergistic effect between the oligonucleotide and dipeptide under the UV radiation. The proposed method showed a new insight to research the genetic code.

Rothschild-Mancinelli B. Horfall L.

Elucidating the Evolution of Metallo-\(\beta\)-Lactamases Through Ancestral Gen Reconstruction [#4226]

Proteins are the core of an organism's survival and adaptation, therefore under-standing their evolutionary history is critical to knowing their ability to survive.