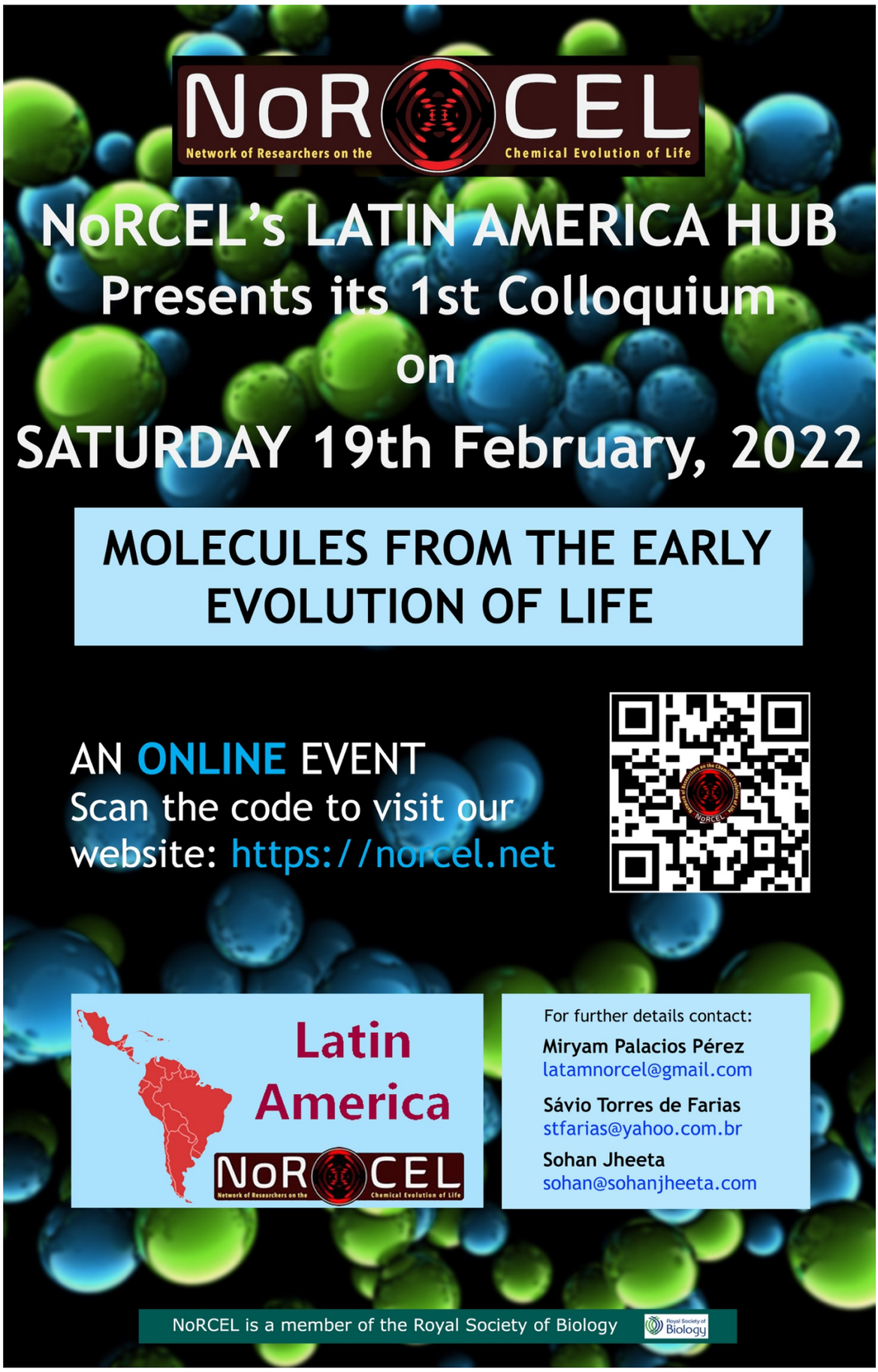


Welcome to the first Colloquium of NorCEL's Latin America Hub. We have brought together scientists from the region who will talk about early evolution of biomolecules from prebiotic processes on one side, and theoretical works on the other

# Speakers and abstracts

SAUL VILLAFAÑE-BARAJAS, *University of Akron in Summit, Ohio, USA*.
Talk: "**Hydrothermal environments as niches of chemical evolution**".

ALICIA NEGRÓN-MENDOZA, *Chemical Evolution Laboratory of the Nuclear Sciences Institute at the Universidad Nacional Autónoma de México, UNAM.*
Talk: "**The possible role of clay minerals in chemical evolution processes**"

FRANCISCO PROSDOCIMI, *Universidade Federal do Rio de Janeiro (UFRJ), Brazil*.
Talk: "**From FUCA to LUCAs: a deep exploration into the world of progenotes**".

MARCO V JOSÉ, *Theoretical Biology Group at the Universidad Nacional Autónoma de México, UNAM.*
Talk: "**Information flow in the evolution of the genetic code**".

ROMEU C GUIMARÃES, *Universidade Federal de Minas Gerais at Belo Horizonte, Brazil*.
Talk: "**Origins of Metabolism and of Self-Referential Genetic Encoding pinpointed to the C1-substrate Gly and Ser pathways**".

SAVIO TORRES DE FARIAS, *Universidade Federal da Paraíba, Brazil*.
Talk: "**Evolution of aminoacyl tRNA-synthetases and their implications to the organization of genetic code**".

**Saúl** VILLAFAÑE-BARAJAS and María Colín García
**"Hydrothermal environments as niches of chemical evolution"**
*University of Akron in Summit, Ohio, USA*

Our current knowledge about the probable environments of the early Earth suggests that hydrothermal systems were common, both at the surface and at submarine conditions. The intense hydrothermal activity could have favoured the interaction of organic molecules with different geochemical variables, and it must have promoted the development of chemical complexity. Although several researchers have pointed out the importance of high-temperature environments in the previous steps that could be involved in the emergence of life, it is necessary to consider the contribution of other parameters (e.g., minerals, pH gradients, metal-organic complexes, dissolved ions, among others) in order to simulate more consistent laboratory models. Moreover, of primary importance is to specify the spatial scale of venting, because the nature and number of experimental variables, as well as the design and scope of the results, are not the same in all system conditions (Fig. 1). Finally, the current perspectives in prebiotic chemistry suggest that the interactions among molecules and environmental parameters could favour the mutualism and synergism between molecules and open the way for new structures with a higher degree of complexity. Hence, the design of complex experiments, including multicomponent environmental variables and the dynamism that is available in hydrothermal systems, seems to be a good starting point. Considering the previous ideas, we have developed some experimental approaches related to the transformation, stability, reactivity, and polymerization of hydrogen cyanide, HCN, under probable hydrothermal conditions. Our results suggest that the contribution of different geochemical variables affect considerably the physicochemical structure of HCN-polymers, as well as their fate in these systems. It is necessary to develop new experimental strategies that consider multicomponent systems to gain better information about the role of some primitive environments and their contribution in chemical evolution and origins of life scenarios.

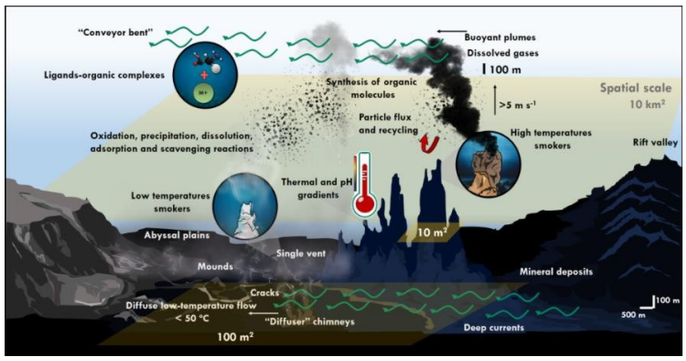


Figure 1. Hydrothermal systems are highly dynamic environments. This dynamism must be considered when designing prebiotic chemistry experiments to gain more insights into the contribution of geochemical variables in the transformation and fate of organic molecules during the early stages of chemical evolution. Credit: Villafañe-Barajas and Colín-García, 2021. Published by Cambridge University.

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**Alicia** NEGRÓN MENDOZA

**"The possible role of clay minerals in chemical evolution processes"**

*Chemical Evolution Laboratory of the Nuclear Sciences Institute at the Universidad Nacional Autónoma de México, UNAM, Cd. Universitaria, 04510 CDMX, México*

Darwinian evolution is a foundational concept in modern biology. If we accept Darwinian evolution, we must postulate another form of evolution before this to explain the synthesis of biological molecules, called chemical evolution. Multi-phase systems would be required to create an adequately replicated environment that may resemble the ancient Earth in this framework. The production of bio-organic molecules and their stability in the harsh circumstances of the early Earth are critical in this regard.

The behavior of the nucleic acid bases (adenine, guanine, thymine, cytosine, and uracil) under irradiation in the presence of minerals such as clays is the focus of this research. All the systems were exposed to a high radiation field to highlight the potential role of clays as ionizing radiation protective agents in prebiotic processes.

Nucleobase behavior was studied in three different systems. In an aqueous solution, as free base. Base adsorbed in sodium montmorillonite (clay), as an example of a mineral surface. A suspension containing sodium montmorillonite as well as the base. Irradiation was conducted with a gamma source at doses of up to 280 kGy. UV spectroscopy and high-performance liquid chromatography were used to examine the bases.

The results reveal that base adsorption occurs primarily at acidic pH. Those bases with a net positive charge at this pH are adsorbed and protected in a high radiation field related to those samples in an aqueous environment (without the clay) that deteriorate quickly, even at low doses of ionizing radiation. Nonetheless, the molecule is relatively stable when the bases are adsorbed on sodium montmorillonite, especially in dry form.

The author thanks the support of PAPIIT Project IN114122.

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**Francisco** PROSDOCIMI

**"From FUCA to LUCAs: a deep exploration into the world of progenotes"**

*Universidade Federal do Rio de Janeiro (UFRJ), Brazil*

The theory of chemical symbiosis (TCS) suggests that biological systems started with the collaboration of two polymeric molecules existing in early Earth: nucleic acids and peptides. Chemical symbiosis emerged when RNA-like nucleic acid polymers happened to fold into 3D structures capable to bind amino acids together, forming a proto peptidyl-transferase center. This folding catalyzed the formation of quasi-random small peptides, some of them capable to bind this ribozyme structure back and starting to form an initial layer that would produce the larger subunit of the ribosome by accretion. TCS suggests that there is no chicken-and-egg problem into the emergence of biological systems as RNAs and peptides were of equal importance to the origin of life. Life has initially emerged when these two macromolecules started to interact in molecular symbiosis. Further, we suggest that life evolved into progenotes and cells due to the emergence of new layers of symbiosis. Mutualism is the strongest force in biology, capable to create novelties by emergent

principles; on which the whole is bigger than the sum of the parts. TCS aims to apply the Margulian view of biology into the origins of life field.

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**Marco** V. JOSÉ

**"Information flow in the evolution of the genetic code"**

*Theoretical Biology Group at the Universidad Nacional Autónoma de México, UNAM, National Autonomous University of Mexico*

The standard genetic code (SGC) performs a mapping between the sequences of the four nucleotides A, U, G, C to the sequences of the 20 amino acids in protein. The Central Dogma was conjured by Francis Crick in response to the discovery of reverse transcription: "There is no information transfer from protein to nucleic acid" There is nothing in the physicochemical world that remotely resembles reactions being determined by a sequence and codes between sequences. The existence of a genome and the genetic code divides living organisms from non-living matter. Herein we calculate the total information given by 61 codons which is equal to 5.931 bits/codon and the maximum amount of information conveyed to a protein is 4.322 bits/residue. The central dogma has not been analysed in the context of the evolution of the SGC. There has been an unbroken chain of transmission of tRNA molecules going back in time to the first organism with a genetic code. Assuming a primeval RNY code the information given by 16 codons is 3 bits/codon and the maximum information of a peptide was 2.161/residue. The information in codons of an extended RNA code is equal to 3.58 bits/codon and, the maximum amount of information obtained by the receiver (protein) was 4.32 bits/residue. Initially, the source resided in the interactions of tRNA and their synthetases, the channel was the peptidyl-transferase centre, and the destination was the protein. There was a major transition of the information flow when DNA took over the role of genetic information storage. The DNA became the receiver, tRNA, synthetases and the ribosome are the channel and protein are the receiver. The maximum amount of a putative protein that evolved purely random but obeying the degeneracy of the SGC is equal to 4.12 bits. Assuming an equal probability of each of the 20 amino acids the information is 4.32; whereas for BLOSUM52, cytochrome C, histone 4, the information is 4.18, 4.45, 4.12, respectively. It is concluded that the degeneracy of the genetic code reduces the effect of errors in protein synthesis.

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**Romeu** C. GUIMARÃES

"**Origins of Metabolism and of Self-Referential Genetic Encoding pinpointed to the C1-substrate Gly and Ser pathways**"

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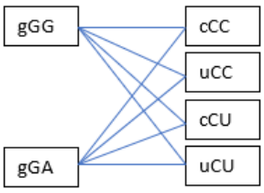
The Self-Referential Model (SRM) proposes that proto-tRNA couples, associated by binding through the (*Life* 2017, *7*(2), 16; https://doi.org/10.3390/life7020016) proto-anticodons are singularities that mimic the ribosome. When the proto-tRNAs in the couples are aminoacylated, the transferase reaction is propitiated, similarly to the laterally-associated couples of tRNAs at translation. At the singular state the transferase reaction is bi(a)directional and the anticodons are concomitantly codons. The peptides produced follow the prebiotic mass gradients of amino acids, which are mostly derived from C1 substrates, especially Gly. Some of the peptides would stay bound to the proto-tRNA – the producers – forming self-referentially stabilized and productive proto-RNPs. These are also precursors to the gene-protein associations. It could be speculated that proto-tRNAs might be reminiscent, *e.g.*, of the PNA, engineered by PE Nielsen and M Egholm 1999. Autotrophic metabolism origins from C1 substrate-driven pathways are varied, e. g., the Ljungdahl-Wood route is indicated by the group of W Martin, the reductive glycine pathway is active in Desulfovibrio desulfurica ns https://doi.org/10.1038/s41467-020-18906-7, and the generic pterin-dependent route is indicated by the phylometabolic analyses of R Braakman and E Smith 2012. The Serine Cycle is active in a widespread class of methylotrophs.




The first-encoded module of anticodon pairs is wGG:wCC and wGA:wCU, respectively, initially Gly:Gly and Ser:Ser, now Pro:Gly and Ser:Ser, Arg.

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**Savio** TORRES DE FARIAS

**"Evolution of aminoacyl tRNA-synthetases and their implications to the organization of genetic code".**

*Universidade Federal da Paraíba, Brazil*

In this talk, I will review recent works on the role that the tRNA molecule played in the early origins of biological systems. tRNAs gave origin to the first genes (mRNA), the peptidyl transferase centre (PTC), the 16S ribosomal molecule, proto-tRNAs were at the core of a proto-translation system, and the anticodon and operational codes appeared in tRNAs molecules. Metabolic pathways emerged from evolutionary pressures of the decoding systems. The transitions from the RNA world to the ribonucleoprotein world to modern biological systems were driven by two kinds of tRNAs transitions, to wit, tRNAs leading to both mRNA and rRNA.

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