

## Assessment of Secondary Structure in Nucleic Acid Produced in Simulated Prebiotic Conditions

K. Glass<sup>1</sup>, Michael Oye<sup>2,3,4</sup>, David Deamer<sup>3</sup> and W. A. Vercoutere<sup>4\*</sup>

<sup>1</sup>Foothill College, Los Altos, CA, <sup>2</sup>San Jose State University, San Jose, CA, <sup>3</sup>UC Santa Cruz, Santa Cruz, CA, <sup>4</sup>Science and Technology Innovation Laboratory, NASA Ames Research Center, Moffett Field, CA

\* e-mail of Correspondence Author

The earliest forms of life would likely have a protocellular form, with a membrane encapsulating some form of linear charged polymer. These polymers could have enzymatic as well as genetic properties. We can simulate plausible prebiotic conditions in the laboratory to test hypotheses related to this concept. In earlier work we have shown that mononucleotides organized within a multilamellar lipid matrix can produce oligomers in the anhydrous phase of dehydration-rehydration cycles [1]. If mononucleotides are in solution at millimolar concentrations, then oligomers resembling RNA are synthesized and exist in a steady state with their monomers [2]. We have used conventional and novel techniques to demonstrate that secondary structures stabilized by hydrogen bonds may be present in the condensation products produced in dehydration-rehydration cycles that simulate hydrothermal fields that were present on the early Earth. Gel electrophoresis data corroborates the presence of 200-base pair length RNA fragments in products of Hydration-Dehydration experiments. Furthermore, hypochromicity measurements demonstrate a degree of hypochromicity found in single RNA strand of known sequence, as well as results that indicate this is true also for a sample of complementary strands of RNA. Analysis of ionic current signatures of known RNA hairpin molecule as measured using a nanopore detector indicate a significant variability in pattern, different from the signatures produced by DNA hairpin molecules. This informs how we may interpret nanopore data gathered from prebiotic simulations.

[1] Deamer D (2012) *Chemical Society Review* 41:5375-5379.

[2] DeGuzman V, Vercoutere W, Hossein S, and Deamer D (2014) *Journal of Molecular Evolution* 78: 251-262.