

Stability and reactions of amino acids in simulated submarine hydrothermal systems

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The discovery of hydrothermal systems in the late 70s brought a new hypothesis to the origin of life. Previously, the Urey-Miller experiment had made waves in this new field, indicating that a reducing atmosphere could form amino acids from basic chemicals. The further discovery of hydrothermal systems with earth prebiotic conditions added another notion to the field. Since then, different kinds of simulation were conducted to test the hypothesis. Initially and autoclave was extensively used due to its robustness and durability, however this system was not an ideal system, hence a flow-type simulator was proposed instead. We tested the stability and reaction of several amino acids using a flow reactor simulating submarine hydrothermal systems at 200—250 °C. This study generally showed that there is a variation in the individual amino acids survivability in the simulators. This is mainly attributed to the following factors; heat time, cold quenching exposure, metal ions and also silica. We observed that, in a rapid heating flow reactor, high aggregation and/or condensation of amino acids could occur even during a heat exposure of 2 min. We also monitored their stability in a reflow-type of simulator for 120 min at 20 min intervals. The non-hydrolyzed and hydrolyzed samples for this system showed a similar degradation only in the absence of metal ions. We also tested the possible condensation that could be forming peptide bonds among the amino acids in one of the flow reactors. We utilized the Lowry protocol to determine the concentration of the peptide bonds in several hydrothermal temperatures. Concentration of peptide bonds was significantly higher when the temperature was at 300 °C. This is despite the decomposition of amino acids by more than half. However, the contribution of peptide bonds in the combined amino acids was less than 10%, even in the 300 °C sample, which showed the highest contribution of peptides. The major heat products were non-peptide amino acid condensates (NPACs) that only possess partial peptide bonds. The role of NPACs should be examined though they were often ignored in the classical chemical evolution scenario so far.

We experimented with Gly, Ala, Asp and Val in the SCWFR at 200 °C, 250 °C and 300 °C. We recorded the recovery of the samples and performed the Lowry method to quantify the peptide bond concentration. Peptide bonds' concentrations are significantly higher when the temperature is at 300 °C. This is despite the decomposition of amino acids by more than half. The highest peptide bond concentration among the samples constitute only about 10% of the total product yield of the amino acid mixture.

We also examined possible formation of amino acid condensates by using single amino acid (Gly, Ala, Asp or Val) and compared the results with those with all of four amino acids.

Keywords: submarine hydrothermal systems, amino acids, origins of life, flow reactor