

Effect of pH on aspartic acid peptides formations under high temperature and pressure

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Proteins are consisted of twenty kinds of L- α -amino acids and play important roles as enzymes in many biological reactions. Amino acids in protein are connected each other with peptide bond bridging the α -amino nitrogen to the α -carboxyl carbon. Two kinds of the proteinogenic amino acids holds two carboxyl groups (i.g., aspartic acid and glutamic acids). Thus, chemically, they can form peptide bonds with β -carboxyl carbon or γ -carboxyl carbon but biologically, α -carboxyl carbon exclusively form the paptide bond. Negatively-charged side chain of Asp and Glu are important for catalytic reactions of proteins.

Hadean deep-seaflor sediments have been proposed as a potential environment for abiotic peptide formation. We investigated the effects by different pH at high temperature and high pressure simulating pore water in deep-sea sediments. Asp solutions buffered at pH 1.3, 2.9, 7.7, and 13.6 were heated and compressed for 1–12 days at 90 °C and 100 MPa. After the incubation, the products were analyzed with liquid chromatography tandem mass spectrometry. Both dimers that connected at α -carbonyl carbon (α -Asp₂) or β -carbonyl carbon (β -Asp₂) formed in acidic and alkaline solutions (pH 1.3, 2.9, and 13.6), whereas β -Asp₂ was below our detection limit in neutral soliuitions (pH 7.7). The yield ratio of α -Asp₂/ β -Asp₂ were 0.76, 0.23, and 0.84 at pH 1.3, 2.9, and 13.6, respectively. The decomposition products of Asp contain glycine, alanine, amines, and organic acids. Yields of these decomposition products do not show significant differences in different pH solutions. These results imply that neutral pH is suitable for abiotic formation of the biologically common peptide bond of Asp.