

Research Paper

Amino Acid Distribution in Meteorites: Diagenesis, Extraction Methods, and Standard Metrics in the Search for Extraterrestrial Biosignatures

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ABSTRACT

The relative abundance of the protein amino acids has been previously investigated as a potential marker for biogenicity in meteoritic samples. However, these investigations were executed without a quantitative metric to evaluate distribution variations, and they did not account for the possibility of interdisciplinary systematic error arising from inter-laboratory differences in extraction and detection techniques. Principal component analysis (PCA), hierarchical cluster analysis (HCA), and stochastic probabilistic artificial neural networks (ANNs) were used to compare the distributions for nine protein amino acids previously reported for the Murchison carbonaceous chondrite, Mars meteorites (ALH84001, Nakhla, and EETA79001), prebiotic synthesis experiments, and terrestrial biota and sediments. These techniques allowed us (1) to identify a shift in terrestrial amino acid distributions secondary to diagenesis; (2) to detect differences in terrestrial distributions that may be systematic differences between extraction and analysis techniques in biological and geological laboratories; and (3) to determine that distributions in meteoritic samples appear more similar to prebiotic chemistry samples than they do to the terrestrial unaltered or diagenetic samples. Both diagenesis and putative interdisciplinary differences in analysis complicate interpretation of meteoritic amino acid distributions. We propose that the analysis of future samples from such diverse sources as meteoritic influx, sample return missions, and *in situ* exploration of Mars would be less ambiguous with adoption of standardized assay techniques, systematic inclusion of assay standards, and the use of a quantitative, probabilistic metric. We present here one such metric determined by sequential feature extraction and normalization (PCA), information-driven automated exploration of classification possibilities (HCA), and prediction of classification accuracy (ANNs).

Key Words: Protein amino acids—Meteorite samples—Principal component analysis—Hierarchical cluster analysis—Stochastic probabilistic artificial neural networks— Standard metric.

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