N89-26348

1985 JUL 177.81

THE SEARCH FOR AND IDENTIFICATION OF AMINO ACIDS, NUCLEOBASES AND NUCLEOSIDES IN SAMPLES RETURNED FROM MARS

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INTRODUCTION:

The Mars Sample Return mission will provide us with a unique source of material from our solar system; material which could advance our knowledge of the processes of chemical evolution.

Investigations based on the Viking datasets have shown that geologically primordial Mars was in many biologically important ways similar to primordial Earth: the presence of surface liquid water, moderate surface temperatures, an atmosphere of carbon dioxide and nitrogen, and high geothermal heat flow.¹ Indeed, it would seem that conditions on Earth and Mars were fundamentally similar during the first one billion years or so. As has been pointed out by McKay¹ and others, Mars may well contain the best preserved record of the events that transpired on the early planets. Examination of the early record will involve an extensive search, ranging from microfossils to isotopic abundance data.

We propose an investigation of the returned Mars samples for biologically important organic compounds, with emphases on amino acids, the purine and pyrimidine bases, and nucleosides. These studies would be conducted on subsurface samples obtained by drilling past the surface oxidizing layer with emphasis on samples containing the largest quantities of organic carbon as determined by the rover GCMS.

A. Sample Extraction

Extraction of these molecules from the returned samples will first be performed using the hydrothermal extraction technique described by Cheng and Ponnamperuma². More rigorous extraction methods will be developed and evaluated, as Hayatsu, *et al.*³ reported improved yields of purines from meteorites with the use of hydrochloric acid. The extract will be analyzed for amino acids, nucleobases and nucleosides.

B. Analysis of Sample Extracts

For analysis of the extract for free amino acids or amino acids present in a bound or peptidic form, aliquots will be analyzed by capillary GCMS both before and after hydrolysis with 6N hydrochloric acid. Establishment of the presence of amino acids would then lead to the next logical step which would be the use of chiral stationary GC phases to determine the enantiomeric composition of the amino acids present, and thus potentially establish their biotic or abiotic origin.

Successful examination of the returned Mars samples for the presence of indigenous amino acids and the determination of their enantiomeric composition will obviously require rigorous exclusion of terrestrial contamination, and our study of the returned lunar samples provides considerable background on matters ranging from sample acquisition, processing and handling to evaluation of the purity of reagents and glassware used.

Confirmational analyses for amino acids would include ion-exchange and reversed-phase liquid chro-

matographic analyses. For analyses of the returned Mars samples for nucleobases and nucleosides, affinity and reversed-phase liquid chromatography would be utilized. This technology coupled with scanning UV detection for identification, presents a powerful tool for nucleobase and nucleoside analysis. Mass spectrometric analysis of these compounds would confirm their presence in samples returned from Mars.

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PROCEDURAL BLANK, HYDROLYZED UNHYDROLYZED 72501.62 APOLLO 17. APOLLO 17,72501.62, HYDROLYZED 10ng AMINO ACID STANDARD SER THR ASP GLY DROLYZED APOLLO 17.70011.37 APOLLO 17.70011.37 YZED 2ng AMINO ACID STAND GLY ASP THR SER

Figure 1. CIE analysis of Apollo 17 lunar fines.