

MARS ANALOG SAMPLE STUDY FOR EXOMARS 2020 ROVER MISSION: Xiang Li¹, Friso van Amerom², Desmond Kaplan³, Andrej Grubisic⁴, Ryan Danell⁵, Stephanie Getty⁴, Marco Castillo⁶, Ricardo Arevalo⁶, Sandra Siljeström⁷, Walter Goetz⁸, and William Brinckerhoff⁴, ¹University of Maryland, Baltimore County, Baltimore, MD 21250. (xiang.li@nasa.gov) ²Mini-Mass Consulting, Inc.; ³KapScience; ⁴NASA/Goddard Space Flight Center; ⁵Danell Consulting, Inc.; ⁶University of Maryland, College Park. ⁷Department of Chemistry and Materials, RISE Research Institutes of Sweden. ⁸Max Planck Institute for Solar System Research.

Introduction: The Mars Organic Molecule Analyzer (MOMA, Figure 1) is a dual-source, ion trap-based instrument capable of both pyrolysis-gas chromatography mass spectrometry (pyr/GC-MS) and laser desorption/ionization mass spectrometry (LDI-MS).[1] The complete instrument, a joint development between NASA and teams in Germany and France, serves as the core astrobiology investigation on the 2020 ExoMars rover. The LDI mode of the MOMA instrument will be conducted at Mars ambient conditions and utilized for the first time on Mars to detect refractory organic compounds and characterize host mineralogy, in achieving the mission's main goal of searching for molecular "signs of life". For more detailed analysis, advanced capabilities like selected ion accumulation (enhancement of specific mass ranges) utilizing Stored Waveform Inverse Fourier Transform (SWIFT) for selected ion ejection (the isolation and enhancement of specific mass ranges) and tandem mass spectrometry (MS/MS, for structural analysis) have also been realized in LDI-MS mode.[2] As the MOMA flight model (FM) has been delivered to the European Space Agency in summer 2018 for integration and test, and the ExoMars landing site selected (Oxia Planum), the next focus will be the continued analysis of Mars analog samples to guide in situ surface operations and mass spectral data interpretation on ExoMars.

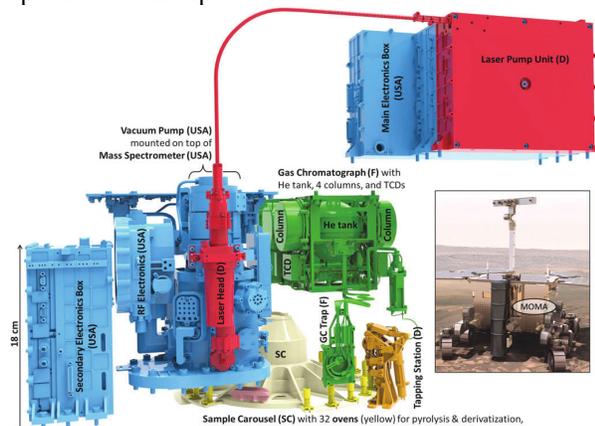


Figure 1. MOMA flight instrument configuration.

Sample Testing on MOMA ETU: The MOMA Engineering Test Unit (ETU) has been used for analog sample testing. Various type of minerals, organic standards, organic spiked samples, and more complex terrestrial analog samples have been tested. The list of analyzed samples includes, carbonates like calcite and

dolomite, silicates such as enstatite and forsterite, spiked samples such as amino acids doped in clay with perchlorate salt, and natural materials such as Yellowstone hot spring samples (e.g., Figure 2) and Atacama samples. The preliminary results are encouraging, demonstrating that the analytical capabilities of the MOMA instrument enable the main scientific goals to: 1. detect and identify organic molecular structures; 2. analyze a range of volatile and nonvolatile compounds; and, 3. derive the inorganic geochemical context of organics. The challenges encountered during simulations of mission operations, such as excessive ion counts and observations of background peaks, underscore the important roles of selected ion accumulation and MS/MS to improve the quality of the spectra and fidelity of interpretations.

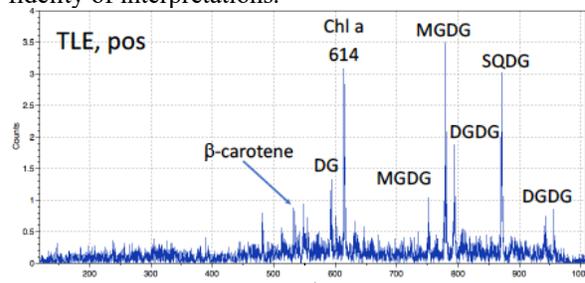


Figure 2. Mass spectrum, obtain from MOMA ETU, of the total lipid extract (TLE) of a Yellowstone hot spring sample. Lipids and other organics detected include diacylglycerols (DG); monogalactosyldiacylglycerol (MGDG); sulfoquinovosyldiacylglycerol (SQDG); digalactosyldiacylglycerol (DGDG); chlorophyll a (Chl a), and β -carotene.

Enhanced Analytical Capabilities: The number and mass range of ions that are generated from LDI of samples could result in complex and dense mass spectra. The ability for MOMA to perform ion isolation and MS/MS allows the targeting of species despite this spectral complexity, thereby supporting detailed chemical identification of unknown species. The measurements collected on the ETU have shown that isolation of mass ranges about 100 Da wide (e.g., 100-200 Da range, 200-300 Da range, and so on) provide more detailed and better resolved mass spectral results compared to wide mass ranges (e.g., 100-1000 Da survey mode).

References: [1] W. Goetz et al. (2016) *Int. J Astro-bio.* 15, 239-250. [2] X. Li et. al.(2017) *IJMS*, 422, 177-187.