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MOMA GC-MS COUPLING

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Introduction: The goals of the joint ESA-Roscosmos Exo-Mars-2018 rover mission is to search for “signs of life” molecules (large, non-volatile organic or biological molecules that suggest existing or prior biosynthetic activity) on the Martian surface and near subsurface and to distinguish between the endogenous and exogenous sources of Martian organics.

The Mars Organic Molecule Analyzer (MOMA) aboard the ExoMars rover will be a key analytical tool in providing chemical (molecular) information from the solid samples, with particular focus on the characterization of organic content. Central to MOMA instrumentation is a gas chromatograph-mass spectrometer (GC-MS) which provides the unique ability to characterize a broad range of compounds allowing chemical analyses of volatile and non-volatile species. Both instruments have been tested separately first and have been coupled in order to test the efficiency of the future MOMA GC-MS instrument.

Instrumental Suite: The French brassboard GC coupled has been coupled to the US brassboard ion trap mass spectrometer in a flight-like configuration (fig 1) for the coupling campaign. The MOMA GC setup is based on the Sample Analysis at Mars (SAM) heritage design with a He reservoir and 4 separate analytical modules including traps, columns and TCDs. Solid samples are sealed and heated in this setup using the manual tapping station (fig. 1), design and built at MPS in Germany, for GC-MS analysis. Then the effluent is ionized by an electron impact ionization source in the MS chamber and analyzed by the linear ion trap mass spectrometer (fig. 1).

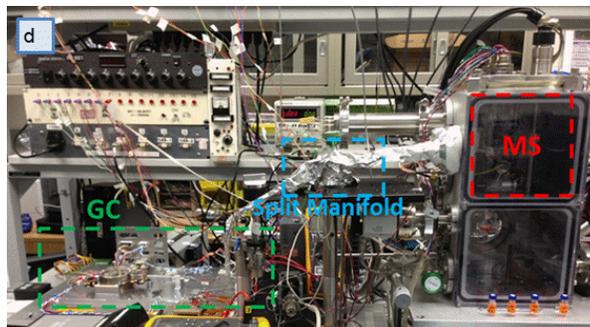
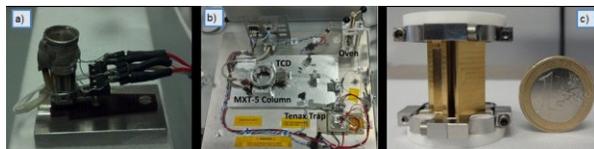


Figure 1: picture of the manual tapping station (a) where sample has been introduced before that it has been trapped, injected in the gas chromatograph (b) and detected in the MS ion trap (c).

MOMA GCMS Results:

Qualitative Analysis: Volatile and non volatile compounds have been injected in the MOMA instrumental suite. Both of these compounds family have been detected by the TCD and by the MS. By using the TCD signal and the retention time we were able to identify each of these injected compounds. MS signal and single mass spectra, by comparison with the NIST libraries, give us an unambiguous confirmation of these identifications (fig 2). The TCD trace (a) and the total ion chromatogram (TIC) from the MS (b) for a standard gas-phase mixture of 100 ppm butane, pentane, hexane and benzene in He. The mass spectra (c-e) arise from an average of 10 spectra averaged from the TIC peaks.



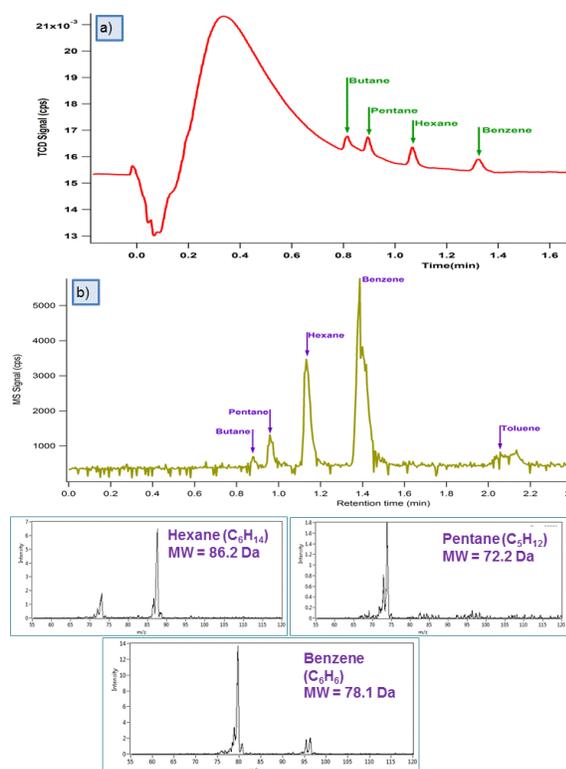


Figure 2: The TCD trace (a) and the total ion chromatogram (TIC) from the MS (b) for a standard gas-phase mixture of 100 ppm butane, pentane, hexane and benzene in He. The mass spectra arise from an average of 10 spectra averaged from the TIC peaks.

Quantitative Analysis: The sensitivity of the end-to-end test of the GC-MS interface depends heavily on the ionization efficiency of the analyte, the quality of the thermal control along the sample path, and the split manifold design. The MOMA requirement for sensitivity in the GC-MS mode for organic molecules is 1 pmol. In this test, sensitivity was determined for the GC TCD and MS response to a dilution series containing IPA, hexane and benzene deposited onto silica beads in the MOMA oven. For the MS, peak areas were integrated in the total ion chromatogram as well as in the resulting mass spectra. Again, IPA was not detected in the MS because the characteristic peaks fell below the low mass cutoff for the instrument. Generally, the MS was found to be 5-10 times more sensitive than the GC TCD for hexane and benzene respectively.

Table 1: TCD and MS sensitivity

Compounds	TCD Sensitivity	MS Sensitivity	
	LOD (pmol)	Peak integrated	LOD (pmol)
Isopropanol	14	ND	ND
Hexane	32	m/z=57	3
		m/z=86	22
		TIC	0.8
Benzene	24	m/z=78	5
		TIC	5

Conclusion: The Mars Organic Molecule Analyzer is a key analytical instrument aboard the ExoMars Rover set to launch in 2018. The results described here demonstrate the current status of the end-to-end performance of the gas chromatography-mass spectrometry mode of operation. Both prototypes individually meet the performance requirements, but this work particularly demonstrates the capabilities of the critical GC-MS interface. Future work will focus on improving detection limits to provide margin to ensure the requirements will be met, as well as analyzing higher molecular weight compounds including derivitized amino acids and thermochemolized compounds.

References: [1] Buch, A. et al. (2009) J Chrom. A, 43, 143-151. [2] Freissinet et al. (2011) J Chrom A, 1306, 59-71. [3] Geffroy-Rodier, C. et al. (2009) JAAP, 85, 454-459.

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