Yersinia intermedia MASE-LG-1, a facultative anaerobic microbe from a Mars analogue environment survives diverse individual and combined simulated Martian stresses.

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Our understanding of the habitability of Mars is hampered by a lack of knowledge of the stress responses of anaerobic organisms. In the project MASE (Mars Analogues for Space Exploration) representative (facultative) anaerobic microorganisms are isolated from Mars analogue environments on Earth and exposed to stresses typical for the Martian environment. The aim is to gain fundamental insights into the limits of anaerobic microbial life on Earth and to use these data to assess the habitability of Mars.

Using systematic anaerobic sampling methods, samples were obtained amongst others from the Icelandic lake Grænavatn. Following an enrichment approach a facultative anaerobic Yersinia strain MASE-LG-1 DSM 102845 was obtained and exposed to the following stress factors separately and in combination: desiccation, low pressure, ionizing radiation, varying temperature, osmotic pressure, and oxidizing chemical compounds. Thereby, the strain showed a high tolerance to desiccation, with a decline of survivability by four orders of magnitude during a storage time of 85 days. Exposure to X-rays resulted in dose-dependent inactivation for exposure up to 600 Gy while applied doses above 750 Gy led to complete inactivation. The effects of the combination of desiccation and irradiation were additive and the survivability was influenced by the order in which they were imposed. Ionizing irradiation and subsequent desiccation was more deleterious than vice versa. By contrast, the presence of perchlorates was not found to significantly affect the survival of the Yersinia strain after ionizing radiation.

These data show that anaerobic organisms have the capacity to survive and grow in physical and chemical stresses, imposed individually or in combination that are associated with Martian environments and they further advance our understanding of the limits and tolerances of the medically and environmentally important genus, Yersinia.

Acknowledgement: EC FP7 project 2014 – 2018, Mars Analoges for Space Exporation, Grant agreement Nr. 607297

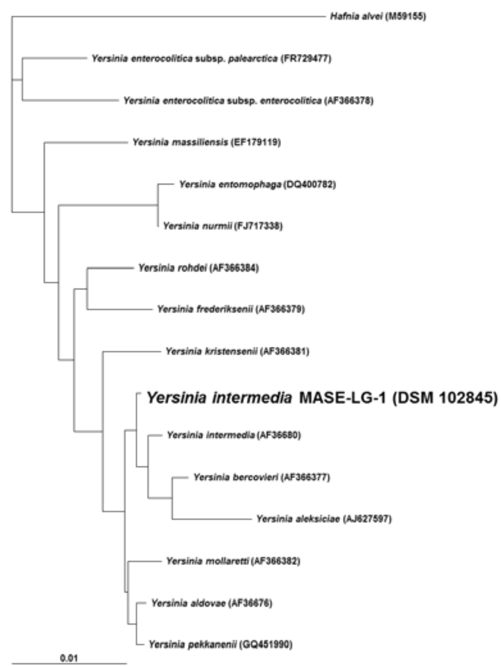

Fig. 1: Neighbor-joining tree based on nearly complete 16S rDNA sequences showing the phylogenetic position of strain *Y. intermedia* MASE-LG-1 related to 14 species of the genus *Yersinia*.

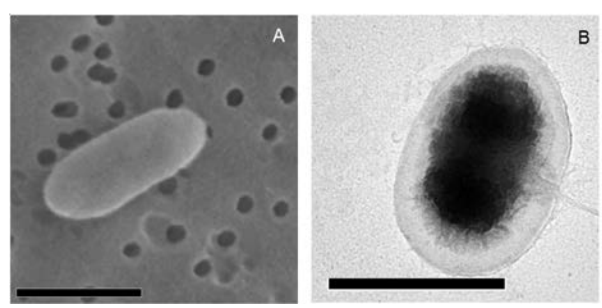

Fig. 2: Scanning and transmission micrographs (bar 1 µm)